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(54) Title: METHODS OF DIAGNOSIS OF CANCER COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF CANCER

(57) Abstract: Described herein are genes whose expression are up-regulated or down-regulated in specific cancers. Related methods and compositions that can be used for diagnosis and treatment of those cancers are disclosed. Also described herein are methods that can be used to identify modulators of selected cancers.

METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF CANCER

CROSS-REFERENCES TO RELATED APPLICATIONS

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This application claims priority to USSN 60/323,469, filed Setember 17, 2001; USSN 60/355,145, filed February 8, 2002; USSN 60/369,899, filed April 4, 2002; USSN 60/323,887, filed September 20, 2001; USSN 60/355,257, filed February 8, 2002; USSN 60/325,114, filed September 25, 2001; USSN 60/340,944, filed October 29, 2001; USSN 60/350,666, filed November 13, 2001; and USSN 60/372,246, filed April 12, 2002; each of which is incorporated herein by reference for all purposes.

FIELD OF THE INVENTION

The invention relates to the identification of nucleic acid and protein expression profiles and nucleic acids, products, and antibodies thereto that are involved in cancer; and to the use of such expression profiles and compositions in the diagnosis, prognosis, and therapy of cancer. The invention further relates to methods for identifying and using agents and/or targets that modulate cancer.

BACKGROUND OF THE INVENTION

Cancer is a major cause of morbidity in the United States. For example, in 1996, the

American Cancer Society estimated that 1,359,150 people were diagnosed with a malignant neoplasm and 554,740 died from one of these diseases. Cancer is responsible for 23.9 percent of all American deaths and is exceeded only by heart disease as a cause of mortality (33 percent). Unfortunately, cancer mortality is increasing and sometime early in this century, cancer is expected to become the leading cause of mortality in the United States as it already is in Japan.

Cancers share the charactaristic of disordered control over normal cell division, growth, and differentiation. Their initial clinical manifestations are extremely heterogeneous, with over 70 types of cancer arising in virtually every organ and tissue of the body. Moreover, some of those similarly classified cancer types may represent multiple different molecular diseases. Unfortunately, some cancers may be virtually asymptomatic until late in the disease course, when treatment is more difficult, and prognosis grim.

Treatment for cancer typically includes surgery, chemotherapy, and/or radiation therapy. Although nearly 50 percent of cancer patients can be effectively treated using these methods, the current therapies all induce serious side effects which diminish quality of life. The identification of novel therapeutic targets and diagnostic markers will be important for improving the diagnosis and treatment of cancer patients.

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Recent advances in molecular medicine have increased the interest in tumor-specific antigens that could serve as targets for various immunotherapeutic or small molecule strategies. Antigens suitable for immunotherapeutic strategies should be highly expressed in cancer tissues, preferably accessible from the vasculature and at the cell surface, and ideally not expressed in normal adult tissues. Expression in tissues that are dispensable for life, however, may be tolerated, e.g., reproductive organs. Examples of antigens that are currently available for the detection and treatment of certain cancers include Her2/neu and the B-cell antigen CD20. Humanized monclonal antibodies directed to Her2/neu (Herceptin®/trastuzumab) are currently in use for the treatment of metastatic breast cancer. See Ross and Fletcher (1998) Stem Cells 16:413-428. Similarly, anti-CD20 monoclonal antibodies (Rituxin®/rituximab) are used to effectively treat non-Hodgkin's lymphoma. See Maloney, et al. (1997) Blood 90:2188-2195; Leget and Czuczman (1998) Curr. Opin. Oncol. 10:548-551.

The elucidation of a role for novel proteins and compounds in disease states for identification of therapeutic targets and diagnostic markers is valuable for improving the current treatment of cancer patients. Accordingly, provided herein are molecular targets for therapeutic intervention in various defined cancers. Additionally, provided herein are methods that can be used in diagnosis and prognosis of cancer. Further provided are methods that can be used to screen candidate bioactive agents for the ability to modulate cancer.

SUMMARY OF THE INVENTION

The present invention provides methods for determining the presence or absence of a pathological cell in a patient, the method comprising detecting a nucleic acid comprising a sequence at least 80% identical to a sequence as described in Tables 2A-68 in a biological sample from the patient, thereby determining the presence or absence of the pathological cell. In certain embodiments of the method, the pathology is described in Table 1, including a cancer; the biological sample comprises isolated nucleic acids; the nucleic acids are mRNA; the biological sample is tissue from an organ which is affected by the pathology of Table 1, including a cancer; a further step is used of amplifying nucleic acids before the step of detecting

the nucleic acid; the detecting is of a protein encoded by the nucleic acid; the nucleic acid comprises a sequence as described in Tables 2A-68; the detecting step is carried out by using a labeled nucleic acid probe, utilizing a biochip comprising at sequence at least 80% identical to a sequence as described in Tables 2A-68, or detecting a polypeptide encoded by the nucleic acid; or the patient is undergoing a therapeutic regimen to treat the pathology of Table 1, or is suspected of having the pathology or cancer.

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Compostions are also provided, e.g., an isolated nucleic acid molecule comprising a sequence as described in Tables 2A-68, including, e.g., those which are labeled; an expression vector comprising such nucleic acid; a host cell comprising such expression vector; an isolated polypeptide which is encoded by such a nucleic acid molecule comprising a sequence as described in Tables 2A-68; or an antibody that specifically binds the polypeptide. In particular embodiments, the antibody is: conjugated to an effector component, is conjugated to a detectable label (including, e.g., a fluorescent label, a radioisotope, or a cytotoxic chemical), an antibody fragment, or is a humanized antibody.

Additional methods are provided, including methods for specifically targeting a compound to a pathological cell in a patient, the method comprising administering to the patient an antibody, as described, thereby providing the targetting. Others include, e.g., methods for determining the presence or absence of a pathological cell in a patient, the methods comprising contacting a biological sample with an antibody, as described. In more particular methods, the antibody is: conjugated to an effector component, or to a fluorescent label; or the biological sample is a blood, serum, urine, or stool sample.

Further methods include those for identifying a compound that modulates a pathology-associated polypeptide, the method comprising steps of: contacting the compound with a pathology-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as described in Tables 2A-68; and determining the functional effect of the compound upon the polypeptide. Another drug screening assay method comprises steps of: administering a test compound to a mammal having a pathology of Table 1 or a cell isolated therefrom; and comparing the level of gene expression of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as described in Tables 2A-68 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of the pathology.

DETAILED DESCRIPTION OF THE INVENTION

In accordance with the objects outlined above, the present invention provides novel methods for diagnosis and prognosis evaluation for various disorders, e.g., angiogenesis, fibrosis, and various defined forms of cancer, including metastatic cancer, as well as methods for screening for compositions which modulate such conditions. Also provided are methods for 5 treating such disorders or cancers. See, e.g., American Society of Clinical Oncology (ed. 2001) ASCO Curriculum: Symptom Management Kendall/Hunt, ISBN: 0787277851; Bonadonna, et al. (2001) Textbook of Breast Cancer (2d ed.) Dunitz Martin, ISBN: 1853178241; Devita and Hellman (eds. 2001) Cancer Principles and Practice of Oncology (2 vols.), Lippincott Williams, ISBN: 0781723876; Howell, et al. (2001) Breast Cancer Isis Medical Media, ISBN: 10 1901865584; Kaye and Laws (2001) Brain Tumours: An Encyclopedic Approach (2d ed.) Churchill Livingstone, ISBN: 0443064261; Mihm, et al. (2001) The Melanocytic Proliferation: A Comprehensive Textbook of Pigmented Lesions Wiley-Liss, ISBN: 0471252719; Montgomery and Aaron (2001) Clinical Pathology of Soft-Tissue Tumors Marcel Dekker, ISBN: 0824702905; Petrovich, et al. (eds. 2001) Combined Modality of Central Nervous 15 System Tumors (Medical Radiology) Springer Verlag, ISBN: 3540660534; Rosen (2001) Rosen's Breast Pathology Lippincott Williams and Wilkins, ISBN: 0781723795; Shah, et al. (2001) Oral Cancer Isis Medical Media, ISBN: 189906687X; Weiss and Goldblum (2001) Enzinger and Weiss's Soft Tissue Tumors (4th ed.) Mosby, ISBN: 0323012000; Abeloff, et al. (eds. 2000) Clinical Oncology (2d ed.) Churchill Livingstone, ISBN: 044307545X; American 20 Society of Clinical Oncology (ed. 2000) Cancer Genetics and Cancer Predisposition Testing Kendall/Hunt, ISBN: 0787276154; Fletcher (2000) Diagnostic Histopathology of Tumors (2 vols. 2d ed.) Churchill Livingstone, ISBN: 0443079927; Vogelzang (ed. 2000) Comprehensive Textbook of Genitourinary Oncology (2d ed.) Lippincott Williams and Wilkins, ISBN: 0683306456; Holland, et al. (eds. 2000) Holland-Frei Cancer Medicine (Book with CD-ROM 25 5th ed.) Decker, ISBN: 1550091131; Turrisi, et al. (2000) Lung Cancer Isis Medical Media, ISBN: 1901865428; Bartolozzi and Lencioni (eds. 1999) Liver Malignancies: Diagnostic and Interventional Radiology (Medical Radiology) Springer Verlag, ISBN: 3540647562; Gasparini (ed. 1999) Prognostic Variables in Node-Negative and Node-Positive Breast Cancer Kluwer, ISBN: 0792384474; Hansen (ed. 1999) The LASLC Textbook of Lung Cancer: International 30 Association for the Study of Lung Cancer Dunitz Martin, ISBN: 1853177083; Raghavan, et al. (eds. 1999) Textbook of Uncommon Cancer (2nd ed.) Wiley, ISBN: 0471929212; Thawley, et

al. (eds. 1999) Comprehensive Management of Head and Neck Tumors (2 vols.) Saunders, ISBN: 0721655823; Whittaker and Holmes (eds. 1999) Leukemia and Related Disorders (3d ed.) Blackwell Science, ISBN: 0865426074; Aapro (ed. 1998) OncoMedia: Medical Oncology (CD-ROM) Elsevier Science, ISBN: 0080427480; Abeloff (1998) Clinical Oncology (Library Version 2 CD-ROM Individual Version 2.0 Windows and Macintosh) Harcourt Brace, ISBN: 5 0443075557; Benson (ed. 1998) Gastrointestinal Oncology (Cancer Treatment and Research, CTAR 98) Kluwer, ISBN: 0792382056; Brambilla and Brambilla (eds. 1998) Lung Tumors: Fundamental Biology and Clinical Management (Vol 124) Marcel Dekker, ISBN: 0824701607; Canellos, et al. (eds. 1998) The Lymphomas Saunders, ISBN: 0721650309; Greenspan and Remagen (1998) Differential Diagnosis of Tumors and Tumor-Like Lesions of Bones and Joints 10 Lippincott Williams and Wilkins Publishers, ISBN: 0397517106; Hiddemann (ed. 1998) Acute Leukemias VII: Experimental Approaches and Novel Therapies (Haematologie Und Bluttransfusion, Vol 39), Springer Verlag, ISBN: 3540635041; Husband and Reznek (1998) Imaging in Oncology (2 vols.) Mosby, ISBN: 1899066489; Leibel and Phillips (eds. 1998) Textbook of Radiation Oncology Saunders, ISBN: 0721653367; Maloney and Miller (eds. 15 1998) Cutaneous Oncology: Pathophysiology, Diagnosis, and Management Blackwell Science, ISBN: 0865425175; Mittal, et al. (eds. 1998) Advances in Radiation Therapy Kluwe, ISBN: 0792399811; Oldham (ed. 1998) Principles of Cancer Biotherapy (3d ed.) Kluwer, ISBN: 0792335074; Ozols (ed. 1998) Gynecologic Oncology Kluwer, ISBN: 0792380703; Parkin, et al. (eds. 1998) Cancer Incidence in Five Continents (Iarc Scientific Publications, No 143) 20 Oxford University Press, ISBN: 9283221435; Perez and Brady (eds. 1998) Principles and Practice of Radiation Oncology Lippincott Williams and Wilkins, ISBN: 0397584164; Black, et al. (eds. 1997) Cancer of the Nervous System Blackwell Science, ISBN: 0865423849; Bonadonna, et al. (1997) Textbook of Breast Cancer: A Clinical Guide to Therapy Blackwell Science, ISBN: 1853173487; Pollock (ed. 1997) Surgical Oncology Kluwer, ISBN: 25 0792399005; Sheaves, et al. (eds. 1997) Clinical Endocrine Oncology Blackwell Science, ISBN: 086542862X; Vahrson (1997) Radiation Oncology of Gynecological Cancers Springer Verlag, ISBN: 0387567682; Walterhouse and Cohn (eds. 1997) Diagnostic and Therapeutic Advances in Pediatric Oncology Kluwer, ISBN: 0792399781; Aisner (ed. 1996) Comprehensive Textbook of Thoracic Oncology Lippincott, Williams and Wilkins, ISBN: 0683000624; 30 Bertino, et al. (eds. 1996) Encyclopedia of Cancer (3 vols.) Academic, ISBN: 012093230X; Cavalli, et al. (1996) Textbook of Medical Oncology Dunitz Martin, ISBN: 1853172901;

Peckham, et al. (eds. 1995) Oxford Textbook of Oncology (2-Vols.) Oxford University Press, ISBN: 0192616854; and Freireich and Kantarjian (eds. 1996) Molecular Genetics and Therapy of Leukemia (Cancer Treatment and Research, V. 84) Kluwer, ISBN: 0792339126.

In particular, identification of markers selectively expressed on defined cancers allows for use of that expression in diagnostic, prognostic, or therapeutic methods. As such, the invention defines various compositions, e.g., nucleic acids, polypeptides, antibodies, and small molecule agonists/antagonists, which will be useful to selectively identify those markers. For example, therapeutic methods may take the form of protein therapeutics which use the marker expression for selective localization or modulation of function (for those markers which have a causative disease effect), for vaccines, identification of binding partners, or antagonism, e.g., using antisense or RNAi. The markers may be useful for molecular characterization of subsets of the diseases, e.g., as provided in Table 1, which subsets may actually require very different treatments. Moreover, the markers may also be important in related diseases to the specific disorders and cancers, e.g., which affect similar tissues in non-malignant diseases, or have similar mechanisms of induction/maintenance. Metastatic processes or characteristics may also be targeted. Diagnostic and prognostic uses are made available, e.g., to subset related but distinct diseases, or to determine treatment strategy. The detection methods may be based upon nucleic acid, e.g., PCR or hybridization techniques, or protein, e.g., ELISA, imaging, IHC, etc. The diagnosis may be qualitative or quantitative, and may detect increases or decreases in expression levels.

Tables 2B-66C provide unigene cluster identification numbers for the nucleotide sequence of genes that exhibit increased or decreased expression in cancer samples, particularly sequences involved in angiogenisis, prostate cancer (including androgen independent and taxol resistant prostate cancer), breast cancer, colorectal cancer, cervical cancer, bladder cancer, lung cancer, ovarian cancer, uterine cancer, glioblastoma, Ewing sarcoma, and lung fibrosis. Tables 2A-67 also provide an exemplar accession number that provides a nucleotide sequence that is part of the unigene cluster.

Definitions

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The term "cancer protein" or "cancer polynucleotide" or "cancer-associated transcript" refers to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologues that: (1) have a nucleotide sequence that has greater than about 60% nucleotide sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably about 92%, 94%, 96%, 97%,

98%, or 99% or greater nucleotide sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to a nucleotide sequence of or associated with a gene of Tables 1-68; (2) bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence encoded by a nucleotide sequence of or associated with a gene of Tables 1-68, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to a nucleic acid sequence, or the complement thereof of Tables 1-68 and conservatively modified variants thereof; or (4) have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, preferably 90%, 91%, 93%, 95%, 97%, 98%, or 99% or greater amino sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more amino acids, to an amino acid sequence encoded by a nucleotide sequence of or associated with a gene of Tables 1-68. A polynucleotide or polypeptide sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or other mammal. A "cancer polypeptide" and a "cancer polynucleotide," include both naturally occurring or recombinant forms.

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A "full length" cancer protein or nucleic acid refers to a cancer polypeptide or polynucleotide sequence, or a variant thereof, that contains elements normally contained in one or more naturally occurring, wild type cancer polynucleotide or polypeptide sequences. The "full length" may be prior to, or after, various stages of post-translational processing or splicing, including alternative splicing.

"Biological sample" as used herein is a sample of biological tissue or fluid that contains nucleic acids or polypeptides, e.g., of a cancer protein, polynucleotide, or transcript. Such samples include, but are not limited to, tissue isolated from primates, e.g., humans, or rodents, e.g., mice, and rats. Biological samples may also include sections of tissues such as biopsy and autopsy samples, frozen sections taken for histologic purposes, archival samples, blood, plasma, serum, sputum, stool, tears, mucus, hair, skin, etc. Biological samples also include explants and primary and/or transformed cell cultures derived from patient tissues. A biological sample is typically obtained from a eukaryotic organism, most preferably a mammal such as a primate e.g., chimpanzee or human; cow; dog; cat; a rodent, e.g., guinea pig, rat, mouse; rabbit; or a bird; reptile; or fish. Livestock and domestic animals are of interest.

"Providing a biological sample" means to obtain a biological sample for use in methods described in this invention. Most often, this will be done by removing a sample of cells from an

animal, but can also be accomplished by using previously isolated cells (e.g., isolated by another person, at another time, and/or for another purpose), or by performing the methods of the invention in vivo. Archival tissues or materials, having treatment or outcome history, will be particularly useful.

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The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same (e.g., about 70% identity, preferably 75%, 80%, 85%, 90%, 91%, 93%, 95%, 97%, 98%, 99%, or higher identity over a specified region, when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using, e.g., a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (see, e.g., NCBI web site http://www.ncbi.nlm.nih.gov/BLAST/ or the like). Such sequences are then said to be "substantially identical." This definition also refers to, or may be applied to, the complement of a test sequence. The definition also includes sequences that have deletions and/or insertions, substitutions, and naturally occurring, e.g., polymorphic or allelic variants, and man-made variants. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is 50-100 amino acids or nucleotides in length.

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Preferably, default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window", as used herein, includes reference to a segment of contiguous positions selected from the group consisting typically of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known.

Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology

algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482-489, by the homology alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48:443-453, by the search for similarity method of Pearson and Lipman (1988) Proc. Nat'l. Acad. Sci. USA 85:2444-2448, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (see, e.g., Ausubel, et al. (eds. 1995 and supplements) Current Protocols in Molecular Biology Wiley).

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Preferred examples of algorithms that are suitable for determining percent sequence identity and sequence similarity include the BLAST and BLAST 2.0 algorithms, which are described in Altschul, et al. (1977) Nuc. Acids Res. 25:3389-3402 and Altschul, et al. (1990) J. Mol. Biol. 215:403-410. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (http://www.ncbi.nlm.nih.gov/). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul, et al., supra). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, e.g., for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negativescoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62

scoring matrix (see Henikoff and Henikoff (1992) <u>Proc. Natl. Acad. Sci. USA</u> 89:10915-919) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences. See, e.g., Karlin and Altschul (1993) Proc. Nat'l. Acad. Sci. USA 90:5873-5787. One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001. Log values may be negative large numbers, e.g., 5, 10, 20, 30, 40, 40, 70, 90, 110, 150, 170, etc.

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An indication that two nucleic acid sequences are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid. Thus, a polypeptide is typically substantially identical to a second polypeptide, e.g., where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent conditions. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequences.

A "host cell" is a naturally occurring cell or a transformed cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be cultured cells, explants, cells in vivo, and the like. Host cells may be prokaryotic cells such as E. coli, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, and the like (see, e.g., the American Type Culture Collection catalog or web site, www.atcc.org).

The terms "isolated," "purified," or "biologically pure" refer to material that is substantially or essentially free from components that normally accompany it as found in its native state. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein or nucleic acid that is the predominant species present in a preparation is substantially purified. In particular, an isolated nucleic acid is separated from some open reading frames that naturally flank the gene and encode proteins other than protein

encoded by the gene. The term "purified" in some embodiments denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Preferably, it means that the nucleic acid or protein is at least about 85% pure, more preferably at least 95% pure, and most preferably at least 99% pure. "Purify" or "purification" in other embodiments means removing at least one contaminant or component from the composition to be purified. In this sense, purification does not require that the purified compound be homogeneous, e.g., 100% pure.

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The terms "polypeptide," "peptide," and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers, those containing modified residues, and non-naturally occurring amino acid polymers.

The term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function similarly to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, e.g., hydroxyproline, γ -carboxyglutamate, and O-phosphoserine. Amino acid analogs refers to compounds that have the same basic chemical structure as a naturally occurring amino acid, e.g., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs may have modified R groups (e.g., norleucine) or modified peptide backbones, but retain somebasic chemical structure as a naturally occurring amino acid. Amino acid mimetic refers to a chemical compound that has a structure that is different from the general chemical structure of an amino acid, but that functions similarly to another amino acid.

Amino acids may be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

"Conservatively modified variant" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical or associated, e.g., naturally contiguous, sequences. Because of the degeneracy of the

genetic code, a large number of functionally identical nucleic acids encode most proteins. For instance, the codons GCA, GCC, GCG, and GCU each encode the amino acid alanine. Thus, at each position where an alanine is specified by a codon, the codon can be altered to another of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations," which are one species of conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes silent variations of the nucleic acid. In certain contexts each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally similar molecule. Accordingly, a silent variation of a nucleic acid which encodes a polypeptide is implicit in a described sequence with respect to the expression product, but not necessarily with respect to actual probe sequences.

As to amino acid sequences, one of skill will recognize that individual substitutions, deletions, or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds, or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention. Typically conservative substitutions include for one another: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M) (see, e.g., Creighton (1984) Proteins: Structure and Molecular Properties Freeman).

Macromolecular structures such as polypeptide structures can be described in terms of various levels of organization. For a general discussion of this organization, see, e.g., Alberts, et al. (eds. 2001) Molecular Biology of the Cell (4th ed.) Garland; and Cantor and Schimmel (1980) Biophysical Chemistry Part I: The Conformation of Biological Macromolecules

Freeman. "Primary structure" refers to the amino acid sequence of a particular peptide.

"Secondary structure" refers to locally ordered, three dimensional structures within a polypeptide. These structures are commonly known as domains. Domains are portions of a

polypeptide that often form a compact unit of the polypeptide and are typically 25 to approximately 500 amino acids long. Typical domains are made up of sections of lesser organization such as stretches of β -sheet and α -helices. "Tertiary structure" refers to the complete three dimensional structure of a polypeptide monomer. "Quaternary structure" refers to the three dimensional structure formed, usually by the noncovalent association of independent tertiary units. Anisotropic terms are also known as energy terms.

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"Nucleic acid" or "oligonucleotide" or "polynucleotide" or grammatical equivalents used herein means at least two nucleotides covalently linked together. Oligonucleotides are typically from about 5, 6, 7, 8, 9, 10, 12, 15, 25, 30, 40, 50, or more nucleotides in length, up to about 100 nucleotides in length. Nucleic acids and polynucleotides are a polymers of any length, including longer lengths, e.g., 200, 300, 500, 1000, 2000, 3000, 5000, 7000, 10,000, etc. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, nucleic acid analogs are included that may have at least one different linkahge, e.g., phosphoramidate, phosphorothioate, phosphorodithioate, or O-methylphophoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach Oxford Univ. Press); and peptide nucleic acid backbones and linkages. Other analog nucleic acids include those with positive backbones; non-ionic backbones, and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7 of Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ACS Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids. Modifications of the ribose-phosphate backbone may be done for a variety of reasons, e.g., to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip. Mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

A variety of references disclose such nucleic acid analogs, including, e.g., phosphoramidate (Beaucage, et al. (1993) Tetrahedron 49:1925-1963 and references therein; Letsinger (1970) J. Org. Chem. 35:3800-3803; Sprinzl, et al. (1977) Eur. J. Biochem. 81:579-589; Letsinger, et al. (1986) Nucl. Acids Res. 14:3487-499; Sawai, et al. (1984) Chem. Lett. 805, Letsinger, et al. (1988) J. Am. Chem. Soc. 110:4470-4471; and Pauwels, et al. (1986) Chemica Scripta 26:141-149), phosphorothioate (Mag, et al. (1991) Nucleic Acids Res. 19:1437-441; and U.S. Patent No. 5,644,048), phosphorodithioate (Brill, et al. (1989) J. Am.

Chem. Soc. 111:2321-2322), O-methylphophoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach, Oxford Univ. Press), and peptide nucleic acid backbones and linkages (see Egholm (1992) J. Am. Chem. Soc. 114:1895-1897; Meier, et al. (1992) Chem. Int. Ed. Engl. 31:1008-1010; Nielsen (1993) Nature 365:566-568; Carlsson, et al. (1996) Nature 380:207, all of which are incorporated by reference). Other 5 analog nucleic acids include those with positive backbones (Denpcy, et al. (1995) Proc. Natl. Acad. Sci. USA 92:6097-101; non-ionic backbones (U.S. Patent Nos. 5,386,023, 5,637,684, 5,602,240, 5,216,141, and 4,469,863; Kiedrowski, et al. (1991) Angew. Chem. Intl. Ed. English 30:423-426; Letsinger, et al. (1988) J. Am. Chem. Soc. 110:4470-4471; Letsinger, et al. (1994) Nucleoside and Nucleotide 13:1597-xxx; Chapters 2 and 3 in Sanghvi and Cook (eds. 1994) 10 Carbohydrate Modifications in Antisense Research ACS Symposium Series 580; Mesmaeker, et al. (1994) Bioorganic and Medicinal Chem. Lett. 4:395-398; Jeffs, et al. (1994) J. Biomolecular NMR 34:17; Horn, et al. (1996) Tetrahedron Lett. 37:743-xxx) and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7 in Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ACS 15 Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids (see Jenkins, et al. (1995) Chem. Soc. Rev. pp 169-176). Several nucleic acid analogs are described in Rawls (page 35, June 2, 1997) C&E News.

Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in at least two advantages. The PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (T_m) for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit a 2-4° C drop in T_m for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9° C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

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The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. The depiction of a single strand also defines the sequence of the complementary strand; thus the sequences described herein also

provide the complement of the sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA, or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and combinations of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine hypoxanthine, isocytosine, isoguanine, etc. "Transcript" typically refers to a naturally occurring RNA, e.g., a pre-mRNA, hnRNA, or mRNA. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus, e.g., the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

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A "label" or a "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, physiological, chemical, or other physical means. In general, labels fall into three classes: a) isotopic labels, which may be radioactive or heavy isotopes; b) immune labels, which may be antibodies, antigens, or epitope tags; and c) colored or fluorescent dyes. The labels may be incorporated into the cancer nucleic acids, proteins, and antibodies. For example, the label should be capable of producing, either directly or indirectly, a detectable signal. The detectable moiety may be a radioisotope, such as ³H, 14C, 32P, 35S, or 125I, electron-dense reagents, a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins or other entities which can be made detectable such as alkaline phosphatase, beta-galactosidase, or horseradish peroxidase. Methods are known for conjugating the antibody to the label. See, e.g., Hunter, et al. (1962) Nature 144:945; David, et al. (1974) Biochemistry 13:1014-1021; Pain, et al. (1981) J. Immunol. Meth. 40:219-230; and Nygren (1982) J. Histochem. and Cytochem. 30:407-412.

An "effector" or "effector moiety" or "effector component" is a molecule that is bound (or linked, or conjugated), either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds, to an antibody. The "effector" can be a variety of molecules including, e.g., detection moieties including radioactive compounds, fluorescent compounds, enzymes or substrates, tags such as epitope tags, toxins; activatable moieties, chemotherapeutic agents; lipases; antibiotics; or radioisotopes, e.g., emitting "hard" beta, radiation.

A "labeled nucleic acid probe or oligonucleotide" is one that is bound, e.g., covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals,

electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe. Alternatively, methods using high affinity interactions may achieve the same results where one of a pair of binding partners binds to the other, e.g., biotin, streptavidin.

As used herein a "nucleic acid probe or oligonucleotide" is a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, e.g., through hydrogen bond formation. As used herein, a probe may include natural (e.g., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, preferably one that does not functionally interfere with hybridization. Thus, e.g., probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. Probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are preferably directly labeled, e.g., with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled, e.g., with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence. Diagnosis or prognosis may be based at the genomic level, or at the level of RNA or protein expression.

The term "recombinant" when used with reference, e.g., to a cell, or nucleic acid, protein, or vector, indicates that the cell, nucleic acid, protein, or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a native nucleic acid or protein, or that the cell is derived from a cell so modified. Thus, e.g., recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed, or not expressed at all. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed in vitro, in general, by the manipulation of nucleic acid, e.g., using polymerases and endonucleases, in a form not normally found in nature. In this manner, operably linkage of different sequences is achieved. Thus an isolated nucleic acid, in a linear form, or an expression vector formed in vitro by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, e.g., using the in vivo cellular machinery of the host cell rather than in vitro manipulations; however, such

nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered recombinant for the purposes of the invention.

Similarly, a "recombinant protein" is a protein made using recombinant techniques, e.g., through the expression of a recombinant nucleic acid as depicted above. A recombinant protein is distinguished from naturally occurring protein by at least one or more characteristics. The protein may be isolated or purified away from some or most of the proteins and compounds with which it is normally associated in its wild type host, and thus may be substantially pure. An isolated protein is unaccompanied by at least some of the material with which it is normally associated in its natural state, preferably constituting at least about 0.5%, more preferably at least about 5% by weight of the total protein in a given sample. A substantially pure protein comprises at least about 75% by weight of the total protein, with at least about 80% being preferred, and at least about 90% being particularly preferred. The definition includes the production of a skin cancer protein from one organism in a different organism or host cell. Alternatively, the protein may be made at a significantly higher concentration than is normally seen, through the use of an inducible promoter or high expression promoter, such that the protein is made at increased concentration levels. Alternatively, the protein may be in a form not normally found in nature, as in the addition of an epitope tag or amino acid substitutions, insertions and deletions, as discussed below.

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The term "heterologous" when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not normally found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences, e.g., from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one source and a coding region from another source. Similarly, a heterologous protein will often refer to two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

A "promoter" is typically an array of nucleic acid control sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A "constitutive" promoter is a promoter that is active under most environmental and developmental conditions. An "inducible" promoter is a promoter that is active under

environmental or developmental regulation. The term "operably linked" refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, e.g., wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

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An "expression vector" is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements that permit transcription of a particular nucleic acid in a host cell. The expression vector can be part of a plasmid, virus, or nucleic acid fragment. Typically, the expression vector includes a nucleic acid to be transcribed in operable linkage to a promoter.

The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule selectively to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (e.g., total cellular or library DNA or RNA).

The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in "Overview of principles of hybridization and the strategy of nucleic acid assays" in Tijssen (1993) Hybridization with Nucleic Probes (Laboratory Techniques in Biochemistry and Molecular Biology) (vol. 24) Elsevier. Generally, stringent conditions are selected to be about 5-10° C lower than the thermal melting point (Tm) for the specific sequence at a defined ionic strength pH. The Tm is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m, 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01-1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C for short probes (e.g., about 10-50 nucleotides) and at least about 60° C for long probes (e.g., greater than about 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is typically at least two times

background, preferably 10 times background hybridization. Exemplary stringent hybridization conditions can be as following: 50% formamide, 5x SSC, and 1% SDS, incubating at 42° C, or, 5x SSC, 1% SDS, incubating at 65° C, with wash in 0.2x SSC, and 0.1% SDS at 65° C. For PCR, a temperature of about 36° C is typical for low stringency amplification, although annealing temperatures may vary between about 32°-48° C depending on primer length. For high stringency PCR amplification, a temperature of about 62° C is typical, although high stringency annealing temperatures can range from about 50-65° C, depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90-95° C for 30-120 sec, an annealing phase lasting 30-120 sec, and an extension phase of about 72° C for 1-2 min. Protocols and guidelines for low and high stringency amplification reactions are provided, e.g., in Innis, et al. (1990) PCR Protocols: A Guide to Methods and Applications, Academic Press, NY.

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37° C, and a wash in 1X SSC at 45° C. A positive hybridization is typically at least twice background. Alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency. Additional guidelines for determining hybridization parameters are provided in numerous references, e.g., Ausubel, et al. (eds. 1991 and supplements) Current Protocols in Molecular Biology Wiley.

The phrase "functional effects" in the context of assays for testing compounds that modulate activity of a cancer protein includes the determination of a parameter that is indirectly or directly under the influence of the cancer protein or nucleic acid, e.g., a physiological, functional, physical, or chemical effect, such as the ability to decrease cancer. It includes ligand binding activity; cell viability; cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis in vivo; mRNA and protein expression in cells undergoing

metastasis; and other characteristics of cancer cells. "Functional effects" include in vitro, in vivo, and ex vivo activities.

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By "determining the functional effect" is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of a cancer protein sequence, e.g., physiological, functional, enzymatic, physical, or chemical effects. Such functional effects can be measured, e.g., changes in spectroscopic characteristics (e.g., fluorescence, absorbance, refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties for the protein, measuring inducible markers or transcriptional activation of the cancer protein, measuring binding activity or binding assays, e.g., binding to antibodies or other ligands, and measuring growth, cellular proliferation, cell viability, cellular transformation, growth factor or serum dependence, tumor specific marker levels, invasiveness into Matrigel, tumor growth and metastasis in vivo, mRNA and protein expression, and other characteristics of cancer cells. The functional effects can be evaluated by many means, e.g., microscopy for quantitative or qualitative measures of alterations in morphological features, measurement of changes in RNA or protein levels for cancer-associated sequences, measurement of RNA stability, identification of downstream or reporter gene expression (CAT, luciferase, β -gal, GFP, and the like), e.g., via chemiluminescence, fluorescence, colorimetric reactions, antibody binding, inducible markers, and ligand binding assays.

"Inhibitors", "activators," and "modulators" of cancer polynucleotide and polypeptide sequences are used to refer to activating, inhibitory, or modulating molecules or compounds identified using in vitro and in vivo assays of cancer polynucleotide and polypeptide sequences. Inhibitors are compounds that, e.g., bind to, partially or totally block activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of cancer proteins, e.g., antagonists. Antisense or inhibitory nucleic acids may seem to inhibit expression and subsequent function of the protein. "Activators" are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate cancer protein activity. Inhibitors, activators, or modulators also include genetically modified versions of cancer proteins, e.g., versions with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, antibodies, small chemical molecules, and the like. Such assays for inhibitors and activators include, e.g., expressing the cancer protein in vitro, in cells, or cell membranes, applying putative modulator compounds, and then determining the functional effects on activity, as described above. Activators and inhibitors of cancer can also be identified

by incubating cancer cells with the test compound and determining increases or decreases in the expression of 1 or more cancer proteins, e.g., 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50, or more cancer proteins, such as cancer proteins encoded by the sequences set out in Tables 1-68.

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Samples or assays comprising cancer proteins that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of inhibition. Control samples (untreated with inhibitors) are assigned a relative protein activity value of 100%. Inhibition of a polypeptide is achieved when the activity value relative to the control is about 80%, preferably 50%, more preferably 25-0%. Activation of a cancer polypeptide is achieved when the activity value relative to the control (untreated with activators) is 110%, more preferably 150%, more preferably 200-500% (e.g., two to five fold higher relative to the control), more preferably 1000-3000% higher.

The phrase "changes in cell growth" refers to any change in cell growth and proliferation characteristics in vitro or in vivo, such as cell viability, formation of foci, anchorage independence, semi-solid or soft agar growth, changes in contact inhibition and density limitation of growth, loss of growth factor or serum requirements, changes in cell morphology, gaining or losing immortalization, gaining or losing tumor specific markers, ability to form or suppress tumors when injected into suitable animal hosts, and/or immortalization of the cell. See, e.g., pp. 231-241 in Freshney (1994) Culture of Animal Cells a Manual of Basic Technique (2d ed.) Wiley-Liss.

"Tumor cell" refers to precancerous, cancerous, and normal cells in a tumor.

"Cancer cells," "transformed" cells or "transformation" in tissue culture, refers to spontaneous or induced phenotypic changes that do not necessarily involve the uptake of new genetic material. Although transformation can arise from infection with a transforming virus and incorporation of new genomic DNA, or uptake of exogenous DNA, it can also arise spontaneously or following exposure to a carcinogen, thereby mutating an endogenous gene. Transformation is associated with phenotypic changes, such as immortalization of cells, aberrant growth control, nonmorphological changes, and/or malignancy. See, Freshney (2000) Culture of Animal Cells: A Manual of Basic Technique (4th ed.) Wiley-Liss.

"Antibody" refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes.

Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD, and IgE, respectively. Typically, the antigen-binding region of an antibody or its functional equivalent will be most critical in specificity and affinity of binding. See Paul (ed. 1999) Fundamental Immunology (4th ed.) Raven.

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An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kD) and one "heavy" chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms variable light chain (V_L) and variable heavy chain (V_H) refer to these light and heavy chains respectively.

Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, e.g., pepsin digests an antibody below the disulfide linkages in the hinge region to produce F(ab)'2, a dimer of Fab which itself is a light chain joined to V_H-C_H1 by a disulfide bond. The F(ab)'2 may be reduced under mild conditions to break the disulfide linkage in the hinge region, thereby converting the F(ab)'2 dimer into an Fab' monomer. The Fab' monomer is essentially Fab with part of the hinge region (see Paul (ed. 1999) Fundamental Immunology (4th ed.) Raven. While various antibody fragments are defined in terms of the digestion of an intact antibody, one of skill will appreciate that such fragments may be synthesized de novo either chemically or by using recombinant DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized de novo using recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries (see, e.g., McCafferty, et al. (1990) Nature 348:552-554).

For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal antibodies, many techniques known. See, e.g., Kohler and Milstein (1975) Nature 256:495-497; Kozbor, et al. (1983) Immunology Today 4:72; Cole, et al. (1985) pp. 77-96 in Reisfeld and Sell (1985) Monoclonal Antibodies and Cancer Therapy Liss; Coligan (1991) Current Protocols in Immunology Lippincott; Harlow and Lane (1988) Antibodies: A Laboratory Manual CSH Press; and Goding (1986) Monoclonal Antibodies: Principles and Practice (2d ed.) Academic Press. Techniques for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce antibodies to polypeptides of this invention. Also, transgenic mice, or other

organisms such as other mammals, may be used to express humanized antibodies.

Alternatively, phage display technology can be used to identify antibodies and heteromeric Fab fragments that specifically bind to selected antigens. See, e.g., McCafferty, et al. (1990) Nature 348:552-554; Marks, et al. (1992) Biotechnology 10:779-783.

A "chimeric antibody" is an antibody molecule in which (a) the constant region, or a portion thereof, is altered, replaced, or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function, and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, e.g., an enzyme, toxin, hormone, growth factor, drug, etc.; or (b) the variable region, or a portion thereof, is altered, replaced, or exchanged with a variable region having a different or altered antigen specificity.

Identification of cancer-associated sequences

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In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a "fingerprint" of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is characteristic of the state of the cell. That is, normal tissue may be distinguished from cancerous or metastatic cancerous tissue, or cancer tissue or metastatic cancerous tissue can be compared with tissue from surviving cancer patients. By comparing expression profiles of tissue in known different cancer states, information regarding which genes are important (including both up-and down-regulation of genes) in each of these states is obtained. Molecular profiling may distinguish subtypes of a currently collective disease designation, e.g., different forms of a cancer.

The identification of sequences that are differentially expressed in cancer versus non-cancer tissue allows the use of this information in a number of ways. For example, a particular treatment regime may be evaluated: does a chemotherapeutic drug act to down-regulate cancer, and thus tumor growth or recurrence, in a particular patient. Alternatively, a treatment step may induce other markers which may be used as targets to destroy tumor cells. Similarly, diagnosis and treatment outcomes may be done or confirmed by comparing patient samples with the known expression profiles. Maliganant disease may be compared to non-malignant conditions. Metastatic tissue can also be analyzed to determine the stage of cancer in the tissue, or origin of primary tumor, e.g., metastasis from a remote primary site. Furthermore, these gene expression

profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; e.g., screening can be done for drugs that suppress the cancer expression profile. This may be done by making biochips comprising sets of the important cancer genes, which can then be used in these screens. These methods can also be done on the protein basis; that is, protein expression levels of the cancer proteins can be evaluated for diagnostic purposes or to screen candidate agents. In addition, the cancer nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense nucleic acids, or the cancer proteins (including antibodies and other modulators thereof) administered as therapeutic drugs.

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Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in cancer relative to normal tissues and/or non-malignant disease, or in different types of related diseases, herein termed "cancer sequences." As outlined below, cancer sequences include those that are up-regulated (e.g., expressed at a higher level) in cancer, as well as those that are down-regulated (e.g., expressed at a lower level). In a preferred embodiment, the cancer sequences are from humans; however, cancer sequences from other organisms may be useful in animal models of disease and drug evaluation; thus, other cancer sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc.) and pets (e.g., dogs, cats, etc.). Cancer sequences from other organisms may be obtained using the techniques outlined below.

Cancer sequences can include both nucleic acid and amino acid sequences. In a preferred embodiment, the skin cancer sequences are recombinant nucleic acids. These nucleic acid sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications; e.g., biochips comprising nucleic acid probes or PCR microtiter plates with selected probes to the cancer sequences.

A cancer sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, e.g., using homology programs or hybridization conditions.

For identifying cancer-associated sequences, the cancer screen typically includes comparing genes identified in different tissues, e.g., normal and cancerous tissues, cancer and

non-malignant conditions, non-malignant conditions and normal tissues, or tumor tissue samples from patients who have metastatic disease vs. non metastatic tissue. Other suitable tissue comparisons include comparing cancer samples with metastatic cancer samples from other cancers, such as lung, stomach, gastrointestinal cancers, etc. Samples of different stages of cancer, e.g., survivor tissue, drug resistant states, and tissue undergoing metastasis, are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated for preparation of mRNA. Suitable biochips are commercially available, e.g., from Affymetrix, Santa Clara, CA. Gene expression profiles as described herein are generated and the data analyzed.

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In one embodiment, the genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, including, and not limited to lung, heart, brain, liver, stomach, kidney, muscle, colon, small intestine, large intestine, spleen, bone, and/or placenta. In a preferred embodiment, those genes identified during the cancer screen that are expressed in a significant amount in other tissues (e.g., essential organs) are removed from the profile, although in some embodiments, this is not necessary (e.g., where organs may be dispensible, e.g., female or male specific). That is, when screening for drugs, it is usually preferable that the target expression be disease specific, to minimize possible side effects on other organs were there expression.

In a preferred embodiment, cancer sequences are those that are up-regulated in cancer; that is, the expression of these genes is higher in the cancer tissue as compared to non-cancer or non-malignant tissue. "Up-regulation" as used herein often means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred. Another embodiment is directed to sequences up-regulated in non-malignant conditions relative to normal. Uniformity among relevant samples is also preferred.

Unigene cluster identification numbers and accession numbers herein are for the GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is available, see, e.g., Benson, et al. (1998) Nuc. Acids Res. 26:1-7; and http://www.ncbi.nlm.nih.gov/. Sequences are also available in other databases, e.g., European Molecular Biology Laboratory (EMBL) and DNA Database of Japan (DDBJ). In some situations, the sequences may be derived from assembly of available sequences or be predicted from genomic DNA using exon prediction algorithms, such as FGENESH. See

Salamov and Solovyev (2000) Genome Res. 10:516-522. In other situations, sequences have been derived from cloning and sequencing of isolated nucleic acids.

In another preferred embodiment, cancer sequences are those that are down-regulated in the cancer; that is, the expression of these genes is lower in cancer tissue as compared to non-cancerous tissue. "Down-regulation" as used herein often means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred.

Informatics

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The ability to identify genes that are over or under expressed in cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure, biosensor development, and other related areas. For example, the expression profiles can be used in diagnostic or prognostic evaluation of patients with cancer or related diseases. See Tables 1 and 3. Or as another example, subcellular toxicological information can be generated to better direct drug structure and activity correlation (see Anderson (June 11-12, 1998) Pharmaceutical Proteomics: Targets, Mechanism, and Function, paper presented at the IBC Proteomics conference, Coronado, CA). Subcellular toxicological information can also be utilized in a biological sensor device to predict the likely toxicological effect of chemical exposures and likely tolerable exposure thresholds (see U.S. Patent No. 5,811,231). Similar advantages accrue from datasets relevant to other biomolecules and bioactive agents (e.g., nucleic acids, saccharides, lipids, drugs, and the like).

Thus, in another embodiment, the present invention provides a database that includes at least one set of assay data. The data contained in the database is acquired, e.g., using array analysis either singly or in a library format. The database can be in a form in which data can be maintained and transmitted, but is preferably an electronic database. The electronic database of the invention can be maintained on any electronic device allowing for the storage of and access to the database, such as a personal computer, but is preferably distributed on a wide area network, such as the World Wide Web.

The focus of the present section on databases that include peptide sequence data is for clarity of illustration only. Similar databases can be assembled for assay data acquired using an assay of the invention.

The compositions and methods for identifying and/or quantitating the relative and/or absolute abundance of a variety of molecular and macromolecular species from a biological sample representing cancer, e.g., the identification of cancer-associated sequences described herein, provide an abundance of information which can be correlated with pathological conditions, predisposition to disease, drug testing, therapeutic monitoring, gene-disease causal linkages, identification of correlates of immunity and physiological status, among others. Although the data generated from the assays of the invention is suited for manual review and analysis, in a preferred embodiment, data processing using high-speed computers is utilized.

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An array of methods for indexing and retrieving biomolecular information is available. For example, U.S. Patents 6,023,659 and 5,966,712 disclose a relational database system for storing biomolecular sequence information in a manner that allows sequences to be catalogued and searched according to one or more protein function hierarchies. U.S. Patent 5,953,727 discloses a relational database having sequence records containing information in a format that allows a collection of partial-length DNA sequences to be catalogued and searched according to association with one or more sequencing projects for obtaining full-length sequences from the collection of partial length sequences. U.S. Patent 5,706,498 discloses a gene database retrieval system for making a retrieval of a gene sequence similar to a sequence data item in a gene database based on the degree of similarity between a key sequence and a target sequence. U.S. Patent 5,538,897 discloses a method using mass spectroscopy fragmentation patterns of peptides to identify amino acid sequences in computer databases by comparison of predicted mass spectra with experimentally-derived mass spectra using a closeness-of-fit measure. U.S. Patent 5.926,818 discloses a multi-dimensional database comprising a functionality for multidimensional data analysis described as on-line analytical processing (OLAP), which entails the consolidation of projected and actual data according to more than one consolidation path or dimension. U.S. Patent 5,295,261 reports a hybrid database structure in which the fields of each database record are divided into two classes, navigational and informational data, with navigational fields stored in a hierarchical topological map which can be viewed as a tree structure or as the merger of two or more such tree structures. See also Baxevanis, et al. (2001) Bioinformatics: A Practical Guuide to the Analysis of Genes and Proteins Wiley; Mount (2001) Bioinformatics: Sequence and Genome Analysis CSH Press, NY; Durbin, et al. (eds. 1999) Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids Cambridge University Press; Baxevanis and Oeullette (eds. 1998) Bioinformatics: A Practical Guide to the

Analysis of Genes and Proteins (2d. ed.) Wiley-Liss; Rashidi and Buehler (1999)

Bioinformatics: Basic Applications in Biological Science and Medicine CRC Press; Setubal, et al. (eds. 1997) Introduction to Computational Molecular Biology Brooks/Cole; Misener and Krawetz (eds. 2000) Bioinformatics: Methods and Protocols Humana Press; Higgins and Taylor (eds. 2000) Bioinformatics: Sequence, Structure, and Databanks: A Practical Approach Oxford University Press; Brown (2001) Bioinformatics: A Biologist's Guide to Biocomputing and the Internet Eaton Pub.; Han and Kamber (2000) Data Mining: Concepts and Techniques Kaufmann Pub.; and Waterman (1995) Introduction to Computational Biology: Maps, Sequences, and Genomes Chap and Hall.

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The present invention provides a computer database comprising a computer and software for storing in computer-retrievable form assay data records cross-tabulated, e.g., with data specifying the source of the target-containing sample from which each sequence specificity record was obtained.

In an exemplary embodiment, at least one of the sources of target-containing sample is from a control tissue sample known to be free of pathological disorders. In a variation, at least one of the sources is a known pathological tissue specimen, e.g., a neoplastic lesion or another tissue specimen to be analyzed for cancer. In another variation, the assay records cross-tabulate one or more of the following parameters for each target species in a sample: (1) a unique identification code, which can include, e.g., a target molecular structure and/or characteristic separation coordinate (e.g., electrophoretic coordinates); (2) sample source; and (3) absolute and/or relative quantity of the target species present in the sample.

The invention also provides for the storage and retrieval of a collection of target data in a computer data storage apparatus, which can include magnetic disks, optical disks, magneto-optical disks, DRAM, SRAM, SGRAM, SDRAM, RDRAM, DDR RAM, magnetic bubble memory devices, and other data storage devices, including CPU registers and on-CPU data storage arrays. Typically, the target data records are stored as a bit pattern in an array of magnetic domains on a magnetizable medium or as an array of charge states or transistor gate states, such as an array of cells in a DRAM device (e.g., each cell comprised of a transistor and a charge storage area, which may be on the transistor). In one embodiment, the invention provides such storage devices, and computer systems built therewith, comprising a bit pattern encoding a protein expression fingerprint record comprising unique identifiers for at least 10 target data records cross-tabulated with target source.

When the target is a peptide or nucleic acid, the invention preferably provides a method for identifying related peptide or nucleic acid sequences, comprising performing a computerized comparison between a peptide or nucleic acid sequence assay record stored in or retrieved from a computer storage device or database and at least one other sequence. The comparison can include a sequence analysis or comparison algorithm or computer program embodiment thereof (e.g., FASTA, TFASTA, GAP, BESTFIT) and/or the comparison may be of the relative amount of a peptide or nucleic acid sequence in a pool of sequences determined from a polypeptide or nucleic acid sample of a specimen.

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The invention also preferably provides a magnetic disk, such as an IBM-compatible (DOS, Windows, Windows95/98/2000, Windows NT, OS/2) or other format (e.g., Linux, SunOS, Solaris, AIX, SCO Unix, VMS, MV, Macintosh, etc.) floppy diskette or hard (fixed, Winchester) disk drive, comprising a bit pattern encoding data from an assay of the invention in a file format suitable for retrieval and processing in a computerized sequence analysis, comparison, or relative quantitation method.

The invention also provides a network, comprising a plurality of computing devices linked via a data link, such as an Ethernet cable (coax or 10BaseT), telephone line, ISDN line, wireless network, optical fiber, or other suitable signal transmission medium, whereby at least one network device (e.g., computer, disk array, etc.) comprises a pattern of magnetic domains (e.g., magnetic disk) and/or charge domains (e.g., an array of DRAM cells) composing a bit pattern encoding data acquired from an assay of the invention.

The invention also provides a method for transmitting assay data that includes generating an electronic signal on an electronic communications device, such as a modem, ISDN terminal adapter, DSL, cable modem, ATM switch, or the like, wherein the signal includes (in native or encrypted format) a bit pattern encoding data from an assay or a database comprising a plurality of assay results obtained by the method of the invention.

In a preferred embodiment, the invention provides a computer system for comparing a query target to a database containing an array of data structures, such as an assay result obtained by the method of the invention, and ranking database targets based on the degree of identity and gap weight to the target data. A central processor is preferably initialized to load and execute the computer program for alignment and/or comparison of the assay results. Data for a query target is entered into the central processor via an I/O device. Execution of the computer

program results in the central processor retrieving the assay data from the data file, which comprises a binary description of an assay result.

The target data or record and the computer program can be transferred to secondary memory, which is typically random access memory (e.g., DRAM, SRAM, SGRAM, or SDRAM). Targets are ranked according to the degree of correspondence between a selected assay characteristic (e.g., binding to a selected affinity moiety) and the same characteristic of the query target and results are output via an I/O device. For example, a central processor can be a conventional computer (e.g., Intel Pentium, PowerPC, Alpha, PA-8000, SPARC, MIPS 4400, MIPS 10000, VAX, etc.); a program can be a commercial or public domain molecular biology software package (e.g., UWGCG Sequence Analysis Software, Darwin); a data file can be an optical or magnetic disk, a data server, a memory device (e.g., DRAM, SRAM, SGRAM, SDRAM, EPROM, bubble memory, flash memory, etc.); an I/O device can be a terminal comprising a video display and a keyboard, a modem, an ISDN terminal adapter, an Ethernet port, a punched card reader, a magnetic strip reader, or other suitable I/O device.

The invention also preferably provides the use of a computer system, such as that described above, which comprises: (1) a computer; (2) a stored bit pattern encoding a collection of peptide sequence specificity records obtained by the methods of the invention, which may be stored in the computer; (3) a comparison target, such as a query target; and (4) a program for alignment and comparison, typically with rank-ordering of comparison results on the basis of computed similarity values. See, e.g., Ewens and Grant (2001) Statistical Methods in Bioinformatics: An Introduction Springer-Verlag. Mathematical approaches can also be used to conclude whether similarities or differences in the gene expression exhibited by different samples are significant. See, e.g., Golub, et al. (1999) Science 286:531-537; Duda, et al. (2001) Pattern Classification Wiley; and Hastie, et al. (2001) The Elements of Statistical Learning:

Data Mining, Inference, and Prediction Springer-Verlag. One approach to determine whether a sample is more similar to or has maximum similarity with a given condition between the sample and one or more pools representing different conditions for comparison; the pool with the smallest vector angle is then chosen as the most similar to the biological sample among the pools compared.

30 Characteristics of cancer-associated proteins

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Cancer proteins of the present invention may be classified as secreted proteins, transmembrane proteins, or intracellular proteins. In one embodiment, the cancer protein is an

Intracellular proteins are involved in all aspects of cellular function and replication (including, e.g., signaling pathways); aberrant expression of such proteins often results in unregulated or disregulated cellular processes (see, e.g., Alberts, et al. (eds. 1994) Molecular Biology of the Cell (3d ed.) Garland). For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity, and the like. Intracellular proteins also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

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An increasingly appreciated concept in characterizing proteins is the presence in the proteins of one or more structural motifs for which defined functions have been attributed. In addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2 domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. These motifs can be identified on the basis of amino acid sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate. One useful database is Pfam (protein families), which is a large collection of multiple sequence alignments and hidden Markov models covering many common protein domains. Versions are available via the internet from Washington University in St. Louis, the Sanger Center in England, and the Karolinska Institute in Sweden. See, e.g., Bateman, et al. (2000) Nuc. Acids Res. 28:263-266; Sonnhammer, et al. (1997) Proteins 28:405-420; Bateman, et al. (1999) Nuc. Acids Res. 27:260-262; and Sonnhammer, et al. (1998) Nuc. Acids Res. 26:320-322.

In another embodiment, the cancer sequences are transmembrane proteins.

Transmembrane proteins are molecules that span a phospholipid bilayer of a cell. They may have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity

and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

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Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors such as G protein coupled receptors (GPCRs) are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Characteristics of transmembrane domains include approximately 17 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the localization and number of transmembrane domains within the protein may be predicted (see, e.g., PSORT web site http://psort.nibb.ac.jp/). Important transmembrane protein receptors include, but are not limited to the insulin receptor, insulin-like growth factor receptor, human growth hormone receptor, glucose transporters, transferrin receptor, epidermal growth factor receptor, low density lipoprotein receptor, epidermal growth factor receptor, leptin receptor, and interleukin receptors, e.g., IL-1 receptor, IL-2 receptor, etc. 20

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are found on receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF, and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, neurotrophic factors, and the like. Extracellular domains also bind to cell-associated molecules. In this respect, they may mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell, e.g., via a glycosylphosphatidylinositol (GPI) anchor, or may themselves

be transmembrane proteins. Extracellular domains may also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

Cancer proteins that are transmembrane are particularly preferred in the present invention as they are readily accessible targets for immunotherapeutics, as are described herein.

In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities. Antibodies may be used to label such readily accessible proteins in situ.

Alternatively, antibodies can also label intracellular proteins, in which case samples are typically permeablized to provide access to intracellular proteins. In addition, some membrane proteins can be processed to release a soluble protein, or to expose a residual fragment.

Released soluble proteins may be useful diagnostic markers, processed residual protein fragments may be useful lung markers of disease.

It will also be appreciated that a transmembrane protein can be made soluble by removing transmembrane sequences, e.g., through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

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In another embodiment, the cancer proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins may have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; e.g., if circulating, they often serve to transmit signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor), an endocrine manner (acting on cells at a distance, e.g., secretion into the blood stream), or exocrine (secretion, e.g., through a duct or to adjacent epithelial surface as sweat glands, sebaceous glands, pancreatic ducts, lacrimal glands, mammary glands, wax producing glands of the ear, etc.). Thus secreted molecules often find use in modulating or altering numerous aspects of physiology. Cancer proteins that are secreted proteins are particularly preferred in the present invention as they serve as good targets for diagnostic markers, e.g., for blood, plasma, serum, or stool tests. Those which are enzymes may be antibody or small molecule targets. Others may be useful as vaccine targets, e.g., via CTL mechanisms.

Use of cancer nucleic acids

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As described above, cancer sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology or linkage to the cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions.

Typically, linked sequences on a mRNA are found on the same molecule.

As detailed elsewhere, percent identity can be determined using an algorithm such as BLAST. A preferred method utilizes the BLASTN module of WU-BLAST-2 set to the default parameters, with overlap span and overlap fraction set to 1 and 0.125, respectively. Alignment may include the introduction of gaps in the sequences to be aligned. In addition, for sequences which contain either more or fewer nucleotides than those of the nucleic acids described, the percentage of homology may be determined based on the number of homologous nucleosides in relation to the total number of nucleosides. Thus, e.g., homology of sequences shorter than those of the sequences identified will be determined using the number of nucleosides in the shorter sequence.

In one embodiment, the nucleic acid homology is determined through hybridization studies. Thus, e.g., nucleic acids which hybridize under high stringency to a described nucleic acid, or its complement, or is also found on naturally occurring mRNAs is considered a cancer sequence. In another embodiment, less stringent hybridization conditions are used; e.g., moderate or low stringency conditions may be used; see Ausubel, supra, and Tijssen, supra.

The cancer nucleic acid sequences of the invention, e.g., the sequences in Tables 1-68, can be fragments of larger genes, e.g., they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, using the sequences provided herein, extended sequences, in either direction, of the cancer genes can be obtained, using techniques well known for cloning either longer sequences or the full length sequences; see Ausubel, et al., supra. Much can be done by informatics and many sequences can be clustered to include multiple sequences corresponding to a single gene, e.g., systems such as UniGene (see, http://www.ncbi.nlm.nih.gov/UniGene/).

Once a cancer nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire cancer nucleic acid coding regions or the entire mRNA sequence. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant cancer nucleic acid can

be further used as a probe to identify and isolate other cancer nucleic acids, e.g., extended coding regions. It can also be used as a "precursor" nucleic acid to make modified or variant cancer nucleic acids and proteins.

The cancer nucleic acids of the present invention are used in several ways. In one embodiment, nucleic acid probes to the cancer nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, e.g., for gene therapy, vaccine, RNAi, and/or antisense applications. Alternatively, cancer nucleic acids that include coding regions of cancer proteins can be put into expression vectors for the expression of cancer proteins, again for screening purposes or for administration to a patient.

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In a preferred embodiment, nucleic acid probes to cancer nucleic acids (both the nucleic acid sequences outlined in the figures and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the cancer nucleic acids, e.g., the target sequence (either the target sequence of the sample or to other probe sequences, e.g., in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under normal reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8-100 bases long, with from about 10-80 bases being preferred, and from about 30-50 bases being particularly preferred. That is, generally whole genes are not used. In some embodiments, much longer nucleic acids can be used, up to hundreds of bases.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a

particular target. The probes can be overlapping (e.g., have some sequence in common), or separate. In some cases, PCR primers may be used to amplify signal for higher sensitivity.

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Nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined. The binding can typically be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is meant one or more of electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent attachment of a molecule, e.g., streptavidin to the support and the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds, and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

In general, the probes are attached to the biochip in a wide variety of ways. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant a material that can be modified for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. Often, the substrate may contain discrete individual sites appropriate for individual partitioning and identification. The number of possible substrates is very large, and include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, TeflonJ, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably fluoresce. See WO 0055627.

Generally the substrate is planar, although other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube for flow-

through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

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In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, e.g., the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxy groups, oxo groups, and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, e.g., using linkers; e.g., homo-or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, oligonucleotides are synthesized, and then attached to the surface of the solid support. Either the 5' or 3' terminus may be attached to the solid support, or attachment may be via linkage to an internal nucleoside. In another embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized in situ, using known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affymetrix GeneChipTM technology.

Often, amplification-based assays are performed to measure the expression level of cancer-associated sequences. These assays are typically performed in conjunction with reverse transcription. In such assays, a cancer-associated nucleic acid sequence acts as a template in an amplification reaction (e.g., Polymerase Chain Reaction, or PCR). In a quantitative amplification, the amount of amplification product will be proportional to the amount of template in the original sample. Comparison to appropriate controls provides a measure of the amount of cancer-associated RNA. Methods of quantitative amplification are well known.

Detailed protocols for quantitative PCR are provided, e.g., in Innis, et al. (1990) <u>PCR Protocols</u>, <u>A Guide to Methods and Applications</u> Academic Press.

In some embodiments, a TaqMan based assay is used to measure expression. TaqMan based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent dye and a 3' quenching agent. The probe hybridizes to a PCR product, but cannot itself be extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, e.g., AmpliTaq, results in the cleavage of the TaqMan probe. This cleavage separates the 5' fluorescent dye and the 3' quenching agent, thereby resulting in an increase in fluorescence as a function of amplification (see, e.g., literature provided by Perkin-Elmer, e.g., www2.perkin-elmer.com).

Other suitable amplification methods include, but are not limited to, ligase chain reaction (LCR) (see Wu and Wallace (1989) Genomics 4:560-569, Landegren, et al. (1988) Science 241:1077-1080, and Barringer, et al. (1990) Gene 89:117-122), transcription amplification (Kwoh, et al. (1989) Proc. Natl. Acad. Sci. USA 86:1173-1177), self-sustained sequence replication (Guatelli, et al. (1990) Proc. Nat. Acad. Sci. USA 87:1874-1878), dot PCR, linker adapter PCR, etc.

Expression of cancer proteins from nucleic acids

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In a preferred embodiment, cancer nucleic acids, e.g., encoding cancer proteins, are used to make a variety of expression vectors to express cancer proteins which can then be used in screening assays, as described below. Expression vectors and recombinant DNA technology are well known (see, e.g., Ausubel, supra, and Fernandez and Hoeffler (eds. 1999) Gene Expression Systems Academic Press) to express proteins. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the cancer protein. The term "control sequences" refers to DNA sequences used for the expression of an operably linked coding sequence in a particular host organism. Control sequences that are suitable for prokaryotes, e.g., include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in

the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is typically accomplished by ligation at convenient restriction sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. Transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the cancer protein. Numerous types of appropriate expression vectors and suitable regulatory sequences are known for a variety of host cells.

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In general, transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences may be either constitutive or inducible promoters. The promoters may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known, and are useful in the present invention.

An expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two organisms, e.g., in mammalian or insect cells for expression and in a prokaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector often contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are available. See, e.g., Fernandez and Hoeffler, supra; and Kitamura, et al. (1995) Proc. Nat'l Acad. Sci. USA 92:9146-9150.

In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known and will vary with the host cell used.

The cancer proteins of the present invention are usually produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding a cancer protein, under the appropriate conditions to induce or cause expression of the cancer protein. Conditions appropriate for cancer protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained through routine experimentation or optimization. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

Appropriate host cells include yeast, bacteria, archaebacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are Saccharomyces cerevisiae and other yeasts, E. coli, Bacillus subtilis, Sf9 cells, C129 cells, 293 cells, Neurospora, BHK, CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells), THP1 cells (a macrophage cell line), and various other human cells and cell lines.

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In a preferred embodiment, the cancer proteins are expressed in mammalian cells. Mammalian expression systems may be used, and include retroviral and adenoviral systems. One expression vector system is a retroviral vector system such as is generally described in PCT/US97/01019 and PCT/US97/01048. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter (see, e.g., Fernandez and Hoeffler, supra). Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenlyation signals include those derived from SV40.

Methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, are available, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

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In a preferred embodiment, cancer proteins are expressed in bacterial systems. Promoters from bacteriophage may also be used. In addition, synthetic promoters and hybrid promoters are also useful; e.g., the tac promoter is a hybrid of the trp and lac promoter sequences. Furthermore, a bacterial promoter can include naturally occurring promoters of nonbacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression vector may also include a signal peptide sequence that provides for secretion of the cancer protein in bacteria. The protein is either secreted into the growth media (grampositive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin, and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan, and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known, and include vectors for Bacillus subtilis, E. coli, Streptococcus cremoris, and Streptococcus lividans, among others (e.g., Fernandez and Hoeffler, supra). The bacterial expression vectors are transformed into bacterial host cells using techniques such as calcium chloride treatment, electroporation, and others.

In one embodiment, cancer proteins are produced in insect cells using, e.g., expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors.

In a preferred embodiment, a cancer protein is produced in yeast cells. Yeast expression systems are well known, and include expression vectors for Saccharomyces cerevisiae, Candida albicans and C. maltosa, Hansenula polymorpha, Kluyveromyces fragilis and K. lactis, Pichia guillerimondii and P. pastoris, Schizosaccharomyces pombe, and Yarrowia lipolytica.

Thus, e.g., for the creation of monoclonal antibodies, if the desired epitope is small, the cancer protein may be fused to a carrier protein to form an immunogen. Alternatively, the cancer protein may be made as a fusion protein to increase expression, or for other reasons. For example, when the cancer protein is a cancer peptide, the nucleic acid encoding the peptide may

be linked to other nucleic acid for expression purposes. Fusion with detection epitope tags can be made, e.g., with FLAG, His6, myc, HA, etc.

In a preferred embodiment, the cancer protein is purified or isolated after expression. Cancer proteins may be isolated or purified in a variety of ways depending on what other components are present in the sample and the requirements for purified product, e.g., natural conformation or denatured. Standard purification methods include ammonium sulfate precipitations, electrophoretic, molecular, immunological, and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the cancer protein may be purified using a standard anticancer protein antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. See, e.g., Walsh (2002) Proteins: Biochemistry and Biotechnology Wiley; Hardin, et al. (eds. 2001) Cloning, Gene Expression and Protein Purification Oxford Univ. Press; Wilson, et al. (eds. 2000) Encyclopedia of Separation Science Academic Press; and Scopes (1993) Protein Purification Springer-Verlag. The degree of purification necessary will vary depending on the use of the cancer protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the cancer proteins and nucleic acids are useful in a number of applications. They may be used as immunoselection reagents, as vaccine reagents, as screening agents, therapeutic entities, for production of antibodies, as transcription or translation inhibitors, etc.

Variants of cancer proteins

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Also included within one embodiment of cancer proteins are amino acid variants of the naturally occurring sequences, as determined herein. Preferably, the variants are preferably greater than about 75% homologous to the wild-type sequence, more preferably greater than about 80%, even more preferably greater than about 85%, and most preferably greater than 90%. In some embodiments the homology will be as high as about 93-95% or 98%. As for nucleic acids, homology in this context means sequence similarity or identity, with identity being preferred. This homology will be determined using standard techniques, as are outlined above for nucleic acid homologies.

Cancer proteins of the present invention may be shorter or longer than the wild type amino acid sequences. Thus, in a preferred embodiment, included within the definition of cancer proteins are portions or fragments of the wild type sequences herein. In addition, as

outlined above, the cancer nucleic acids of the invention may be used to obtain additional coding regions, and thus additional protein sequence.

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In one embodiment, the cancer proteins are derivative or variant cancer proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative cancer peptide will often contain at least one amino acid substitution, deletion, or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion, or deletion may occur at many residue positions within the cancer peptide.

Also included within one embodiment of cancer proteins of the present invention are amino acid sequence variants. These variants typically fall into one or more of three classes: substitutional, insertional, or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the cancer protein, using cassette or PCR mutagenesis or other techniques, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above. However, variant cancer protein fragments having up to about 100-150 residues may be prepared by in vitro synthesis using established techniques. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the cancer protein amino acid sequence. The variants typically exhibit a similar qualitative biological activity as a naturally occurring analogue, although variants can also be selected which have modified characteristics.

While the site or region for introducing an amino acid sequence variation is often predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed cancer variants screened for the optimal combination of desired activity. Techniques for making substitution mutations at predetermined sites in DNA having a known sequence are well known, e.g., M13 primer mutagenesis and PCR mutagenesis. Screening of mutants is often done using assays of cancer protein activities.

Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1-20 amino acids, although considerably larger insertions may be tolerated. Deletions generally range from about 1-20 residues, although in some cases deletions may be much larger.

Substitutions, deletions, insertions, or combination thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the

alteration of the molecule. However, larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of the cancer protein are desired, substitutions are generally made in accordance with the amino acid substitution relationships described.

The variants typically exhibit essentially the same qualitative biological activity and will elicit the same immune response as a naturally-occurring analog, although variants also are selected to modify the characteristics of cancer proteins as needed. Alternatively, the variant may be designed such that a biological activity of the cancer protein is altered. For example, glycosylation sites may be added, altered, or removed.

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Substantial changes in function or immunological identity are sometimes made by selecting substitutions that are less conservative than those described above. For example, substitutions may be made which more significantly affect: the structure of the polypeptide backbone in the area of the alteration, for example the alpha-helical or beta-sheet structure; the charge or hydrophobicity of the molecule at the target site; or the bulk of the side chain. Substitutions which generally are expected to produce the greatest changes in the polypeptide's properties are those in which (a) a hydrophilic residue, e.g., serine or threone is substituted for (or by) a hydrophobic residue, e.g., leucine, isoleucine, phenylalanine, valine, or alanine; (b) a cysteine or proline is substituted for (or by) another residue; (c) a residue having an electropositive side chain, e.g., lysine, arginine, or histidine, is substituted for (or by) an electronegative residue, e.g., glutamic or aspartic acid; (d) a residue having a bulky side chain, e.g., phenylalanine, is substituted for (or by) one not having a side chain, e.g., glycine; or (e) a proline residue is incorporated or substituted, which changes the degree of rotational freedom of the peptidyl bond.

Variants typically exhibit a similar qualitative biological activity and will elicit the same immune response as the naturally-occurring analog, although variants also are selected to modify the characteristics of the skin cancer proteins as needed. Alternatively, the variant may be designed such that the biological activity of the cancer protein is altered. For example, glycosylation sites may be altered or removed.

Covalent modifications of cancer polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a cancer polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N-or C-terminal residues of a cancer polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking cancer polypeptides to a water-

insoluble support matrix or surface for use in a method for purifying anti-cancer polypeptide antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, e.g., esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-((p-azidophenyl)dithio)propioimidate.

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Other modifications include deamidation of glutaminyl and asparaginyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of serinyl, threonyl, or tyrosyl residues, methylation of the amino groups of the lysine, arginine, and histidine side chains (e.g., pp. 79-86, Creighton (1992) Proteins: Structure and Molecular Properties Freeman), acetylation of the N-terminal amine, and amidation of a C-terminal carboxyl group.

Another type of covalent modification of the cancer polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide.

"Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence cancer polypeptide, and/or adding one or more glycosylation sites that are not present in the native sequence cancer polypeptide.

Glycosylation patterns can be altered in many ways. Different cell types to express cancer-associated sequences can result in different glycosylation patterns.

Addition of glycosylation sites to cancer polypeptides may also be accomplished by altering the amino acid sequence thereof. The alteration may be made, e.g., by the addition of, or substitution by, one or more serine or threonine residues to the native sequence cancer polypeptide (for O-linked glycosylation sites). The cancer amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the cancer polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the cancer polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. See, e.g., WO 87/05330; pp. 259-306 in Aplin and Wriston (1981) <u>CRC Crit. Rev. Biochem.</u>

Removal of carbohydrate moieties present on the cancer polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for

amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are applicable. See, e.g., Sojar and Bahl (1987) <u>Arch. Biochem. Biophys.</u> 259:52-57 and Edge, et al. (1981) <u>Anal. Biochem.</u> 118:131-137. Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo-and exo-glycosidases. See, e.g., Thotakura, et al. (1987) <u>Meth. Enzymol.</u> 138:350-359.

Another type of covalent modification of cancer comprises linking the cancer polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192, or 4,179,337.

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Cancer polypeptides of the present invention may also be modified in a way to form chimeric molecules comprising a cancer polypeptide fused to another heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of a cancer polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino-or carboxylterminus of the cancer polypeptide. The presence of such epitope-tagged forms of a cancer polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the cancer polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of a cancer polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are available. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; HIS6 and metal chelation tags, the flu HA tag polypeptide and its antibody 12CA5 (Field, et al. (1988) Mol. Cell. Biol. 8:2159-2165); the c-myc tag and the 8F9, 3C7, 6E10, G4, B7, and 9E10 antibodies thereto (Evan, et al. (1985) Molecular and Cellular Biology 5:3610-3616); and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody (Paborsky, et al. (1990) Protein Engineering 3(6):547-553). Other tag polypeptides include the Flag-peptide (Hopp, et al. (1988) BioTechnology 6:1204-1210); the KT3 epitope peptide (Martin, et al. (1992) Science 255:192-194); tubulin epitope peptide (Skinner, et al. (1991) J. Biol. Chem. 266:15163-15166); and the T7 gene 10 protein peptide tag (Lutz-Freyermuth, et al. (1990) Proc. Natl. Acad. Sci. USA 87:6393-6397).

Also included are other cancer proteins of the cancer family, and cancer proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related cancer proteins from humans or other organisms. Particularly useful probe and/or PCR primer sequences include the unique areas of the cancer nucleic acid sequence. Preferred PCR primers are from about 15-35 nucleotides in length, with from about 20-30 being preferred, and may contain inosine as needed. The conditions for PCR reaction have been well described (e.g., Innis, PCR Protocols, supra).

In addition, cancer proteins can be made that are longer than those encoded by the nucleic acids of the Tables, e.g., by the elucidation of extended sequences, the addition of epitope or purification tags, the addition of other fusion sequences, etc.

Cancer proteins may also be identified as being encoded by cancer nucleic acids. Thus, cancer proteins are encoded by nucleic acids that will hybridize to the sequences of the sequence listings, or their complements, as outlined herein.

15 Antibodies to cancer proteins

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In a preferred embodiment, when the cancer protein is to be used to generate antibodies, e.g., for immunotherapy or immunodiagnosis, the cancer protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is typically meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller cancer protein will be able to bind to the full-length protein, particularly linear epitopes. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity. In a preferred embodiment, the epitope is selected from a protein sequence set out in the tables.

Methods of preparing polyclonal antibodies exist (e.g., Coligan, supra; and Harlow and Lane, supra). Polyclonal antibodies can be raised in a mammal, e.g., by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a nucleic acid of Tables 1-68 or fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum

albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). Various immunization protocols may be used.

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The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein (1975) Nature 256:495. In a hybridoma method, a mouse, harnster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized in vitro. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of the tables or fragment thereof, or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (e.g., pp. 59-103 in Goding (1986) Monoclonal Antibodies: Principles and Practice Academic Press). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine, or human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens or that have binding specificities for two epitopes on the same antigen. In one embodiment, one of the binding specificities is for a protein encoded by a nucleic acid of the tables or a fragment thereof, the other one is for another antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific. Alternatively, tetramer-type technology may create multivalent reagents.

In a preferred embodiment, the antibodies to cancer protein are capable of reducing or eliminating a biological function of a cancer protein, in a naked form or conjugated to an effector moiety, as is described below. That is, the addition of anti-cancer protein antibodies (either polyclonal or preferably monoclonal) to cancer tissue (or cells containing cancer) may reduce or eliminate the cancer. Generally, at least a 25% decrease in activity, growth, size, or the like is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

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In a preferred embodiment the antibodies to the cancer proteins are humanized antibodies (e.g., Xenerex Biosciences, Medarex, Inc., Abgenix, Inc., Protein Design Labs, Inc.) Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')2 or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat, or rabbit having the desired specificity, affinity, and capacity. In some instances, Fv framework residues of a human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, a humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework (FR) regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will typically comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-329; and Presta (1992) Curr. Op. Struct. Biol. 2:593-596). Humanization can be essentially performed following the method of Winter and co-workers (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-327; Verhoeyen, et al. (1988) Science 239:1534-1536), by substituting rodent CDRs or CDR sequences for corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by corresponding sequence from a non-human species.

Human antibodies can also be produced using phage display libraries (Hoogenboom and Winter (1992) J. Mol. Biol. 227:381-388; Marks, et al. (1991) J. Mol. Biol. 222:581-597) or human monoclonal antibodies (e.g., p. 77, Cole, et al. in Reisfeld and Sell (1985) Monoclonal Antibodies and Cancer Therapy Liss; and Boerner, et al. (1991) J. Immunol. 147:86-95). Similarly, human antibodies can be made by introducing human immunoglobulin loci into 5 transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in nearly all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, e.g., in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the 10 following scientific publications: Marks, et al. (1992) Bio/Technology 10:779-783; Lonberg, et al. (1994) Nature 368:856-859; Morrison (1994) Nature 368:812-13; Fishwild, et al. (1996) Nature Biotechnology 14:845-851; Neuberger (1996) Nature Biotechnology 14:826; and Lonberg and Huszar (1995) Intern. Rev. Immunol. 13:65-93.

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By immunotherapy is meant treatment of cancer with an antibody raised against cancer proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. The antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen, leading to an immune response.

In a preferred embodiment the cancer proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment may bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted cancer protein, e.g., in autocrine signaling.

In another preferred embodiment, the cancer protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment may bind the extracellular domain of the cancer protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The antibody may cause down-regulation of the transmembrane cancer protein. The antibody may be a competitive, non-

competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the cancer protein. The antibody may also be an antagonist of the cancer protein. Further, the antibody may prevent activation of the transmembrane cancer protein, or may induce or suppress a particular cellular pathway. In one aspect, when the antibody prevents the binding of other molecules to the cancer protein, the antibody prevents growth of the cell. The antibody may also be used to target or sensitize the cell to cytotoxic agents, including, but not limited to TNF-α, TNF-β, IL-1, INF-γ, and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody may belong to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity or antigen-dependent cytotoxicity (ADCC). Thus, cancer may be treated by administering to a patient antibodies directed against the transmembrane cancer protein. Antibody-labeling may activate a co-toxin, localize a toxin payload, or otherwise provide means to locally ablate cells.

In another preferred embodiment, the antibody is conjugated to an effector moiety. The effector moiety can be various molecules, including labeling moieties such as radioactive labels or fluorescent labels, or can be a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of a cancer protein. In another aspect the therapeutic moiety may modulate the activity of molecules associated with or in close proximity to a cancer protein. The therapeutic moiety may inhibit enzymatic or signaling activity such as protease or collagenase or protein kinase activity associated with cancer, or be an attractant of other cells, such as NK cells.

In a preferred embodiment, the therapeutic moiety can also be a cytotoxic agent. In this method, targeting the cytotoxic agent to cancer tissue or cells results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with cancer. Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin, saporin, auristatin, and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against cancer proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane cancer proteins not only serves to increase the local

concentration of therapeutic moiety in the cancer afflicted area, but also serves to reduce deleterious side effects that may be associated with the untargeted therapeutic moiety.

In another preferred embodiment, the cancer protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the cancer protein can be targeted within a cell, e.g., the nucleus, an antibody thereto may contain a signal for that target localization, e.g., a nuclear localization signal.

The cancer antibodies of the invention specifically bind to cancer proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a K_d of at least about 0.1 mM, more usually at least about 1 μ M, preferably at least about 0.1 μ M or better, and most preferably, 0.01 μ M or better. Selectivity of binding to the specific target and not to related sequences is often also important.

15 Detection of cancer sequence for diagnostic and therapeutic applications

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In one aspect, the RNA expression levels of genes are determined for different cellular states in the cancer phenotype. Expression levels of genes in normal tissue (e.g., not undergoing cancer) and in cancer tissue (and in some cases, for varying severities of cancer that relate to prognosis, as outlined below), or in non-malignant disease are evaluated to provide expression profiles. A gene expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state of the cell. While two states may have a particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is reflective of the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be performed or confirmed to determine whether a tissue sample has the gene expression profile of normal or cancerous tissue. This will provide for molecular diagnosis of related conditions.

"Differential expression," or grammatical equivalents as used herein, refers to qualitative or quantitative differences in the temporal and/or cellular gene expression patterns within and among cells and tissue. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, e.g., normal versus cancer tissue. Genes may be turned on or turned off in a particular state, relative to another state thus

permitting comparison of two or more states. A qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques. Some genes will be expressed in one state or cell type, but not in both. Alternatively, the difference in expression may be quantitative, e.g., in that expression is increased or decreased; e.g., gene expression is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays. See, Lockhart (1996) Nature Biotechnology 14:1675-1680. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, northern analysis, and RNase protection. As outlined above, preferably the change in expression (e.g., upregulation or downregulation) is at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably at least about 200%, with from 300 to at least 1000% being especially preferred.

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Evaluation may be at the gene transcript or the protein level. The amount of gene expression may be monitored using nucleic acid probes to the RNA or DNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, e.g., with antibodies to the cancer protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Proteins corresponding to cancer genes, e.g., those identified as being important in a cancer or disease phenotype, can be evaluated in a cancer diagnostic test. In a preferred embodiment, gene expression monitoring is performed simultaneously on a number of genes. Multiple protein expression monitoring can be performed as well.

In this embodiment, the cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of cancer sequences in a particular cell. The assays are further described below in the example. PCR techniques can be used to provide greater sensitivity.

In a preferred embodiment nucleic acids encoding the cancer protein are detected. Although DNA or RNA encoding the cancer protein may be detected, of particular interest are methods wherein an mRNA encoding a cancer protein is detected. Probes to detect mRNA can be a nucleotide/deoxynucleotide probe that is complementary to and hybridizes with the mRNA and includes, but is not limited to, oligonucleotides, cDNA, or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after

immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method, detection of the mRNA is performed in situ. In this method permeabilized cells or tissue samples are contacted with a detectably labeled nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxygenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding a cancer protein is detected by binding the digoxygenin with an anti-digoxygenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl phosphate.

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In a preferred embodiment, various proteins from the three classes of proteins as described herein (secreted, transmembrane, or intracellular proteins) are used in diagnostic assays. The cancer proteins, antibodies, nucleic acids, modified proteins, and cells containing cancer sequences are used in diagnostic assays. This can be performed on an individual gene or corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

As described and defined herein, cancer proteins, including intracellular, transmembrane, or secreted proteins, find use as markers of cancer, e.g., for prognostic or diagnostic purposes. Detection of these proteins in putative cancer tissue allows for detection, prognosis, or diagnosis of cancer or similar disease, and for selection of therapeutic strategy. In one embodiment, antibodies are used to detect cancer proteins. A preferred method separates proteins from a sample by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be another type of gel, including isoelectric focusing gels and the like). Following separation of proteins, the cancer protein is detected, e.g., by immunoblotting with antibodies raised against the cancer protein.

In another preferred method, antibodies to the cancer protein find use in in situ imaging techniques, e.g., in histology. See, e.g., Asai, et al. (eds. 1993) Methods in Cell Biology:

Antibodies in Cell Biology (vol. 37) Academic Press. In this method, cells are contacted with from one to many antibodies to the cancer protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a

detectable label. In another method the primary antibody to the cancer protein(s) contains a detectable label, e.g., an enzyme marker that can act on a substrate. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of cancer proteins. Many other histological imaging techniques are also provided by the invention.

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In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

In another preferred embodiment, antibodies find use in diagnosing cancer from blood, serum, plasma, stool, and other samples. Such samples, therefore, are useful as samples to be probed or tested for the presence of cancer proteins. Antibodies can be used to detect a cancer protein by previously described immunoassay techniques including ELISA, immunoblotting (western blotting), immunoprecipitation, BIACORE technology and the like. Conversely, the presence of antibodies may indicate an immune response against an endogenous cancer protein.

In a preferred embodiment, in situ hybridization of labeled cancer nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including cancer tissue and/or normal tissue, are made. In situ hybridization (see, e.g., Ausubel, supra) is then performed. When comparing the fingerprints between an individual and a standard, a diagnosis, a prognosis, or a prediction may be based on the findings. It is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis and molecular profiling of the condition of the cells may lead to distinctions between responsive or refractory conditions or may be predictive of outcomes.

In a preferred embodiment, the cancer proteins, antibodies, nucleic acids, modified proteins, and cells containing cancer sequences are used in prognosis assays. As above, gene expression profiles can be generated that correlate to cancer, clinical, pathological, or other information, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. Single or multiple genes may be useful in various combinations. As above, cancer probes may be attached to biochips for the detection and quantification of cancer sequences in a tissue or patient. The assays proceed as outlined above for diagnosis. PCR method may provide more sensitive and accurate quantification.

Assays for therapeutic compounds

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In a preferred embodiment, the proteins, nucleic acids, and antibodies as described herein are used in drug screening assays. The cancer proteins, antibodies, nucleic acids, modified proteins, and cells containing cancer sequences are used in drug screening assays or by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques, to allow monitoring for expression profile genes after treatment with a candidate agent (e.g., Zlokarnik, et al. (1998) Science 279:84-88; Heid (1996) Genome Res. 6:986-994.

In a preferred embodiment, the cancer proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified cancer proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the cancer phenotype or an identified physiological function of a cancer protein. As above, this can be done on an individual gene level or by evaluating the effect of drug candidates on a "gene expression profile". In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques, to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, supra.

Having identified the differentially expressed genes herein, a variety of assays may be performed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene as up regulated in cancer, test compounds can be screened for the ability to modulate gene expression or for binding to the cancer protein. "Modulation" thus includes both an increase and a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal versus tissue undergoing cancer, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4-fold increase in cancer tissue compared to normal tissue, a decrease of about four-fold is often desired; similarly, a 10-fold decrease in cancer tissue compared to normal tissue often provides a target value of a 10-fold increase in expression to be induced by the test compound.

The amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be

monitored, e.g., through the use of antibodies to the cancer protein and standard immunoassays. Proteomics and separation techniques may also allow quantification of expression.

In a preferred embodiment, gene expression or protein monitoring of a number of entities, e.g., an expression profile, is monitored simultaneously. Such profiles will typically involve a plurality of those entities described herein.

In this embodiment, the cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of cancer sequences in a particular cell.

Alternatively, PCR may be used. Thus, a series, e.g., of microtiter plate, may be used with dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for each well.

Modulators of cancer

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Expression monitoring can be performed to identify compounds that modify the expression of one or more cancer-associated sequences, e.g., a polynucleotide sequence set out in the tables. Generally, in a preferred embodiment, a test modulator is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that modulate cancer, modulate cancer proteins, bind to a cancer protein, or interfere with the binding of a cancer protein and an antibody or other binding partner.

The term "test compound" or "drug candidate" or "modulator" or grammatical equivalents as used herein describes a molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or indirectly alter the cancer phenotype or the expression of a cancer sequence, e.g., a nucleic acid or protein sequence. In preferred embodiments, modulators alter expression profiles, or expression profile nucleic acids or proteins provided herein. In one embodiment, the modulator suppresses a cancer phenotype, e.g., to a normal or non-malignant tissue fingerprint. In another embodiment, a modulator induced a cancer phenotype. Generally, a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, e.g., at zero concentration or below the level of detection.

Drug candidates encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than 100 and less than about 2,500 daltons. Preferred small molecules are less than 2000, or

less than 1500, or less than 1000, or less than 500 D. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Candidate agents are also found among biomolecules including peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs, or combinations thereof. Particularly preferred are peptides.

In one aspect, a modulator will neutralize the effect of a cancer protein. By "neutralize" is meant that activity of a protein is inhibited or blocked and the consequent effect on the cell.

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In certain embodiments, combinatorial libraries of potential modulators will be screened for an ability to bind to a cancer polypeptide or to modulate activity. Conventionally, new chemical entities with useful properties are generated by identifying a chemical compound (called a "lead compound") with some desirable property or activity, e.g., inhibiting activity, creating variants of the lead compound, and evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis. See, e.g., Janzen (2002) High Throughput Screening: Methods and Protocols Humana; Devlin (ed. 1997) High Throughput Screening: The Discovery of Bioactive Substances Dekker; and Mei and Czarnik (eds. 2002) Integrated Drug Discovery Techniques Dekker.

In one preferred embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such "combinatorial chemical libraries" are then screened in one or more assays to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library, such as a polypeptide (e.g., mutein) library, is formed by combining a set of chemical building blocks called amino acids in every possible way for a given compound length (e.g., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be

synthesized through such combinatorial mixing of chemical building blocks (Gallop, et al. (1994) J. Med. Chem. 37:1233-1251).

Preparation and screening of combinatorial chemical libraries is well known. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent No. 5,010,175, Furka (1991) Pept. Prot. Res. 37:487-493, Houghton, et al. (1991) Nature 5 354:84-88), peptoids (PCT Publication No WO 91/19735), encoded peptides (PCT Publication WO 93/20242), random bio-oligomers (PCT Publication WO 92/00091), benzodiazepines (U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs, et al. (1993) Proc. Nat. Acad. Sci. USA 90:6909-6913, vinylogous polypeptides (Hagihara, et al. (1992) J. Amer. Chem. Soc. 114:6568-570), nonpeptidal peptidomimetics with a Beta-D-10 Glucose scaffolding (Hirschmann, et al. (1992) J. Amer. Chem. Soc. 114:9217-9218), analogous organic syntheses of small compound libraries (Chen, et al. (1994) J. Amer. Chem. Soc. 116:2661-662), oligocarbamates (Cho, et al. (1993) Science 261:1303-1305), and/or peptidyl phosphonates (Campbell, et al. (1994) J. Org. Chem. 59:658-xxx). See, generally, Gordon, et al. (1994) J. Med. Chem. 37:1385-1401, nucleic acid libraries (see, e.g., Stratagene, 15 Corp.), peptide nucleic acid libraries (see, e.g., U.S. Patent 5,539,083), antibody libraries (see, e.g., Vaughn, et al. (1996) Nature Biotechnology 14(3):309-314, and PCT/US96/10287), carbohydrate libraries (see, e.g., Liang, et al. (1996) Science 274:1520-1522, and U.S. Patent No. 5,593,853), and small organic molecule libraries (see, e.g., benzodiazepines, page 33 Baum (Jan 18, 1993) C&EN; isoprenoids, U.S. Patent No. 5,569,588; thiazolidinones and 20 metathiazanones, U.S. Patent No. 5,549,974; pyrrolidines, U.S. Patent Nos. 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent No. 5,506,337; benzodiazepines, U.S. Patent No. 5,288,514; and the like).

Devices for the preparation of combinatorial libraries are commercially available (see, e.g., 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY, Symphony, Rainin, Woburn, MA, 433A Applied Biosystems, Foster City, CA, 9050 Plus, Millipore, Bedford, MA).

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A number of well known robotic systems have also been developed for solution phase chemistries. These systems include automated workstations like the automated synthesis apparatus developed by Takeda Chemical Industries, LTD. (Osaka, Japan) and many robotic systems utilizing robotic arms (Zymate II, Zymark Corporation, Hopkinton, Mass.; Orca, Hewlett-Packard, Palo Alto, Calif.), which mimic the manual synthetic operations performed by a chemist. The above devices are suitable for use with the present invention. The nature and

implementation of modifications to these devices (if any) so that they can operate as discussed herein will be apparent. In addition, numerous combinatorial libraries are themselves commercially available (see, e.g., ComGenex, Princeton, N.J., Asinex, Moscow, Ru, Tripos, Inc., St. Louis, MO, ChemStar, Ltd, Moscow, RU, 3D Pharmaceuticals, Exton, PA, Martek Biosciences, Columbia, MD, etc.).

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The assays to identify modulators are amenable to high throughput screening. Preferred assays thus detect enhancement or inhibition of cancer gene transcription, inhibition, or enhancement of polypeptide expression, and inhibition or enhancement of polypeptide activity.

High throughput assays for the presence, absence, quantification, or other properties of particular nucleic acids or protein products are well known. Similarly, binding assays and reporter gene assays are similarly well known. Thus, e.g., U.S. Patent No. 5,559,410 discloses high throughput screening methods for proteins, U.S. Patent No. 5,585,639 discloses high throughput screening methods for nucleic acid binding (e.g., in arrays), while U.S. Patent Nos. 5,576,220 and 5,541,061 disclose high throughput methods of screening for ligand/antibody binding.

In addition, high throughput screening systems are commercially available (see, e.g., Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman Instruments, Inc. Fullerton, CA; Precision Systems, Inc., Natick, MA, etc.). These systems typically automate entire procedures, including sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. The manufacturers of such systems provide detailed protocols for various high throughput systems. Thus, e.g., Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like.

In one embodiment, modulators are proteins, often naturally occurring proteins or fragments of naturally occurring proteins. Thus, e.g., cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of proteins may be made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred. Particularly useful test

compound will be directed to the class of proteins to which the target belongs, e.g., substrates for enzymes or ligands and receptors.

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In a preferred embodiment, modulators are peptides of from about 5-30 amino acids, with from about 5-20 amino acids being preferred, and from about 7-15 being particularly preferred. The peptides may be digests of naturally occurring proteins, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that each nucleic acid and peptide consists of essentially random nucleotides and amino acids, respectively. Since generally these random peptides (or nucleic acids, discussed below) are chemically synthesized, they may incorporate a nucleotide or amino acid at any position. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. For example, in a preferred embodiment, the nucleotides or amino acid residues are randomized within a defined class, e.g., of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines, or histidines for phosphorylation sites, etc., or to purines, etc.

Modulators of cancer can also be nucleic acids, as defined above.

As described above generally for proteins, nucleic acid modulating agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. For example, digests of prokaryotic or eukaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate compounds are organic chemical moieties, a wide variety of which are available in the literature.

After the candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing a target sequence to be analyzed is added to the biochip. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR performed as appropriate. For example, an in

vitro transcription with labels covalently attached to the nucleotides is performed. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

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In a preferred embodiment, the target sequence is labeled with, e.g., a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as, alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

These assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos. 5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670, 5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246, and 5,681,697, all of which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

A variety of hybridization conditions may be used in the present invention, including high, moderate, and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allows formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration, pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

The reactions outlined herein may be accomplished in a variety of ways. Components of the reaction may be added simultaneously, or sequentially, in different orders, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents. These include salts, buffers, neutral proteins, e.g., albumin, detergents, etc. which may be used

to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may also be used as appropriate, depending on the sample preparation methods and purity of the target.

The assay data are analyzed to determine the expression levels, and changes in expression levels as between states of individual genes, forming a gene expression profile.

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Screens are performed to identify modulators of the cancer phenotype. In one embodiment, screening is performed to identify modulators that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. In another embodiment, e.g., for diagnostic applications, having identified differentially expressed genes important in a particular state, screens can be performed to identify modulators that alter expression of individual genes. In an another embodiment, screening is performed to identify modulators that alter a biological function of the expression product of a differentially expressed gene. Again, having identified the importance of a gene in a particular state, screens are performed to identify agents that bind and/or modulate the biological activity of the gene product.

In addition, screens can be done for genes that are induced in response to a candidate agent or treatment process. After identifying a modulator based upon its ability to suppress a cancer expression pattern leading to a normal expression pattern (or its converse), or to modulate a single cancer gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated cancer tissue reveals genes that are not expressed in normal tissue or cancer tissue, but are expressed in agent treated tissue. These agent-specific sequences can be identified and used by methods described herein for cancer genes or proteins. In particular, these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics to the treated cancer tissue sample.

Thus, in one embodiment, a test compound is administered to a population of cancer cells that have an associated cancer expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell

surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (e.g., a peptide) may be put into a viral construct such as an adenoviral or retroviral construct, and added to the cell, such that expression of the peptide agent is accomplished, e.g., PCT US97/01019. Regulatable gene therapy systems can also be used.

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Once a test compound has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

Thus, e.g., cancer or non-malignant tissue may be screened for agents that modulate, e.g., induce or suppress a cancer phenotype. A change in at least one gene, preferably many, of the expression profile indicates that the agent has an effect on cancer activity. By defining such a signature for the cancer phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein need to change.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of either the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "cancer proteins" or a "cancer modulatory protein". The cancer modulatory protein may be a fragment, or alternatively, be the full length protein to the fragment encoded by the nucleic acids of the Tables. Preferably, the cancer modulatory protein is a fragment. In a preferred embodiment, the cancer amino acid sequence which is used to determine sequence identity or similarity is encoded by a nucleic acid of the Tables. In another embodiment, the sequences are naturally occurring allelic variants of a protein encoded by a nucleic acid of the Tables. In another embodiment, the sequences are sequence variants as further described herein.

Preferably, the cancer modulatory protein is a fragment of about 14-24 amino acids long. More preferably the fragment is a soluble fragment. Preferably, the fragment includes a non-transmembrane region. In a preferred embodiment, the fragment has an N-terminal Cys to aid in solubility. In one embodiment, the C-terminus of the fragment is kept as a free acid and the N-terminus is a free amine to aid in coupling, e.g., to cysteine.

In one embodiment the cancer proteins are conjugated to an immunogenic agent as discussed herein. In one embodiment the cancer protein is conjugated to BSA.

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Measurements of cancer polypeptide activity, or of cancer or the cancer phenotype can be performed using a variety of assays. For example, the effects of the test compounds upon the function of the cancer polypeptides can be measured by examining parameters described above. A suitable physiological change that affects activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as, in the case of cancer associated with tumors, tumor growth, tumor metastasis, neovascularization, hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g., northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as cGMP. In the assays of the invention, mammalian cancer polypeptide is typically used, e.g., mouse, preferably human.

Assays to identify compounds with modulating activity can be performed in vitro. For example, a cancer polypeptide is first contacted with a potential modulator and incubated for a suitable amount of time, e.g., from 0.5-48 hours. In one embodiment, the cancer polypeptide levels are determined in vitro by measuring the level of protein or mRNA. The level of protein is typically measured using immunoassays such as western blotting, ELISA, and the like with an antibody that selectively binds to the cancer polypeptide or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or hybridization assays, e.g., northern hybridization, RNAse protection, dot blotting, are preferred. The level of protein or mRNA is typically detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or enzymatically labeled antibodies, and the like, as described herein.

Alternatively, a reporter gene system can be devised using a cancer protein promoter operably linked to a reporter gene such as luciferase, green fluorescent protein, CAT, or β -gal. The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the expression of the gene or

the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "cancer proteins." The cancer protein may be a fragment, or alternatively, the full length protein to a fragment shown herein.

In one embodiment, screening for modulators of expression of specific genes is performed. Typically, the expression of only one or a few genes are evaluated. In another embodiment, screens are designed to first find compounds that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate structure activity relationships.

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In a preferred embodiment, binding assays are done. In general, purified or isolated gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the cancer proteins can be used in the assays.

Thus, in a preferred embodiment, the methods comprise combining a cancer protein and a candidate compound, and determining the binding of the compound to the cancer protein. Preferred embodiments utilize the human cancer protein, although other mammalian proteins may also be used, e.g., for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative cancer proteins may be used.

Generally, in a preferred embodiment of the methods herein, the cancer protein or the candidate agent is non-diffusably bound to an insoluble support, preferably having isolated sample receiving areas (e.g., a microtiter plate, an array, etc.). The insoluble supports may be made of a composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface of such supports may be solid or porous and of a convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes, and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflonTM, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular manner of binding of the composition is typically not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition, and is nondiffusable. Preferred methods of binding include the use of antibodies (which do not

sterically block either the ligand binding site or activation sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein, or other innocuous protein or other moiety.

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In a preferred embodiment, the cancer protein is bound to the support, and a test compound is added to the assay. Alternatively, the candidate agent is bound to the support and the cancer protein is added. Novel binding agents include specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled in vitro protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.), and the like.

The determination of the binding of the test modulating compound to the cancer protein may be done in a number of ways. In a preferred embodiment, the compound is labeled, and binding determined directly, e.g., by attaching all or a portion of the cancer protein to a solid support, adding a labeled candidate agent (e.g., a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps may be utilized as appropriate.

In some embodiments, only one of the components is labeled, e.g., the proteins (or proteinaceous candidate compounds) can be labeled. Alternatively, more than one component can be labeled with different labels, e.g., ¹²⁵I for the proteins and a fluorophor for the compound. Proximity reagents, e.g., quenching or energy transfer reagents are also useful.

In one embodiment, the binding of the test compound is determined by competitive binding assay. The competitor may be a binding moiety known to bind to the target molecule (e.g., a cancer protein), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding between the compound and the binding moiety, with the binding moiety displacing the compound. In one embodiment, the test compound is labeled. Either the compound, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at a temperature which facilitates optimal activity, typically between about 4-40° C. Incubation

periods are typically optimized, e.g., to facilitate rapid high throughput screening. Typically between 0.1-1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

In a preferred embodiment, the competitor is added first, followed by a test compound. Displacement of the competitor is an indication that the test compound is binding to the cancer protein and thus is capable of binding to, and potentially modulating, the activity of the cancer protein. In this embodiment, either component can be labeled. Thus, e.g., if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent.

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Alternatively, if the test compound is labeled, the presence of the label on the support indicates displacement.

In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the test compound is bound to the cancer protein with a higher affinity. Thus, if the test compound is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the test compound is capable of binding to the cancer protein.

In a preferred embodiment, the methods comprise differential screening to identity agents that are capable of modulating the activity of the cancer proteins. In one embodiment, the methods comprise combining a cancer protein and a competitor in a first sample. A second sample comprises a test compound, a cancer protein, and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the cancer protein.

Alternatively, differential screening is used to identify drug candidates that bind to the native cancer protein, but cannot bind to modified cancer proteins. The structure of the cancer protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect the activity of a cancer protein are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

Positive controls and negative controls may be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results. Incubation of all samples is for a time sufficient for the binding of the agent to the protein.

Following incubation, samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

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A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g., albumin, detergents, etc., which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in an order that provides for the requisite binding.

In a preferred embodiment, the invention provides methods for screening for a compound capable of modulating the activity of a cancer protein. The methods comprise adding a test compound, as defined above, to a cell comprising cancer proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes a cancer protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, e.g., hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including chemotherapeutics, radiation, carcinogenics, or other cells (e.g., cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

In this way, compounds that modulate cancer agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the cancer protein. Once identified, similar structures are evaluated to identify critical structural feature of the compound.

In one embodiment, a method of inhibiting cancer cell division is provided. The method comprises administration of a cancer inhibitor. In another embodiment, a method of inhibiting cancer is provided. The method may comprise administration of a cancer inhibitor. In a further embodiment, methods of treating cells or individuals with cancer are provided, e.g., comprising administration of a cancer inhibitor.

In one embodiment, a cancer inhibitor is an antibody as discussed above. In another embodiment, the cancer inhibitor is an antisense molecule.

A variety of cell growth, proliferation, viability, and metastasis assays are available, as described below.

Soft agar growth or colony formation in suspension

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Normal cells require a solid substrate to attach and grow. When the cells are transformed, they lose this phenotype and grow detached from the substrate. For example, transformed cells can grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft agar. The transformed cells, when transfected with tumor suppressor genes, regenerate normal phenotype and require a solid substrate to attach and grow. Soft agar growth or colony formation in suspension assays can be used to identify modulators of cancer sequences, which when expressed in host cells, inhibit abnormal cellular proliferation and transformation. A therapeutic compound would reduce or eliminate the host cells' ability to grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft.

Techniques for soft agar growth or colony formation in suspension assays are described, e.g., in Freshney (1998) <u>Culture of Animal Cells: A Manual of Basic Technique</u> (3d ed.) Wiley-Liss; Freshney (2000) <u>Culture of Animal Cells: A Manual of Basic Technique</u> (4th ed.) Wiley-Liss; and Garkavtsev, et al. (1996) <u>Nature Genet.</u> 14:415-20.

Contact inhibition and density limitation of growth

Normal cells typically grow in a flat and organized pattern in a petri dish until they touch other cells. When the cells touch one another, they are contact inhibited and stop growing. When cells are transformed, however, the cells are not contact inhibited and continue to grow to high densities in disorganized foci. Thus, the transformed cells grow to a higher saturation density than normal cells. This can be detected morphologically by the formation of a disoriented monolayer of cells or rounded cells in foci within the regular pattern of normal surrounding cells. Alternatively, labeling index with (³H)-thymidine at saturation density can be used to measure density limitation of growth. See Freshney (2000), supra. The transformed cells, when transfected with tumor suppressor genes, regenerate a normal phenotype and become contact inhibited and would grow to a lower density.

In this assay, labeling index with (³H)-thymidine at saturation density is a preferred method of measuring density limitation of growth. Transformed host cells are transfected with a cancer-associated sequence and are grown for 24 hours at saturation density in non-limiting medium conditions. The percentage of cells labeling with (³H)-thymidine is determined autoradiographically. See, Freshney (1998), supra.

Growth factor or serum dependence

Transformed cells typically have a lower serum dependence than their normal counterparts (see, e.g., Temin (1966) <u>J. Natl. Cancer Insti.</u> 37:167-175; Eagle, et al.(1970) <u>J. Exp. Med.</u> 131:836-879); Freshney, supra. This is in part due to release of various growth factors by the transformed cells. Growth factor or serum dependence of transformed host cells can be compared with that of control.

Tumor specific markers levels

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Tumor cells release an increased amount of certain factors (hereinafter "tumor specific markers") than their normal counterparts. For example, plasminogen activator (PA) is released from human glioma at a higher level than from normal brain cells (see, e.g., Gullino "Angiogenesis, tumor vascularization, and potential interference with tumor growth" pp. 178-184 in Mihich (ed. 1985) Biological Responses in Cancer Plenum. Similarly, tumor angiogenesis factor (TAF) is released at a higher level in tumor cells than their normal . counterparts. See, e.g., Folkman (1992) Sem. Cancer Biol. 3:89-96.

Various techniques which measure the release of these factors are described in Freshney (1998), supra. Also, see, Unkeless, et al. (1974) <u>J. Biol. Chem.</u> 249:4295-4305; Strickland and Beers (1976) <u>J. Biol. Chem.</u> 251:5694-5702; Whur, et al. (1980) <u>Br. J. Cancer</u> 42:305-312; Gullino "Angiogenesis, tumor vascularization, and potential interference with tumor growth" pp. 178-184 in Mihich (ed. 1985) <u>Biological Responses in Cancer</u> Plenum; Freshney (1985) Anticancer Res. 5:111-130.

Invasiveness into Matrigel

The degree of invasiveness into Matrigel or some other extracellular matrix constituent can be used as an assay to identify compounds that modulate cancer-associated sequences.

Tumor cells exhibit a good correlation between malignancy and invasiveness of cells into Matrigel or some other extracellular matrix constituent. In this assay, tumorigenic cells are typically used as host cells. Expression of a tumor suppressor gene in these host cells would decrease invasiveness of the host cells.

Techniques described in Freshney (1994), supra, can be used. Briefly, the level of invasion of host cells can be measured by using filters coated with Matrigel or some other extracellular matrix constituent. Penetration into the gel, or through to the distal side of the filter, is rated as invasiveness, and rated histologically by number of cells and distance moved,

or by prelabeling the cells with ¹²⁵I and counting the radioactivity on the distal side of the filter or bottom of the dish. See, e.g., Freshney (1984), supra.

Tumor growth in vivo

Effects of cancer-associated sequences on cell growth can be tested in transgenic or immune-suppressed mice. Knock-out transgenic mice can be made, in which the cancer gene is disrupted or in which a cancer gene is inserted. Knock-out transgenic mice can be made by insertion of a marker gene or other heterologous gene into the endogenous cancer gene site in the mouse genome via homologous recombination. Such mice can also be made by substituting the endogenous cancer gene with a mutated version of the cancer gene, or by mutating the endogenous cancer gene, e.g., by exposure to carcinogens.

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A DNA construct is introduced into the nuclei of embryonic stem cells. Cells containing the newly engineered genetic lesion are injected into a host mouse embryo, which is reimplanted into a recipient female. Some of these embryos develop into chimeric mice that possess germ cells partially derived from the mutant cell line. Therefore, by breeding the chimeric mice it is possible to obtain a new line of mice containing the introduced genetic lesion (see, e.g., Capecchi, et al. (1989) Science 244:1288-1292). Chimeric targeted mice can be derived according to Hogan, et al. (1988) Manipulating the Mouse Embryo: A Laboratory Manual CSH Press; and Robertson (ed. 1987) Teratocarcinomas and Embryonic Stem Cells: A Practical Approach IRL Press, Washington, D.C.

Alternatively, various immune-suppressed or immune-deficient host animals can be used. For example, genetically athymic "nude" mouse (see, e.g., Giovanella, et al. (1974) <u>J. Natl. Cancer Inst.</u> 52:921-930), a SCID mouse, a thymectomized mouse, or an irradiated mouse (see, e.g., Bradley, et al. (1978) <u>Br. J. Cancer</u> 38:263-272; Selby, et al. (1980) <u>Br. J. Cancer</u> 41:52-61) can be used as a host. Transplantable tumor cells (typically about 10⁶ cells) injected into isogenic hosts will produce invasive tumors in a high proportions of cases, while normal cells of similar origin will not. In hosts which developed invasive tumors, cells expressing a cancer-associated sequences are injected subcutaneously. After a suitable length of time, preferably 4-8 weeks, tumor growth is measured (e.g., by volume or by its two largest dimensions) and compared to the control. Tumors that have statistically significant reduction (using, e.g., Student's T test) are said to have inhibited growth.

Polynucleotide modulators of cancer Antisense and RNAi Polynucleotides

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In certain embodiments, the activity of a cancer-associated protein is down-regulated, or entirely inhibited, by the use of an inhibitory or antisense polynucleotide, e.g., a nucleic acid complementary to, and which can preferably hybridize specifically to, a coding mRNA nucleic acid sequence, e.g., a cancer protein mRNA, or a subsequence thereof. Binding of the antisense polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

In the context of this invention, antisense polynucleotides can comprise naturally-occurring nucleotides, or synthetic species formed from naturally-occurring subunits or their close homologs. Antisense polynucleotides may also have altered sugar moieties or inter-sugar linkages. Exemplary among these are the phosphorothioate and other sulfur containing species. Analogs are comprehended by this invention so long as they function effectively to hybridize with the cancer protein mRNA. See, e.g., Isis Pharmaceuticals, Carlsbad, CA; Sequitor, Inc., Natick, MA.

Such antisense polynucleotides can readily be synthesized using recombinant means, or can be synthesized in vitro. Equipment for such synthesis is sold by several vendors, including Applied Biosystems. The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known.

Antisense molecules as used herein include antisense or sense oligonucleotides. Sense oligonucleotides can, e.g., be employed to block transcription by binding to the anti-sense strand. The antisense and sense oligonucleotide comprise a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for cancer molecules. A preferred antisense molecule is for a cancer sequences in the Tables, or for a ligand or activator thereof. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14-30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, e.g., Stein and Cohen (1988) Cancer Res. 48:2659-2668; and van der Krol, et al. (1988) BioTechniques 6:958-976.

RNA interference is a mechanism to suppress gene expression in a sequence specific manner. See, e.g., Brumelkamp, et al. (2002) <u>Sciencexpress</u> (21March2002); Sharp (1999) <u>Genes Dev.</u> 13:139-141; and Cathew (2001) <u>Curr. Op. Cell Biol.</u> 13:244-248. In mammalian cells, short, e.g., 21 nt, double stranded small interfering RNAs (siRNA) have been shown to be

effective at inducing an RNAi response. See, e.g., Elbashir, et al. (2001) <u>Nature</u> 411:494-498. The mechanism may be used to downregulate expression levels of identified genes, e.g., treatment of or validation of relevance to disease.

Ribozymes

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In addition to antisense polynucleotides, ribozymes can be used to target and inhibit transcription of cancer-associated nucleotide sequences. A ribozyme is an RNA molecule that catalytically cleaves other RNA molecules. Different kinds of ribozymes have been described, including group I ribozymes, hammerhead ribozymes, hairpin ribozymes, RNase P, and axhead ribozymes (see, e.g., Castanotto, et al. (1994) <u>Adv. in Pharmacology</u> 25: 289-317 for a general review of the properties of different ribozymes).

The general features of hairpin ribozymes are described, e.g., in Hampel, et al. (1990)

Nucl. Acids Res. 18:299-304; European Patent Publication No. 0 360 257; U.S. Patent No.
5,254,678. Methods of preparation are described in, e.g., WO 94/26877; Ojwang, et al. (1993)

Proc. Natl. Acad. Sci. USA 90:6340-6344; Yamada, et al. (1994) Human Gene Therapy 1:39-45; Leavitt, et al. (1995) Proc. Natl. Acad. Sci. USA 92:699-703; Leavitt, et al. (1994) Human

Gene Therapy 5:1151-120; and Yamada, et al. (1994) Virology 205: 121-126.

Polynucleotide modulators of cancer may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of cancer may be introduced into a cell containing the target nucleic acid sequence, e.g., by formation of an polynucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

Thus, in one embodiment, methods of modulating cancer in cells or organisms are provided. In one embodiment, the methods comprise administering to a cell an anti-cancer antibody that reduces or eliminates the biological activity of an endogenous cancer protein.

Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic

acid encoding a cancer protein. This may be accomplished in any number of ways. In a preferred embodiment, e.g., when the cancer sequence is down-regulated in cancer, such state may be reversed by increasing the amount of cancer gene product in the cell. This can be accomplished, e.g., by overexpressing the endogenous cancer gene or administering a gene encoding the cancer sequence, using known gene-therapy techniques. In a preferred embodiment, the gene therapy techniques include the incorporation of the exogenous gene using enhanced homologous recombination (EHR), e.g., as described in PCT/US93/0386.

Alternatively, e.g., when the cancer sequence is up-regulated in cancer, the activity of the endogenous cancer gene is decreased, e.g., by the administration of a cancer antisense or other inhibitor, e.g., RNAi.

In one embodiment, the cancer proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to cancer proteins. Similarly, the cancer proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify cancer antibodies useful for production, diagnostic, or therapeutic purposes. In a preferred embodiment, the antibodies are generated to epitopes unique to a cancer protein; that is, the antibodies show little or no cross-reactivity to other proteins. The cancer antibodies may be coupled to standard affinity chromatography columns and used to purify cancer proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the cancer protein.

20 Methods of identifying variant cancer-associated sequences

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Without being bound by theory, expression of various cancer sequences is correlated with cancer. Accordingly, disorders based on mutant or variant cancer genes may be determined. In one embodiment, the invention provides methods for identifying cells containing variant cancer genes, e.g., determining all or part of the sequence of at least one endogenous cancer gene in a cell. In a preferred embodiment, the invention provides methods of identifying the cancer genotype of an individual, e.g., determining all or part of the sequence of at least one cancer gene of the individual. This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced cancer gene to a known cancer gene, e.g., a wild-type gene.

The sequence of all or part of the cancer gene can then be compared to the sequence of a known cancer gene to determine if any differences exist. This can be done using known

homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the cancer gene of the patient and the known cancer gene correlates with a disease state or a propensity for a disease state, as outlined herein.

In a preferred embodiment, the cancer genes are used as probes to determine the number of copies of the cancer gene in the genome.

In another preferred embodiment, the cancer genes are used as probes to determine the chromosomal localization of the cancer genes. Information such as chromosomal localization finds use in providing a diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in the cancer gene locus.

10 Administration of pharmaceutical and vaccine compositions

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In one embodiment, a therapeutically effective dose of a cancer protein or modulator thereof, is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable using known techniques. See, e.g., Ansel, et al. (1999)

Pharmaceutical Dosage Forms and Drug Delivery Lippincott; Lieberman (1992) Pharmaceutical Dosage Forms (vols. 1-3) Dekker, ISBN 0824770846, 082476918X, 0824712692, 0824716981; Lloyd (1999) The Art, Science and Technology of Pharmaceutical Compounding Amer. Pharmaceut. Assn.; and Pickar (1998) Dosage Calculations Thomson. Adjustments for cancer degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration, drug interaction and the severity of the condition may be necessary. U.S. Patent Application No. 09/687,576, further discloses the use of compositions and methods of diagnosis and treatment in cancer.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals. Thus the methods are applicable to both human therapy and veterinary applications. In the preferred embodiment the patient is a mammal, preferably a primate, and in the most preferred embodiment the patient is human.

The administration of the cancer proteins and modulators thereof of the present invention can be done in a variety of ways, including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, or intraocularly. In some instances, e.g., in the treatment of wounds and inflammation, the cancer proteins and modulators may be directly applied as a solution or spray.

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The pharmaceutical compositions of the present invention comprise a cancer protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid, and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid, and the like. "Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts, and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose, lactose, com and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

The pharmaceutical compositions can be administered in a variety of unit dosage forms depending upon the method of administration. For example, unit dosage forms suitable for oral administration include, but are not limited to, powder, tablets, pills, capsules and lozenges. It is recognized that cancer protein modulators (e.g., antibodies, antisense constructs, ribozymes, small organic molecules, etc.) when administered orally, should be protected from digestion. This is typically accomplished either by complexing the molecule(s) with a composition to render it resistant to acidic and enzymatic hydrolysis, or by packaging the molecule(s) in an appropriately resistant carrier, such as a liposome or a protection barrier. Means of protecting agents from digestion are available.

The compositions for administration will commonly comprise a cancer protein modulator dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers can be used, e.g., buffered saline and the like. These solutions are sterile and generally free of undesirable matter. These compositions may be sterilized by conventional, well known sterilization techniques. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents, and the like, e.g., sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate, and the like. The concentration of active agent in these formulations can vary widely, and will be selected primarily based on fluid volumes, viscosities, body weight, and the like in accordance with the particular mode of administration selected and the patient's needs (e.g., (1980) Remington's Pharmaceutical Science (18th ed.) Mack, and Hardman and Limbird (eds. 2001) Goodman and Gilman: The Pharmacologial Basis of Therapeutics (10th ed.) McGraw-Hill.

Thus, a typical pharmaceutical composition for intravenous administration would be about 0.1 to 10 mg per patient per day. Dosages from 0.1 up to about 100 mg per patient per day may be used, particularly when the drug is administered to a secluded site and not into the blood stream, such as into a body cavity or into a lumen of an organ. Substantially higher dosages are possible in topical administration. Actual methods for preparing parenterally administrable compositions will be known or apparent.

The compositions containing modulators of cancer proteins can be administered for therapeutic or prophylactic treatments. In therapeutic applications, compositions are administered to a patient suffering from a disease (e.g., a cancer) in an amount sufficient to cure or at least partially arrest the disease and its complications. An amount adequate to accomplish this is defined as a "therapeutically effective dose." Amounts effective for this use will depend upon the severity of the disease and the general state of the patient's health. Single or multiple administrations of the compositions may be administered depending on the dosage and frequency as required and tolerated by the patient. In any event, the composition should provide a sufficient quantity of the agents of this invention to effectively treat the patient. An amount of modulator that is capable of preventing or slowing the development of cancer in a mammal is referred to as a "prophylactically effective dose." The particular dose required for a prophylactic treatment will depend upon the medical condition and history of the mammal, the particular cancer being prevented, as well as other factors such as age, weight, gender,

administration route, efficiency, etc. Such prophylactic treatments may be used, e.g., in a mammal who has previously had cancer to prevent a recurrence of the cancer, or in a mammal who is suspected of having a significant likelihood of developing cancer based, at least in part, upon gene expression profiles. Vaccine strategies may be used, in either a DNA vaccine form, or protein vaccine.

It will be appreciated that the present cancer protein-modulating compounds can be administered alone or in combination with additional cancer modulating compounds or with other therapeutic agent, e.g., other anti-cancer agents or treatments.

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In numerous embodiments, one or more nucleic acids, e.g., polynucleotides comprising nucleic acid sequences set forth in the Tables, such as RNAi, antisense polynucleotides or ribozymes, will be introduced into cells, in vitro or in vivo. The present invention provides methods, reagents, vectors, and cells useful for expression of cancer-associated polypeptides and nucleic acids using in vitro (cell-free), ex vivo or in vivo (cell or organism-based) recombinant expression systems.

The particular procedure used to introduce the nucleic acids into a host cell for expression of a protein or nucleic acid is application specific. Many procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection, plasma vectors, viral vectors, and other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA, or other foreign genetic material into a host cell (see, e.g., Berger and Kimmel (1987) Guide to Molecular Cloning Techniques from Methods in Enzymology (vol. 152) Academic Press; Ausubel, et al. (eds. 1999 and supplements) Current Protocols Lippincott; and Sambrook, et al. (2001) Molecular Cloning: A Laboratory Manual (3d ed., Vol. 1-3) CSH Press.

In a preferred embodiment, cancer proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, cancer genes (including both the full-length sequence, partial sequences, or regulatory sequences of the cancer coding regions) can be administered in a gene therapy application. These cancer genes can include inhibitory applications, e.g., as inhibitory RNA, gene therapy (e.g., for incorporation into the genome), or antisense compositions.

Cancer polypeptides and polynucleotides can also be administered as vaccine compositions to stimulate HTL, CTL, and antibody responses. Such vaccine compositions can

include, e.g., lipidated peptides (see, e.g., Vitiello, et al. (1995) J. Clin. Invest. 95:341-349), peptide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres (see, e.g., Eldridge, et al. (1991) Molec. Immunol. 28:287-294,; Alonso, et al. (1994) Vaccine 12:299-306; Jones, et al. (1995) Vaccine 13:675-681), peptide compositions contained in immune stimulating complexes (ISCOMS) (see, e.g., Takahashi, et al. (1990) Nature 344:873-5 875; Hu, et al. (1998) Clin Exp Immunol. 113:235-243), multiple antigen peptide systems (MAPs) (see, e.g., Tam (1988) Proc. Natl. Acad. Sci. USA 85:5409-5413; Tam (1996) J. Immunol. Methods 196:17-32), peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, et al., p. 379, in Kaufmann (ed. 1996) Concepts in Vaccine Development de Gruyter; Chakrabarti, et al. 10 (1986) Nature 320:535-537; Hu, et al. (1986) Nature 320:537-540; Kieny, et al. (1986) Bio/Technology 4:790-795; Top, et al. (1971) J. Infect. Dis. 124:148-154; Chanda, et al. (1990) Virology 175:535-547), particles of viral or synthetic origin (see, e.g., Kofler, et al. (1996) J. Immunol. Methods 192:25-35; Eldridge, et al. (1993) Sem. Hematol. 30:16-24; Falo, et al. (1995) Nature Med. 1:649-653), adjuvants (Warren, et al. (1986) Annu. Rev. Immunol. 4:369-15 388; Gupta, et al. (1993) Vaccine 11:293-306), liposomes (Reddy, et al. (1992) J. Immunol. 148:1585-1589; Rock (1996) Immunol. Today 17:131-137), or, naked or particle absorbed cDNA (Ulmer, et al. (1993) Science 259:1745-1749; Robinson, et al. (1993) Vaccine 11:957-960; Shiver, et al., p 423, in Kaufmann (ed. 1996) Concepts in Vaccine Development de Gruyter; Cease and Berzofsky (1994) Annu. Rev. Immunol. 12:923-989; and Eldridge, et al. 20 (1993) Sem. Hematol. 30:16-24). Toxin-targeted delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

Vaccine compositions often include adjuvants. Many adjuvants contain a substance

designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, Bortadella pertussis, or

Mycobacterium tuberculosis derived proteins. Certain adjuvants are commercially available as, e.g., Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI);

Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham,

Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron, or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes;

biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

Vaccines can be administered as nucleic acid compositions wherein DNA or RNA encoding one or more of the polypeptides, or a fragment thereof, is administered to a patient. This approach is described, for instance, in Wolff et. al. (1990) Science 247:1465-1468, as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; WO 98/04720; and in more detail below. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivicaine, polymers, peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (see, e.g., U.S. Patent No. 5,922,687).

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For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus, e.g., as a vector to express nucleotide sequences that encode cancer polypeptides or polypeptide fragments. Upon introduction into a host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover, et al. (1991) Nature 351:456-460. A wide variety of other vectors are availablel for therapeutic administration or immunization, e.g., adeno and adeno-associated virus vectors, retroviral vectors, Salmonella typhi vectors, detoxified anthrax toxin vectors, and the like. See, e.g., Shata, et al. (2000) Mol Med Today 6:66-71; Shedlock, et al. (2000) J. Leukoc. Biol. 68:793-806; Hipp, et al. (2000) In Vivo 14:571-85.

Methods for the use of genes as DNA vaccines are well known, and include placing a cancer gene or portion of a cancer gene under the control of a regulatable promoter or a tissue-specific promoter for expression in a cancer patient. The cancer gene used for DNA vaccines can encode full-length cancer proteins, but more preferably encodes portions of the cancer proteins including peptides derived from the cancer protein. In one embodiment, a patient is immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived from a cancer gene. For example, cancer-associated genes or sequence encoding subfragments of a cancer protein are introduced into expression vectors and tested for their immunogenicity in the context of Class I MHC and an ability to generate cytotoxic T cell responses. This procedure

provides for production of cytotoxic T cell responses against cells which present antigen, including intracellular epitopes.

In a preferred embodiment, DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the cancer polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are available.

In another preferred embodiment, cancer genes find use in generating animal models of cancer. When the cancer gene identified is repressed or diminished in cancer tissue, gene therapy technology, e.g., wherein inhibitory or antisense RNA directed to the cancer gene will also diminish or repress expression of the gene. Animal models of cancer find use in screening for modulators of a cancer-associated sequence or modulators of cancer. Similarly, transgenic animal technology, including gene knockout technology, e.g., as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence or increased expression of the cancer protein. When desired, tissue-specific expression or knockout of the cancer protein may be necessary.

It is also possible that the cancer protein is overexpressed in cancer. As such, transgenic animals can be generated that overexpress the cancer protein. Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene. Animals generated by such methods will find use as animal models of cancer and are additionally useful in screening for modulators to treat cancer.

Kits for Use in Diagnostic and/or Prognostic Applications

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For use in diagnostic, research, and therapeutic applications suggested above, kits are also provided by the invention. In diagnostic and research applications, such kits may include at least one of the following: assay reagents, buffers, cancer-specific nucleic acids or antibodies, hybridization probes and/or primers, antisense polynucleotides, ribozymes, dominant negative cancer polypeptides or polynucleotides, small molecule inhibitors of cancer-associated sequences etc. A therapeutic product may include sterile saline or another pharmaceutically acceptable emulsion and suspension base.

In addition, the kits may include instructional materials containing instructions (e.g., protocols) for the practice of the methods of this invention. While the instructional materials

typically comprise written or printed materials, they are not limited to such. A medium capable of storing such instructions and communicating them to an end user is contemplated by this invention. Such media include, but are not limited to, electronic storage media (e.g., magnetic discs, tapes, cartridges, chips), optical media (e.g., CD ROM), and the like. Such media may include addresses to internet sites that provide such instructional materials.

The present invention also provides for kits for screening for modulators of cancer-associated sequences. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise one or more of the following materials: a cancer-associated polypeptide or polynucleotide, reaction tubes, and instructions for testing cancer-associated activity. Optionally, the kit contains biologically active cancer protein. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user. Diagnosis would typically involve evaluation of a plurality of genes or products. The genes will typically be selected based on correlations with important parameters in disease which may be identified in historical or outcome data.

EXAMPLES

Example 1: Gene Chip Analysis

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Molecular profiles of various normal and cancerous tissues were determined and analyzed using gene chips. RNA was isolated and gene chip analysis was performed as described (Glynne, et al. (2000) Nature 403:672-676; Zhao, et al. (2000) Genes Dev. 14:981-993).

Table 1 lists medical conditions, abnormatities, or organs affected by disease, referred to in Tables 2A-68, for which markers have been identified, and other related medical conditions (including various stages and/or metastases) in which those markers will also be useful, e.g., in therapeutic, diagnostic, prognostic, subsetting, vaccine, and other uses.

blood vessels/anglogenests; hemangtomas, lymphengtomas, wound healing, tissue remodeling, psoriasis, ischemic, heart disease, inflammatory diseases (e.g., arthitis, asthma, chronic branchilis), atherosclerosis, endometricois, presumed coular histoplasmosis syndrome, hypoda, solid tumors, lymphomas, autoimmune diseases (e.g., arthrus, asthma, chronic arthritis, pigmented vitionodular synovitis, etc.), retinal newascutarization syndromes (e.g., diabetic retinopathy, macular degeneration, presumed ocular histoplasmosis syndrome, etc.), scientisconjunctivitis, hypertrophic scars (kelokl), birth control, utarine fibroids 5

bladder: carcinoma in situ, papilary carcinomas, transitional cell carcinoma bone marrow: Ewing sarcoma, sarcomas arising from skeletal and extraskeletal connective tissues, including the peripheral nervous system

brain: glioblastoma, oligodendroglioma, anablastic astrocytoma, meningioma, medulablastoma, neuroblastoma, ependymoma, schwannoma, cranlopharyngioma, pineoblastoma, 10

breast: ductal carcinoma in situ, lobular carcinoma in situ

cervix: cancer of the cervix, vagina, or vulva

colon/rectum: precancerous colorectal disease (e.g., neoplastic polyps (adenomas), familial adenomatous polyposis, utcerative colitis), colon cancer, e.g., epithelial tumor (e.g., adenocarcinoma, muchous adenocarcinoma, signet-ring cell adenocarcinoma, squamous cell carcinoma, adenosquamous carcinoma, undifferentiated carcinoma, unclassified carcinoma, carinoid tumor (e.g., argentaffin, nonargentaffin, composite), non-epithelial tumor (e.g., leimyo sarcoma, others), inflammatory bowel disease (e.g., utcerative colitis, 15 Crohn's disease (granulomatous colitis), dysptasia), rectal cancer, cancer of the anal region (e.g., squamous cell carcinoma, transitional carcinoma, adenocarcinoma, carcinoma, papillary viltous carcinoma, mucinous adenocarcinoma, melanoma)

esophagus: premalignant or predisposing conditions (e.g., esophagitis), squarmous cell cancers (e.g., cancers of the head and neck, hung, or cervix), gastrodigestive carcinomas 20

- (e.g., cencers of the stornach, colon, or rectum)
 fibrosis: lung fibrosis (idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, interstitial pneumonitis, nonspecific idiopathic pneumonitis), chronic obstructive pulmonary disease (e.g., emphysema, chronic bronchitis), asthma, bronchiectasis, cirrhosis (liver fibrosis), renal fibrosis, scleroderma, wound healing
- head and neck: turnors of the nesal cavity, paransasi sinuses, nasopharyno, oral cavity, oral pharyno, tip, laryno, hypopharyno, salivary glands, paragangliomas, esophagus kidney: clear cell (nonpapillary) carcinoma, papillary carcinoma, chromophobe renal carcinoma, hypemephroma, adenocarcinoma, sporadic renal carcinomas, hereditary renal carcinomas (von Hippel-Lindau disease), carcinoma of the renal pelvis, ureteral carcinoma, fibroma, papillary adenoma, anglomyolipoma, oncocytoma 25
- leukocytes; acute lymphoblastic leukemia/lymphoma, malignant transformation of immature, precursor 8 (pre-8) or precursor T (pre-T) lymphocytes, or lymphoblasts, arthritis, inflammation, wound healing
 - liver: hepatitis (e.g., types A, B, C), benign epithelial tumors and tumor bile conditions, primary malignant epithelial tumors, primary malignant mesenchymal tumors, tumors of the gallbladder or bile duct
- geninavora or una outo.

 lung: lung carcinoma (eat cell carcinoma), non-small cell carcinomas (e.g., squamous cell carcinoma, adenocarcinoma, large cell lung carcinoma, carcinoid, granulomatous), fibrosis (idiopathic pulmonary fibrosis, hypersensitivity pneumonitis; interstitial pneumonitis, nonspecific idiopathic pneumonitis), chronic obstructive pulmonary disease (e.g., emphysema, chronic bronchitis), asthma, bronchiectasis, esophageal cancer ovary: ovarian carcinoma (e.g., epithelial (serous lumors, mucinous lumors, endometrioid lumors), germ cell (e.g., teratomas, choriocarcinomas, polyembryomas, embryomal 30
- carcinoma, endodermal sinus lumor, dysgerminoma, gonadoblastoma), stromal carcinomas (e.g., granulosal stromal cell tumors)), falloplan tube carcinoma, pertioneal carcinoma, 35
 - pancreas: adenocarcinoma, ductal adenocarcinoma, mucinous cyst adenocarcinoma, acinar cell carcinoma, unclassified large cell carcinoma, small cell carcinoma, pancreas: adenocarcinoma, ductactatic mucin-hypersecreting tumor, mucinous cyst adenoma, papillary cystic neoplasm, serous cyst adenoma, diabetes melitis, chronic pancreatitis prostate: epithelial neoplasms (e.g., adenocarcinoma, small cell tumors, transitional cell carcinoma, carcinoma in situ, and basal cell carcinoma), carcinosarcoma, non-epithelial neoplasms (e.g., mesenchymal and lymphoma), germ cell tumors, prostatic intraepithelial neoplasia (PIN), hormone independent prostate cancer, benign prostate hyperplasia,
 - skin/melanoma: melanoma, lentigo (common benign localized hyperplasia of melanocytes), nevocellular nevi (congenital or acquired neoplasm of melanocytes), actinic keratosis (overgrowth of outer layers of skin), basal cell carcinoma, Markel cell carcinoma, benign fibrous histiocytoma (dermal neoplasms of fibroblasts and histiocytes), dermatofibrosarcoma protuberans (well differentiated fibrosarcoma of the skin), xenthomas (tumor-like collections of foamy histicoytes within the demis), dermat vascular tumors, sebormelic keratoses (benign tumor), acanthosis nigricans (benign or malignant hyperplasia and hyperpigmentation of skin), and squamous cell carcinomas of the skin, lung, cervix, esophagus, uterus, head, neck, or bladder
 - stomach: edenocarcinoma, squamous cell carcinoma, adenoacanthoma, carcinoid, leiomyosarcoma, gastritis (chronic atrophic, H. pylori associated), hyperplastic polyps, lipoma, leiomyoma, esophageal adenocarcinomas
 - testicles: germ cell tumors (including seminomas, embryonal carcinomas, teratomas, chorlocarcinomas, yolk sac tumors), sex chord stromal tumors (including Leydig cell tumors, Sertoli cell turnors, and Granulosa cell turnors), garm cell and gonadal stromal elements (e.g., gonadoblastomas), adnexal and paratesticular turnors (e.g., mesotheliomas, soft
 - tissue sarcomas, and adnexal of the rete testes), miscellaneous neoplasms (including carcinold, hymphoma, and cysts)
 uterus: epithelial tumors (e.g., endometrioid, papillary endometrioid, papillary serous, clear cell, mucinous), mesenchymal tumors (e.g., endometrial stromal sarcoma, leiomyosarcoma, nonspecific sarcomas), mixed tumors (e.g., malignant mixed mullerian tumors, adenosarcoma)
- Tables 28-66C list accession numbers for Pkeys tacking UnigenelD's for Tables 2A-66C, respectively. For each probeset is listed gene cluster number from which oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using 55 Clustering and Alignment Tools (DoubleTwist, Oakland California). Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.
- Tables 2C-66C list genomic positioning for Pkeys lacking Unigene ID's and accession numbers in Tables 2A-66C, respectively. For each predicted exon is listed genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed. 60

TABLE 2A: ABOUT 1031 GENES UP-REGULATED IN ACUTE LYMPHOCYTIC LEUKEMIA (ALL)

Table 2A issued 1031 genes up-regulated in acute lymphocytic leukemia (ALL) compared to normal adult tissues. These were selected from 35403 probesets on the Affymetriz/Eos Hu01 GeneChip array such that the ratio of "average" leukemia to "average" normal adult tissues was greater than or equal to 1.7. The "average" leukemia level was set to the 75th percentile amongst various ALL samples. The "everage" normal adult tissue level was set to the 85th percentile amongst various non-malignant tissues. In order to 65 remove gene-specific background levels of non-specific hybridization, the 7.5th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Unique Eos probeset identifier number Pkey:

Exemplar Accession number, Genbank accession number ExAcon:

70 UnigenelD: Unigene number Unigene Title: Unigene gene title

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R1: Ratio of leukemia to normal body tissue

	Pkev	ExAcc	UniGeneID	UniGene Title	R1
75	100458	874019	Hs.247979	pre-B lymphocyte gene 1	46.8
	113089	T40707	Hs.270862	ESTs	20.4
	106956	R06428	Hs.226351	ESTs	15.8
	101447	M21305		gb:Human alpha satellite and satellite 3	13.8
	113009	T23699	Hs.7245	ESTs	12.5
80	126947	Z40778	Hs.191837	ESTs	11.4
	100893	BE245294	Hs.180789	S164 protein	11.1
	101050	AU077324	Hs.1832	neuropeptide Y	11.0
	132114	NM_006152	Hs.40202	lymphold-restricted membrane protein	10.7

	101304 AA001021	Hs.6685	thyroid hormone receptor interactor 8	10.4 9.1
	105667 AA767526	Hs.22030 Hs.15069	paired box gene 5 (B-cell lineage specif ESTs	9.0
	112727 T91029 109788 T79971	Hs.12432	Homo sapiens clone 24407 mRNA sequence	8.7
5	113374 T79925	Hs.269165	ESTs, Wealdy similar to ALU1_HUMAN ALU S	7.8 7.7
	130466 W19744	Hs.180059	Homo sapiens cDNA FLJ20653 fis, clone KA	7.7 7.6
	109384 AA219172 112602 AW004045	Hs.86849 Hs.203365	ESTs ESTs	6.6
	112602 AW004045 125278 Al218439	Hs.129998	enhancer of polycomb 1	6.5
10	112167 N99591	Hs.25587	ESTs, Weakly similar to T00329 hypotheti	6.4 5.8
	116355 AA789133	Hs.88650	ESTS	5.5
	123440 Al733692 100918 AK001335	Hs.112488 Hs.31137	ESTs protein tyrosine phosphatase, receptor t	5.4
	101879 AA176374	Hs.243886	nuclear autoantigenic sperm protein (his	5.4
15	109260 AW978515	Hs.131915	KIAA0863 protein	5.4 5.4
	129213 Al146494	Hs.109525	ESTs, Weakly similar to IRX2_HUMAN IROQU gb:EST52657 Fetal heart II Homo saptens	5.4 5.4
	120809 AA346495 105498 H68279	Hs.24937	transformer-2 alpha (hira-2 alpha)	5.1
	114840 AA447591	Hs.87359	ESTs, Highly similar to RB18_HUMAN RAS-R	5.0
20	103304 BE561801	Hs.2484	T-cell leukemia/lymphoma 1A	4.9 4.8
	113983 W87415	Hs.55296	HLA-B associated transcript-1 hypothetical protein MGC5370	4.8
	115844 Al373062 120712 AF193339	Hs.332938 Hs.102506	eukaryotic translation initiation factor	4.8
	107794 AA019255	113.102500	gb:ze56e10.s1 Soares retina N2b4HR Homo	4.7
25	135101 U82275	Hs.94498	leukocyte immunoglobulin-like receptor,	4.6 4.6
	129898 Al672731	Hs.13256	ESTs ESTs	4.6
	113494 T91451 115004 AA329340	Hs.86538 Hs.4867	mannosyl (alpha-1,3-)-glycoprotein beta-	4.5
	113074 AK001335		protein tyrosine phosphatase, receptor t	4.5
30	112326 R55822	Hs.4268	ESTs	4.4 4.4
	105169 BE245294		S164 protein EST	4.3
	117048 H89732 123133 AA487264	Hs.230113 Hs.154974	Homo saplens mRNA; cDNA DKFZp667N084 (fr	4.3
	111394 AA412227		hypothetical protein FLJ12876	4.3
35	106112 AL117518		KIAA0978 protein	4.2 4.2
	114414 AW152160 125219 Al804331	6 Hs.182113 Hs.99423	ESTs ATP-dependent RNA helicase	4.2
	125219 Al804331 114995 AA769266		ESTs	4.2
• •	123338 AA504249		ESTs	4.1 4.1
40	126666 AA648886		ESTs	4.1
	112908 BE281000 116640 X89984) Hs.3530 Hs.211563	TLS-associated serine-arginine protein 2 B-celt CLL/lymphoma 7A	4.0
	109292 AW97574		KIAA1702 protein	4.0
	131724 AK00133	5 Hs.31137	protein tyrosine phosphatase, receptor t	4.0 4.0
45	119772 AJ250839		gene for serine/threonine protein kinase	4.0
	134453 Al272141 123562 AA17708		SRY (sex determining region Y)-box 4 ESTs	4.0
	103226 X75042	Hs.44313	v-rel avian reticuloendotheliosis viral	3.9
50	127610 AA96086		ESTs, Highly similar to unnamed protein	3.9 3.9
50	119873 Al660149		lymphoid enhancer-binding factor 1 transcription factor (SMIF gene)	3.9
	115553 AJ27598 131844 Al419294		ESTs	3.8
	123360 AA53271		ESTs	3.8
<i>E E</i>	111180 AI798851		hemoglobin, gamma G	3.8 3.8
55	129426 AF07795 105434 AA25211		Protein inhibitor of activated STAT X ESTs	3.8
	119073 BE24536		ESTs	3.8
	127003 AW8165	15 Hs.173540	ATPase, Class V, type 10D	3.7 3.7
<i>4</i> 0	119325 T51136	Hs.90489	ESTs ribosomal protein L44	3.7
60	115998 AA44848 119830 AW0549		Homo sapiens cDNA FLJ12366 fis, clone MA	3.7
	104584 AA7045		ESTs	3.6
	105212 AA2053	34 Hs.324278	Homo sapiens mRNA; cDNA DKFZp566M063 (f	3.6 3.6
65	109223 AW0007		ESTs ESTs	3.5
65	112605 R79374 105733 AA7676		ESTS	3.5
	120562 BE2445		hypothetical protein FLJ10330	3.5
	112268 W39609		solute carrier family 6 (neurotransmitte	3.5 3.5
70	127834 AW3010		EST hypothetical protein MGC2454	3.5
70	115147 AA7457 115185 BE2996		hypothetical protein FLJ20357	3.5
	113921 AW976		hypothetical protein FLJ22402	3.5
	115835 AA5214	110 Hs.41371	ESTs	3.5 3.5
75	123503 AW975		ESTs, Weakly similar to 178885 serine/th transcription factor 3 (E2A immunoglobul	3.4
75	128527 AA5045 128743 R44284		transcription factor 3 (E2A literatioglobus heterogeneous nuclear ribonucleoprotein	3.4
	117031 H88353		gb:yw21a02.s1 Morton Fetal Cochlea Homo	3.4
	123149 Al7341	79 Hs.105676	ESTs	3.4 3.4
80	102581 AU0771		enhancer of zeste (Drosophila) homolog 2 hematopoietically expressed homeobox	3.4
00	103158 BE242 107599 AW664		ESTs	3.4
	125556 AB033	064 Hs.334806	KIAA1238 protein	3.4 3.4
	103331 Al8254	63 Hs.147996	•	3.4
			05	

	114387	AI655141	Hs.107720	ESTs, Wealtly similar to A54295 Interfer	3.4
	119040	R02394	Hs.269435	ESTs, Moderately similar to PC4259 femi	3.4
	100305	NM_004941		DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	3.4
5	129818 133445	171092 AC005262	Hs.172572	hypothetical protein FLJ20093	3.3
_	132111	AW500857	Hs.73797 Hs.40137	guantine nucleotide binding protein (G pr anaphase-promoting complex 1; melotic ch	3.3
	105292	AF128542	Hs.166846	polymerase (DNA directed), epsilon	3.3 3.3
	118397	BE139479	Hs.161492	EST8	3.3
10	118922	AW206193	Hs.91065	hypothetical protein DXFZp761B2423	3.2
10	132344 129889	AW977189 AA810932	Hs.45719 Hs.131899	KIAA0823 protein	3.2
	123670	Al189844	Hs.112708	ESTs, Wealdy similar to T00370 hypotheti ESTs, Moderately similar to ZN91_HUMAN Z	3.2 3.2
	116291	AW410377	Hs.41502	hypothetical protein FLJ21276	3.2
15	105289	AB020638	Hs.103000	KIAA0831 protein	3.2
15	105583	AA278907	Hs.3530	TLS-associated serine-arginine protein	3.2
	104796 111657	BE620712 R07364	Hs.33026 Hs.268667	hypothetical protein PP2447	3.2
	134174	AF283770	Hs.79630	ESTs, Weakly similar to ALU1_HUMAN ALU CD79A antigen (immunoglobulin-associated	3.2 3.2
20	126077	M78772	Hs.210836	ESTs	3.1
20	133733	AK000476	Hs.75798	hypothetical protein	3.1
	124847 127879	W07701	Hs.304177	Homo sapiens clone FLB8503 PRO2286 mRNA,	3.1
	113108	AA768098 AW516695	Hs.189079 Hs.8438	ESTs ESTs	3.1
	110343	AW136703	Hs.17268	ESTs	3.1 3.1
25	102935	BE561850	Hs.80506	small nuclear ribonucleoprotein polypept	3.1
	111676	AB040882	Hs.109778	KIAA1449 protein	3.1
	127311 108830	AA492582 AA131743	Hs.322404	hypothetical protein MGC4175	3.1
	111330	BE247767	Hs.193352 Hs.18166	ESTs KIAA0870 protein	3.1
30	104246	AF016032	Hs.201377	lysosomal apyrase-like 1	3.1 3.1
	126668	AA011616	Hs.269877	EST8	3.1
	124724	H20816	Hs.112423	Homo saplens mRNA; cDNA DKFZp586i1420 (f	3.1
	114794 134599	A1751157 X99226	Hs.101395 Hs.284153	hypothetical protein MGC11352	3.1
35	130314	NM_014674		Fancori anemia, complementation group A KIAA0212 gene product	3.0
	100265	D38521	Hs.112396	KIAA0077 protein	3.0 3.0
	115005	A1760825	Hs.111339	ESTs	3.0
	123433	AW450922	Hs.112478	ESTs	3.0
40	127798 117403	AA737068 H84455	Hs.294078 Hs.40639	ESTs ESTs	3.0
	107111	Al298448	Hs.22670	chromodomain helicase DNA binding protel	3.0 3.0
	105698	AW957300	Hs.294142	ESTs, Weakly similar to C55663 oligodend	3.0
	108358	M81933	Hs.1634	cell division cycle 25A	3.0
45	132066	A1929392	Hs.181195	OnaJ (Hsp40) homolog, subfamily B, membe	2.9
43	130303 104596	BE245294 AF067804	Hs.180789 Hs.15423	S164 protein hypothetical protein HDCMC04P	2.9
	112197	NM_003655		ESTs	2.9 2.9
	132809	AF036144	Hs.5734	meningioma expressed antigen 5 (hyaturon	2.9
50	100877	X80821	Hs.27973	KIAA0874 protein	29
50	108147 133674	AJ972094 AW851121	Hs.286221 Hs.75497	Homo sepiens cDNA FLJ13741 fis, clone PL	2.9
	129001	AA443323	Hs.107812	Homo sapiens cDNA: FLJ22139 fis, clone H BPOZ protein	2.9 2.9
	131920	BE002320	Hs.287864	Homo sapiens cDNA FLJ14030 fis, clone HE	2.9
55	134709	NM_006290		tumor necrosts factor, alpha-induced pro	2.8
<i>JJ</i>	113577 115839	AJ300699 BE300266	Hs.278937 Hs.28935	PRO0470 protein	2.8
	129969	N57818	16.20333	transducin-like enhancer of split 1, hom gb:yv59d07.s1 Soares fetal liver spleen	2.8 2.8
	128659	AW630087	Hs.103315	trinucleotide repeat containing 1	2.8
60	105011	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	2.8
00	129294	AF172940	Hs.184542	CGI-127 protein	2.8
	104518 107796	H20816 AA058848	Hs.112423 Hs.60797	Homo sapiens mRNA; cDNA DKFZpS8611420 (f ESTs	2.7 2.7
	106331	AB037742	Hs.24336	KIAA1321 protein	2.7
65	127692	Al021912	Hs.187983	EST8	2.7
05	131916 124971	AA025976	Hs.34569	ESTs .	2.7
	129428	T23800 AA256906	Hs.151001 Hs.111364	hypothetical protein FLJ14728 ESTs, Weakly similar to ubiquitous TPR m	2.7
	118348	AW408586	Hs.91052	ESTs, Moderately similar to ALU5_HUMAN A	2.7 2.7
70	113219	T59257	Hs.269528	ESTs, Moderately similar to ALU8_HUMAN A	27
70	131720	Z68128	Hs.3109	Rho GTPase activating protein 4	2.7
	109593 135359	AW196801 AF043722	Hs.6685 Hs.99491	thyroid hormone receptor interactor 8	27
	131689	AB012124	Hs.30696	RAS guanyl releasing protein 2 (calcium transcription factor-like 5 (basic helix	2.7 2.7
75	117457	N29682	Hs.44071	ESTs, Wealthy similar to ALU5_HUMAN ALLU	27
75	121073	H46199	Hs.112184	DKFZP588J0619 protein	2.7
	125069 116456	H81306 Al381911	Hs.194485 Hs.334859	ESTs	2.7
	124271	AW293223	Hs.8928	KIAA1814 protein hypothetical protein FLJ20291	2.7 2.7
00	112369	AW966243	Hs.4243	hypothetical protein FLJ12650	2.7
80	115866	AW062629	Hs.52081	KIAA0867 protein	2.7
	132543 124494	BE568452 N54831	Hs.5101 He 271381	protein regulator of cytokinesis 1	2.7
	104799	AA029703	Hs.271381	ESTs, Weakly similar to 138022 hypothet gb:ze95h08.s1 Soares_fetal_heart_NbHH19W	27 27
				Annual Annual Annual Community (April 1944	4-1

	120510 Al796395 Hs.111	77 ESTs	2.6
	129781 AA306090 Hs.124	07 ESTs	26
	122698 AA456112 Hs.994		26 26
5	106995 AB023139 Hs.378 105502 BE464016 Hs.238		2.6
,	128671 Al885045 Hs.211	586 phosphoinositide-3-kinase, regulatory s	2.6
	107059 BE614410 Hs.230		2.6 2.6
	126502 T10077 Hs.134 129703 BE388665 Hs.179	ago Homo saoiens, clone IMAGE:3457003, mRNA	26
10	111219 N68836 Hs.192	47 ESTs, Moderately similar to ALUC_HUMAN	26
	133529 W45623 Hs.745		2.6 2.6
	125626 Al038854 Hs.180 111189 N67603 Hs.272		2.6
	111189 N67603 Hs.272 113146 BE151985 Hs.572		2.6
15	125562 Al494372 Hs.989	68 hypothetical protein FLJ23058	2.6 2.6
	102263 U29171 Hs.756		2.6
	118835 AA535246 Hs.504 103141 X66113 Hs.754		2.6
	109598 R40515 Hs.21	MR FSTs	2.6
20	127262 AA828125	gb:od71e09.s1 NCL_CGAP_Ov2 Homo saplens	2.6 2.6
	129620 D79338 Hs.23		26
	125905 Al678638 Hs.64 123255 AA830335 Hs.10		26
	133160 N54968 Hs.66	309 hypothetical protein MGC11061	2.6 2.6
25	109638 AW977747 Hs.11		2.6
	119896 AA731836 Hs.13 134770 M89957 Hs.89		2.6
	119403 AL117554 Hs.11	9908 nucleolar protein NOP5/NOP5B	2.6
00	129563 AF119664 Hs.27		2.6 2.6
30	111719 AI655806 Hs.17		2.6
	103982 AA218558 Hs.79 125032 T74884	gb:vc58d02.s1 Stratagene liver (937224)	2.5
	131426 AL122045 Hs.26	703 CCR4-NOT transcription complex, subunit	2.5 2.5
25	131938 AF176085 Hs.3		2.5
35	102450 U48251 Hs.7 133761 AF041430 Hs.7		2.5
•	126339 AA152106 Hs.4		2.5
	118967 Al668670 Hs.2	16756 ESTs	2.5 . 2.5
40		93510 EST 4825 ESTs, Weakly similar to KIAA1503 protein	2.5
40	114092 H81213 Hs.1 113247 T63856 Hs.1	3430 ESTs, Weakly similar to 2109260A B cell	2.5
		39433 ESTs	2.5 2.5
	106657 AW854339 Hs.3	hypothetical protein FLJ11937	25 25
45	126127 N95428	gb:zb80d09.s1 Soares_senescent_fibroblas 5119 ESTs, Weakly similar to YEX0_YEAST HYPOT	2.5
43		24751 ESTs	2.5
	120132 W57554 Hs.1	25019 ESTs	2.5 2.5
		72106 ESTs, Weakly similar to 138022 hypotheti 8008 ESTs	2.5
50		8008 ESTs 8661 Homo sapiens cDNA FLJ10071 fis, clone HE	2.5
50		63988 ESTs	2.5 2.5
		18178 hypothetical protein FLJ23468 15319 ribonucleotide reductase M2 polypeptide	2.5
		75319 ribonucleotide reductase M2 polypepude 806155 chorionic somatomammotropin hormone 1 (p	2.5
55		78915 GA-binding protein transcription factor,	2.5
	105393 AF167570 Hs.	256583 interleukin enhancer binding factor 3, 9	2.5 2.5
		78546 ATPase, Ca++ transporting, ptasma membra 88500 mitogen-activated protein kinase 8 inte	2.5
		284288 hqp0256 protein	2.5
60	113283 T66813 Hs.	12947 EST	2.5 2.5
		47790 EST 96820 ESTs	2.5
		96820 ESTs 236463 Homo saplens mRNA; cDNA DKFZp586l0521 (f	2.5
		193044 potassium inwardly-rectifying channel, s	2.5 2.5
65		30348 ESTs 172182 poly(A)-binding protein, cytoplasmic 1	2.5
		172182 poly(A)-binding protein, cytoplasmic 1 6685 thyroid hormone receptor interactor 8	2.5
	113947 W84768	gb:zh53d03.s1 Soares_fetal_liver_spleen_	2.5
70	132112 AL021938 Hs	40154 jumonji (mouse) homolog	2.5 2.4
70		.158210 hypothetical protein MGC2555 .43005 RAB9-like protein	2.4
		.40838 ESTs	2.4
	113119 T47910	gb:yb18b11.s1 Stratagene fetal spleen (9	2.4 2.4
75	133726 AJ803188 H	.252716 oxysterol-binding protein-related protei	2.4
75		.187634 ESTs .98132 ESTs	2.4
	131136 AB033099 H	.23413 KIAA1273 protein	24
	126589 AW027809 H	:.187698 Homo sapiens cytomegalovirus partial fus	24 24
80		. 40193 hypothetical protein KIAA1259 s. 183842 ubiquitin B	24
50		£144941 ESTs	2.4
	124457 AK000680 H	s.266175 phosphoprotein associated with GEMs	2.4 2.4
	113721 AF143885 H	s.18190 EST	2.4

		AK000157	Hs.108502	hypothetical protein FLJ20150	24
		AA608705	Hs.187772	ESTs	2.4 2.4
		AA805331 R50752	Hs.112637 Hs.23856	ESTs hypothetical protein MGCS297	24
5		F13687	Hs.227976	EST	2.4
•	101759	M80244	Hs.184601	solute carrier family 7 (cationic amino	24
	131686	NM_012296	Hs.30687	GRB2-associated blinding protein 2	24
	127841	AW136558	Hs.125246	ESTs	24
10	102737	R51790	Hs.239483	Human clone 23933 mRNA sequence	2.4 2.4
10	129673 133095	D38552 BE046490	Hs.1191 Hs.180677	KIAA0073 protein zinc finger protein 162	2.4
	124540	N63232	115.100077	gb:yz39a12.s1 Morton Fetal Cochlea Homo	24
	113609	T93263	Hs.16875	ESTs, Wealdy similar to S23650 retrovtr	2.4
	128826	Z40313	Hs.106330	Homo saplens clone IMAGE:23371, mRNA seq	2.4
15	129059	AW069534	Hs.279583	CGI-81 protein	24
	134092	AA218558	Hs.7905	sorting nextn 9	2.4
	132317	BE262438	Hs.44592	beta-1,4 mannosyltransferase	2.4 2.4
	135278	AA399542	Hs.229671	EST, Moderately similar to PEPTIDYL-PROL putative translation initiation factor	24
20	128468 127407	T23625 AW089514	Hs.150580 Hs.279681	heterogeneous nuclear ribonucleoprotein	24
20	132342	AW162758	Hs.45232	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.4
	113518		Hs.323954	postmeiolic segregation increased 2-lik	2.4
	100330	AW410976		minichromosome maintenance deficient (S.	2.4
0.5	116046	BE395293	Hs.94491	hypothetical protein FLJ20297	2.4
25	123910	AA621262	Hs.179923	ESTs, Weakly similar to S65657 alpha-1C-	2.4 2.4
	101651	AL037111	Hs.75641	galactose-1-phosphate uridylyltransferas	24
	100114 125038	X02308 AA812234	Hs.82962 Hs.270134	thymidylate synthetase hypothetical protein FLJ20280	2.4
	135191	X16866	Hs.301086	cytochrome P450, subfamily IID (debrisog	2.4
30	123258	AA490929	Hs.105274	ESTs, Weakly similar to RMS1_HUMAN REGUL	2.4
50	132380	AW373665	Hs.46853	ESTs	24
	114046	BE018658	Hs.141003	Homo sapiens cDNA: FLJ21691 fis, clone C	2.3
	133582	BE391579	Hs.75087	Fas-activated serine/threonine kinase	23
25	134839	D63479	Hs.115907	diacylglycerol kinase, delta (130kD)	23 23
35	105734	AI952797	Hs.10888 Hs.250959	hypothetical protein FLJ21709 histatin 1	. 23
•	101086 118349	AA382524 N63786	Hs.94149	ESTs, Wealty similar to ALU1_HUMAN ALU S	2.3
	101194	L20971	Hs.188	phosphodiesterase 4B, cAMP-specific (dun	2.3
	130588	AL030996	Hs.16411	hypothetical protein LOC57187	2.3
40	101875	BE241753	Hs.74592	special AT-rich sequence binding protein	2.3
	118751	N74210	Hs.50454	ESTs	2.3
	125174	W51835	Hs.231082	EST	2.3 2.3
	105966	AA142984	Hs.5344 Hs.184721	adaptor-related protein complex 1, gamma ESTs	2.3
45	104624 131263	AA353125 AU077002	Hs.24950	regulator of G-protein signalling 5	2.3
1.5	105014	AA121123	Hs.269267	ESTs, Weakly similar to AF161361 1 HSPC	2.3
	123423	AA598484		gb:ae38f04.s1 Gessler Wilms turnor Homo s	23
	128531	H03721	Hs.2953	ribosomal protein \$15a	23
50	108876	Al733860	Hs.191453	ESTs	2.3 2.3
50	130215 132232	BE301883 Al522273	Hs.152707 Hs.42640	glioblastoma amplified sequence ESTs	23
	132664	AJ740461	Hs.54542	ESTs	2.3
	105991	AA215701	Hs.186541	ESTs, Wealdy similar to 138022 hypotheti	2.3
	100253	D38024	Hs.157425	double homeobox, 2	2.3
55	105574	AA045281		phosphoprotein associated with GEMs	2.3
	100780			Immunoglobulin heavy constant mu	2.3 2.3
	134964	AI803516	Hs.272891	htppocatcin-like protein 4 hypothetical protein MGC2668	23
	132786 104952			desmoplakin (DPI, DPII)	2.3
60	119127			ESTs	23
• • •	104857		Hs.19058	ESTs, Moderately similar to S65657 alpha	2.3
	107592			ESTs	2.3
	113378		Hs.14757	ESTs	2.3 2.3
65	129228		Hs.239307	tyrosyl-IRNA synthetase	2.3
65	106898 130734			Hamo saplens cDNA FLJ14302 fis, clone PL KIAA1052 protein	2.3
	125728			B-cell CLL/lymphoma 11B (zinc finger pro	2.3
	113697		Hs.17992	Homo sepiens mRNA; cDNA DKFZp434J1726 (f	2.3
	107104	AU076640		nucleolar protein 1 (120kD)	2.3
70	134267			RAE1 (RNA export 1, S.pombe) homolog	23
	105777		Hs.23096	· ESTs	2.3 2.3
	115306			ESTs	2.3
	133363 129535			chimerin (chimaerin) 1	2.3
75	121520			ESTs	2.3
, ,	123808			gb:ee58g11.s1 Stratagene lung carcinoma	2.3
	105700) AW58083	0 Hs.35254	hypothetical protein FLB6421	23
	120820			EST	2.3
٥٨	12872			phosphoprotein associated with GEMs	2.3 2.3
80	10771		Hs.220687	ESTs MAD (mothers against decapentaplegic, Dr	23
	102564 13186		Hs.79067 16 Hs.33532	zinc finger protein 151 (pHZ-67)	2.3
	12233			ESTs, Moderately similar to T34561 hypot	2.3
				00	

		. =05.405	11- 54520	FOT-	2.3
			Hs.54530 Hs.6755	ESTs RaP2 interacting protein 8	2.3
		E379867	Hs.76038	Isopentenyl-diphosphate delta isomerase	2.3
5			Hs.24567	ESTs, Weakly similar to KBF3_HUMAN NUCL	2.3 2.3
3			Hs.184211 Hs.142569	peptidase (mitochondrial processing) bet ESTs, Weakly similar to 138022 hypotheti	2.3
			Hs.180461	ESTs	2.3
			Hs.180789	S164 protein	2.3 2.3
10			Hs.193195	ESTs, Weakly similar to 2109260A B cell delta steep inducing peptide, immunoreac	2.2
10		1036883 V04606	Hs.75450 Hs.171637	hypothetical protein MGC2628	2.2
		85692	Hs.40730	ESTs	2.2
		223858	Hs.143375	Homo sapiens, clone IMAGE:3840937, mRNA,	2.2 2.2
15		A558677	Hs.8928	hypothetical protein FLJ20291 hypothetical protein FLJ14824	2.2
13		vas31016 R69751	Hs.22399	gb:yi40a10.s1 Soares placenta Nb2HP Homo	2.2
		87179	Hs.16346	ESTs, Wealdy similar to S57447 HPBRII-7	2.2
		W978731	Hs.301824	hypothetical protein PRO1331	2.2 2.2
20		V87353	Hs.89421	CBF1 interacting corepressor gb:nr60h01.s1 NCI_CGAP_Lym3 Homo sapiens	2.2
20		NA642974 N793211	Hs.165372	ESTs, Moderately similar to ALU1_HUMAN A	2.2
		AB040922	Hs.20237	DKFZP566C134 protein	2.2
	105561	AA262881	Hs.323836	ESTs, Weakly similar to alternatively s	2.2 2.2
25		H41694	11- 070004	gb:yo06b06.r1 Soares adult brain N2b5HB5 hetarogeneous nuclear ribonucleoprotein	2.2
25		BE513050 AA984531	Hs.279681 Hs.159293	ESTs	2.2
		AA350256	Hs.323875	EST, Weakly similar to 2109260A B cell	2.2
	131392	AA235153	Hs.26320	TRABID protein	2.2
20		AW503976	Hs.10649	basement membrane-induced gene PAX transcription activation domain inte	2.2
30		U80735 W46653	Hs.173854 Hs.251928	nuclear pore complex interacting protein	2.2
		BE259039	Hs.129953	Ewing sercoma breakpoint region 1	2.2
		AU077018	Hs.3235	keratin 4	2.2 2.2
25	109252	BE440157	Hs.85944	ESTs ESTs	2.2
35	131163 115292	AA099524 AA279956	Hs.23754 Hs.88672	ESTs	2.2
•	122591	Al188219	Hs.99311	ESTs, Weakly similar to HSJ2_HUMAN DNAJ	2.2
	124977	F04819	Hs.190452	KIAA0365 gene product	2.2 2.2
40	103319	X83492	Hs.82359	tumor necrosis factor receptor superfami	2.2
40	100370 128992	D79989 H04150	Hs.184884 Hs.107708	KIAA0167 gene product ESTs	2.2
	129928	Al338993	Hs.134535	ESTs	2.2
	108451	AA079195		gb:zm92h12.s1 Stratagene ovarian cancer	2.2
15	133910	AW835281	Hs.77500	ublquitin specific protease 4 (proto-onc	2.2 2.2
45	106288 134125	AB037742 NM_01478	Hs.24336 1 Hs.50421	KIAA1321 protein KIAA0203 gene product	2.2
	101379	X02994	Hs.1217	adenosine deaminase	2.2
	112276	R53442	Hs.26038	ESTs, Weakly similar to 138022 hypothet	2.2 2.2
50	106251	R12607	Hs.35101	proline-rich Gla (G-carboxyglutamic acid ESTs, Weakly similar to 178885 serine/th	2.2
50	125394 103392	BE178502 X94563	Hs.173772	gb:H.sapiens dbi/acbp gene exon 1 & 2.	2.2
	112853	T02843		gb:FB11H5 Fetal brain, Stratagene Homo s	2.2
	133195	A1434760	Hs.279949	KIAA1007 protein	2.2 2.2
55	135060	AK001887	Hs.259842	protein kinase, AMP-activated, gamma 2 n collagen, type XVI, alpha 1	2.2
55	131381 134104	M92642 L35253	Hs.26208 Hs.79107	mitogen-activated protein kinase 14	2.2
	105225	AA211777		gb:zn57d02.s1 Stratagene muscle 937209 H	2.2
	131320	AA505691	Hs.145696	splicing factor (CC1.3)	2.2 2.2
60	11,4419	Al248013 BE541733	Hs.106532	ESTs, Weakly similar to 138588 reverse t H3 histone, family 38 (H3.38)	2.2
00	103634 134624	AF035119		deleted in liver cancer 1	2.2
	126524	Z45455	Hs.182447	heterogeneous nuclear ribonucleoprotein	2.2
	115556	AL031778		nuclear transcription factor Y, alpha	2.2 2.2
65	111898	R38944	Hs.183475 Hs.75822	Homo sapiens clone 25061 mRNA sequence TGFB1-induced anti-apoptotic factor 1	2.2
UJ	100415 103898	D86970 AA248884		gb:k3517.seq.F Human fetal heart, Lambda	2.2
	129501	AI631811	Hs.180403	ŠTRIN protein	2.2
	127251			ESTs	2.2 2.2
70	100613		Hs.101047	transcription factor 3 (E2A immunoglobul chromosome 6 open reading frame 1	2.2
70	116332 128897	AA49120 AW97913		hypothetical protein	2.2
	111777) Hs.41690	desmocollin 3	2.2
	128604	AI879099	Hs.102397	GIOT-3 for gonadotropin inducible transc	2.2 2.2
75	125585			SON DNA binding protein CGI-76 protein	22
13	129584 114461			ESTs	2.2
	121387			gb:zu66g08.s1 Soares_testis_NHT Homo sap	2.2
	109339	AA31455	4 Hs.27774	ESTs, Highly similar to AF161349 1 HSPC0	2.2
٥٥	129179			ESTs	2.2 2.2
80	106711 106424		5 Hs.143187 Hs.37902	hypothetical protein ESTs	2.2
	123949			EST	2.2
	127256			ESTs, Moderately similar to ALU8_HUMAN	2.2
					90

	404000	4547000	11- 80000		
	104858 132984	AF173867 BE539199	Hs.28906 Hs.62112	glucocorticoid modulatory element bindin zinc finger protein 207	2.2 2.2
	126383	AB032977	Hs.6298	KIAA1151 protein	2.2
_	130557	H51825	Hs.268911	ESTs, Weakly similar to S65824 reverse	2.2
5	119232	AI655226	Hs.117659	ESTs, Wealdy similar to T46481 hypotheti	2.2
	105715	BE621800	Hs.29444	putative small membrane protein NID67	2.2
	124691 113649	R05835 N94768	Hs.110153	ESTs	2.2 2.2
	117049	AW970600	Hs.16400 Hs.303261	ESTs, Weakly similar to KIAA1435 protein ESTs	22
10	128767	M85169	Hs.1050	pleckstrin homology, Sec7 and coiled/coi	2.2
	120602	AA808018	Hs.109302	ESTs	2.2
	107182	AJ311782	Hs.20013	GCIP-Interacting protein p29	2.2
	107357	U63973	Hs.103501	rhodopsin kinase	2.2 2.1
15	125499 126872	H10543 AW450979		gb:ym04c06.r1 Soares infant brain 1NIB H gb:Ui-H-Bi3-ela-a-12-0-UI.s1 NCI_CGAP_Su	2.1
10	113233	T61955	Hs.279867	CGI-59 protein	2.1
	128367	AW611791	Hs.150742	ESTs	2.1
	127432	AW067708	Hs.170311	heterogeneous nuclear ribonucleoprotein	2.1
20	114021	AW235215	Hs.16145	ESTs	21
20	104455 134966	AL110261 AW402389	Hs.157211 Hs.920	DKFZP586B0621 protein modulator recognition factor I	2.1 2.1
	129765	M86933	Hs.1238	amelogenin (Y chromosome)	21
	133461	NM_000762		cytochrome P450, subfamily IIA (phenobar	21
25	109639	AA082650	Hs.6217	Homo saplens cDNA FLJ12521 fis, clone NT	21
25	129794 134869	AF161399 AL157518	Hs.23259 Hs.90421	hypothetical protein FLJ13433 PRO2463 protein	21 21
	110256	H63947	Hs.237955	RAB7, member RAS oncogene family	2.1
	128817	BE395776	Hs.168640	ankylosis, progressive (mouse) homolog	2.1
20	120906	NM_000734	Hs.97087	CD3Z antigen, zeta polypeptide (TIT3 com	2.1
30	134354	M90391	Hs.82127	Interleukin 16 (lymphocyte chemoattracta	2.1
	106048	AW883367	Hs.301732	hypothetical protein MGC5306	2.1 2.1
	128352 115348	AW137413 AA281562	Hs.169942 Hs.292100	ESTs .	21
	123474	AA599209	113.232100	gb:ag34b11.s1 Jia bone marrow stroma Hom	2.1
35	107121	AB015427	Hs.250493	zinc finger protein 219	2.1
	118509	N22617	Hs.4322B	Homo saplens cDNA FLJ11835 fis, clone HE	21
	135051	AJ272141	Hs.83484 Hs.86999	SRY (sex determining region Y)-box 4	2.1 2.1
	109442 126561	AW296134 AA009835	Hs.269521	ESTs, Weakly similar to S65657 atpha-1C- ESTs	2.1
40	129270	AA357185	Hs.109918	ras homolog gene family, member H	21
	125568	AW615396	Hs.105613	ESTs	2.1
	132867	AF226667	Hs.58553	CTP synthase II	2.1
	124656	AW297702	Hs.102915	ESTs	2.1 2.1
45	128954 132985	AA346839 AL045579	Hs.209100 Hs.62113	DKFZP434C171 protein KIAA0717 protein	2.1
	119247	BE269047	Hs.65234	hypothetical protein FLJ20596	2.1
	106686	N66397	Hs.334825	Homo sapiens cDNA FLJ14752 fis, clone NT	21
	131009	AF169802	Hs.22142	cytochrome b5 reductase b5R.2	21
50	112170 130755	BE246743 BE293520	Hs.288529 Hs.18910	hypothetical protein FLJ22635 prostate cancer overexpressed gene 1	2.1 2.1
50	117357	N24829	ns.10310	gb:yx98h12.s1 Soares melanocyte 2NbHM Ho	2.1
	101613	M24283	Hs.168383	intercellular adhesion molecule 1 (CD54)	2.1
	127644	N88858	Hs.155101	ATP synthase, H+ transporting, mitochond	2.1
55	101183	AA442324	Hs.795	H2A histone family, member O	2.1 2.1
55	100420 129879	D86983 AK001696	Hs.118893 Hs.13109	Melanoma associated gene Ran binding protein 11	2.1
	122311		Hs.131915	KIAA0863 protein	2.1
	130566	R85474	Hs.16073	ESTs	21
60	113517	AI874223	Hs.293560	ESTs	21
00	115810	AA426026 Al580150	Hs.187615	ESTs ESTe	2.1 2.1
	129255	Al961727	Hs./10/4 Hs.109804	H1 histone family, member X	2.1
	120766	AA764879	Hs.12570	tubulin-specific chaperone d	21
65	126893	AJ252060	Hs.26320	TRABID protein	2.1
65	115254	AA279024	Hs.269316	ESTs, Weakly similar to \$65657 alpha-1C	2.1 2.1
	105865 120999	BE279383 AI972375	Hs.26557 Hs.29626	plakophilin 3 hypothetical brain protein my038	2.1
	125636	H12382	Hs.25119	ESTs, Weakly similar to YEX0_YEAST HYPOT	21
7 0	117997	N52090	Hs.47420	EST	2.1
70	104333	D82418	Hs.29626	hypothetical brain protein my038	2.1
	134315	AA291183	Hs.81648	hypothetical protein FLJ11021 similar to hypothetical protein FLJ23058	21 21
	135332 107279	AW393883 S57296	Hs.98968 Hs.323910	v-erb-b2 avian erythroblastic leukemia	21
	133097	W03512	Hs.6479	hypothetical protein MGC13272	21
75	112563	AW961220	Hs.29282	mitogen-activated protein kinase kinase	2.1
	121782		Hs.334698	Homo septens, clone MGC:15203, mRNA, com	21
	111567 133912	F12628 H42679	Hs.334786 Hs.77522	hypothetical protein MGC16040 major histocompatibility complex, class	2.1 2.1
	134076		110.11 (16.6	gb:Homo saptens full length insert cONA	21
80	116665	F04405		gb:HSC2SB082 normalized infant brain cDN	2.1
	133562		Hs.74870	H2.0 (Drosophila)-like homeo box 1	21
	129092 106869		Hs.63525 Hs.292679	poly(rC)-binding protein 2 ESTs	2.1 2.1
				· -	

		hypothetical protein FLJ21012	2.1
	130820 AL353934 Hs.288798 126277 AB037847 Hs.15441	Crm (Cramped Drosophila)-like	2.1
	126277 AB037847 Hs.15441 106392 BE350058 Hs.36787	chromodomain helicase DNA binding protei	2.1
_	131902 AA180145 Hs.34348	Homo sapiens mRNA; cDNA DKFZp434P0235 (f	21 21
5	120734 AA299948	gb:EST12544 Uterus tumor I Homo sapiens KIAA1151 protein	21
	113070 AB032977 Hs.6298 116031 AA452239 Hs.103329	KIAA0970 protein	2.1
	116031 AA452239 Hs.103329 123869 AA620924 Hs.112923	EST	21
	106145 AA424791 Hs.5734	meningioma expressed antigen 5 (hyaluron	2.1 2.1
10	109061 AA160896	gb:zo79c07.s1 Stratagene pancreas (93720 Homo sapiens cDNA FLJ13992 fis, clone Y7	2.1
	126348 T16243 Hs.6473	hypothetical protein FLJ20510	2.1
	133231 AK000517 Hs.6844 123132 Al061582 Hs.324179	Homo sapiens cDNA FLJ12371 fis, clone MA	2.1
	117452 N34687 Hs.44054	ninein (GSK3B interacting protein)	2.1 2.1
15	128538 R44214 Hs.101189	ESTs	21
	111945 R40663 Hs.124944	ESTs ESTs, Moderately similar to ALU1_HUMAN	2.1
	119155 R61715 Hs.310598 124362 AL046406 Hs.103483	KIAA1798 protein	2.1
	129198 N57532 Hs.109315	KIAA1415 protein	2.1
20	122059 AA431737 Hs.98749	EST, Moderately similar to T42671 hypoth	21 20
	115643 AA404276 Hs.123253	hypothetical protein FLJ22009 hypothetical protein FLJ10759	20
	112558 AK001621 Hs.15921 115355 AA262292 Hs.88445	FSTs	2.0
	115355 AA262292 Hs.88445 130724 AK001507 Hs.306084	Homo sapiens clone FLB6914 PRO1821 mRNA,	20
25	125360 AW898892 Hs.189741	ESTs	2.0 2.0
	104926 BE298808 Hs.33363	DKFZP434N093 protein	2.0
	119468 Al911535 Hs.6657	hypothetical protein bK1048E9.5 U2(RNU2) small nuclear RNA auxillary fac	2.0
	132891 BE267143 Hs.59271 100237 D30715 Hs.306333	Human PAP (pancreatitis-associated prot	2.0
30	105335 AW291165 Hs.25447	ESTs	2.0
50	106727 AA357001 Hs.34045	hypothetical protein FLJ20764	2.0 2.0
	126053 H64450	gb:yu62d01.r1 Weizmann Otfactory Epithel hypothetical protein FLJ10618	2.0
	115084 BE383668 Hs.42484 128408 Al183407 Hs.143704	EST	2.0
35	128408 Al183407 Hs.143704 132311 Al765559 Hs.20072	myosin regulatory light chain Interactin	2.0
55	113626 T94318 Hs.17359	ESTs, Moderately similar to RL44_HUMAN 6	2.0 2.0
	116379 AA448588 Hs.71252	hypothetical protein DKFZp761C169	2.0
	105474 AL134843 Hs.219614	f-box and leucine-rich repeat protein 11	2.0
40	108922 AA115268 Hs.269263	ESTs EST	2.0
40	123720 AA609734 Hs.112755 128902 AA036637 Hs.107052	ESTs	2.0
	113226 Al821008 Hs.10697	ESTs	2.0
	106798 BE252749 Hs.20558	hypothetical protein FLJ20345	2.0 2.0
4.50	106665 BE090009 Hs.323164		2.0
45	105952 Al767152 Hs.181400	gb:EST75015 Pineal gland II Homo sapiens	2.0
	127248 AA364195 112972 Al684745 Hs.165983		2.0
	128148 AA918175 Hs.126637	ESTs	2.0 2.0
	116176 AA311152 Hs.288708		2.0
50	126457 AA007489 Hs.50382	ESTs serine/threonine protein kinase MASK	2.0
	112610 AW500106 Hs.23643 109249 AA194730 Hs.268189		2.0
	121292 AA401807	gb:zv65f11.s1 Soares_total_fetus_Nb2HF8_	2.0
	128505 AW058113 Hs.102403	Mad4 homolog	2.0 2.0
55	127705 AJ003322	gb:AJ003322 Selected chromosome 21 cDNA KIAA0154 protein; ADP-ribosylation facto	2.0
	134674 AF219139 Hs.87726 107529 BE515065 Hs.29658		2.0
	107529 BE515065 Hs.29658 116411 AA608897 Hs.32161		2.0
	111576 T88827 Hs.15489	ESTs	2.0 2.0
60	127002 AL353940 Hs.24979		2.0
	112662 R85436 Hs.26881		2.0
	126250 AL050391 Hs.32124 101045 J05614	oh-Human proliferating cell nuclear anti	2.0
	117186 H98988 Hs.42612	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.0
65	122110 Al123000 Hs.30124	metanocortin 1 receptor (alpha metanocyt	2.0 2.0
	119849 Al074585 Hs.58440	ESTs ESTs, Weakly similar to 138022 hypotheti	20
	124395 N29963 Hs.27209 131600 NM_004377 Hs.2933		2.0
	131600 NM_004377 Hs.2933 112774 R95770 Hs.3545	t FSTs	2.0
70	109751 AB033492 Hs.6679	hHDC for homolog of Drosophila headcase	2.0
	102377 U40343 Hs.2965		2.0 2.0
	115197 R18656 Hs.6749	ESTs nuclear RNA helicase, DECD variant of DE	2.0
	102808 BE242818 Hs.1796 128869 AA768242 Hs.8061		2.0
75	128869 AA768242 Hs.8061 111229 AW389845 Hs.1108	55 FSTs	20
, ,	129330 AL079310 Hs.9226	0 high-mobility group protein 2-like 1	2.0 2.0
	105448 NM_001186 Hs.1542	76 BTB and CNC homology 1, basic leucine zi	2.0
	127391 AW380893 Hs.1103		2.0
80	102337 AI814663 Hs.1701 121897 AA427419 Hs.2291		2.0
30	107902 AA026627 Hs.6135	8 ESTs	2.0
	129340 H75334 Hs.1105	60 F-box only protein 9	2.0 2.0
	101097 BE245301 Hs.8941	4 chemokine (C-X-C molif), receptor 4 (fus	20

	124864	AW970168	Hs.185706	ESTs	2.0
	118485	AA508515	Hs.291049	ESTs	2.0
	116715	AL117440	Hs.170263	tumor protein p53-binding protein, 1	2.0
5	130743 118677	AL049266 AW971146	Hs.18724 Hs.293187	Homo saptens mRNA; cDNA DKFZp564F093 (fr ESTs	2.0 2.0
•	100020	A1137 1140	113.233107	2013	20
	123252	AW968776	Hs.2875B6	Homo sapiens cDNA FLJ13648 fis, clone PL	2.0
	134977	AL044963	Hs.306121	teukocyte receptor cluster (LRC) encoded	2.0 2.0
10	115334 111790	AA702972 AW769683	Hs.65300 Hs.6734	ESTs ESTs, Wealdy similar to \$26650 DNA-blindi	2.0
10	129101	NM_013403		zinedin	20
	132676	N92589	Hs.261038	ESTs, Wealdy similar to 138022 hypothet	2.0
	111018	AI287912	Hs.3628	mitogen-activated protein kinase kinase	2.0 2.0
15	105933 110679	AF078544 AA004798	Hs.194686 Hs.108311	solute carrier (amily 25 (mitochondrial ESTs, Wealdy similar to T00351 hypotheti	2.0
	120861	AA350394	Hs.96952	ESTs .	2.0
	132430	AW973652	Hs.283105	ESTs .	2.0
	115026 128660	AA251972 AA011597	Hs.188718 Hs.177398	ESTs ESTs	2.0 2.0
20	134554	Al184316	Hs.85273	retinoblastoma-binding protein 6	2.0
	109592	Al198059	Hs.26370	ESTs	2.0
	123636	AA609263	11. 5000	gb:af13c08.s1 Soares_testis_NHT Homo sap	20
	132610 122652	AA160511 AA454641	Hs.5326	amino acid system N transporter 2; porcu gb:zx99d05.s1 Soares_NhHMPu_S1 Homo sapi	20 20
25	120467	AW292562	Hs.187628	ESTs	2.0
	126046	AA804957	Hs.119840	ESTs	20
	128179	AW293689	Hs.127116	ESTs cofactor required for Sp1 transcriptiona	2.0 2.0
	123349 106208	AB033042 AK001674	Hs.29679 Hs.22630	cofactor required for Sp1 transcriptiona	2.0
30	125832	AA628600	Hs.117587	ESTs	2.0
	133317	AC005258	Hs.70830	U6 snRNA-associated Sm-like protein LSm7	2.0
	132886 127447	AW978168 AA386192	Hs.5912 Hs.193482	F-box only protein 7 Homo seplens cDNA FLJ11903 fis, clone HE	2.0 2.0
	133149	AA370045	Hs.6607	AXIN1 up-regulated	2.0
35	120468	AW967675	Hs.96487	ESTs, Highly similar to S08228 ribosomal	2.0
•	106487	A1697340	Hs.135265	Homo sapiens clone FLB8435 PRO2277 mRNA,	2.0 2.0
	126770 120592	A1292320 AA830664	Hs.81361 Hs.143974	heterogeneous nuclear ribonucleoprotein ESTs	2.0
	100944	L07518	Hs.159593	mucin 6, gastric	2.0
40	101887	AW967413	Hs.83958	transducin-like enhancer of split 4, hom	2.0
	125324	R07785	LI ₀ 77401	gb:yf15c06.r1 Soares fetal liver spleen	2.0 2.0
	133906 113408	BE386038 NM 005908	Hs.77492 Hs.115945	heterogeneous nuclear ribonucleoprotein mannosidase, beta A, lysosomal	2.0
	115613	AW136951	Hs.173946	hypothetical protein FLJ 10486	2.0
45	107468	AA740979	Hs.91389	ESTs SUA partial a	2.0
	100554 120476	M95923	Hs.104305	gb:Human 12-lipoxygenase mRNA, partial c death effector filament-forming Ced-4-li	2.0 2.0
	117160	AA322302	Hs.183302	PCTAIRE protein kinase 2	2.0
	115582	AW245047	Hs.136164	cutaneous T-cell lymphoma-associated tu	2.0
50	125536	F08266	Hs.77948	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.0 2.0
	100842 133207	U05597 Al561173	Hs.67688	gb:Human anion exchanger 3 cardiac isofo ESTs	2.0
	122053	AI637498	Hs.98745	ESTs	2.0
55	121080	AA617830	Hs.28310	ESTs	2.0
33	113316 113137	170318 AW952129	Hs.268581 Hs.293225	ESTs ESTs, Weakly similar to FLDED-1 [H.saple	2.0 1.9
	100416	AW505086		minor histocompatibility antigen HA-1	1.9
	133975	C18356	Hs.295944	tissue factor pathway inhibitor 2	1.9
60	103872	AI816078 AK001942	Hs.21756	translation factor sui1 homolog hypothetical protein DKFZp566A1524	1.9 1.9
OO	132439 126082	H81188	Hs.4863 Hs.269571	ESTs	1.9
	124677	R01073		gb:ye84c03.s1 Soares fetal liver spleen	1.9
	123385		Hs.17767	KIAA1554 protein	1.9
65	103138 104867		Hs.225979	gb:H.sapiens SOD-2 gene for manganese su hypothetical protein similar to small G	1.9 1.9
05	128668		Hs.103422	Homo sapiens cDNA FLJ14630 fis, clone NT	1.9
	125826		Hs.7594	solute carrier family 2 (facilitated glu	1.9
	113701		Hs.18026	ESTs	1.9 1.9
70	134447 128895		Hs.83428 Hs.106985	nuclear factor of kappa light polypeptid ESTs	1.9
. •	112719	AI200957	Hs.19301	Homo sapiens, Similar to Nedd-4-like ubi	1.9
	102552		6 Hs.44585	turnor protein p53-binding protein, 2	1.9
	131186 133347		Hs.246112 Hs.71475	KIAA0788 protein acid cluster protein 33	1.9 1.9
75	133388			heterogeneous nuclear ribonucleoprotein	1.9
	112266	AI652534	Hs.25934	ESTs, Wealdy similar to HSHU11 histone H	1.9
	100336		Hs.8127	KIAA0144 gene product	1.9 1.9
	113479 135231		Hs.10739 Hs.74280	ESTs hypothetical protein FLJ22237	1.9
80	123783	AA610112		gb:a/19g05.s1 Soares_lotal_fetus_Nb2HF8_	1.9
	113016		7 Hs.127649	KIAA0414 protein	1.9 1.9
	132761 128536		Hs.323502 Hs.101150	nuclear RNA export factor 1 Horno sapiens, clone IMAGE:4054156, mRNA,	1.9
				p,	

	400000	18/540430	U- 404007	ECTA	1.9
		W518478 A305729	Hs.181297 Hs.18272	ESTs amino acid transporter system A1	1.9
		W591428	Hs.27556	hypothetical protein FLJ22405	1.9
_		W207000	Hs.126857	Homo sapiens cDNA FLJ12936 fis, clone NT	1.9
5		W970672	Hs.9247	protein kinase, AMP-activated, alpha 1 c	1.9
		A1825838	Hs.75206	protein phosphatase 3 (formerly 2B), cat	1.9 1.9
		AJ271379	Hs.76194	ribosomal protein S5	1.9
		A1378328 AL080155	Hs.77256 Hs.226372	enhancer of zeste (Drosophila) homolog 2 DKFZP434J154 protein	1.9
10		T80270	Hs.104788	hypothetical protein LOC55565	1.9
10		BE276738	Hs.74578	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	1.9
		R55094	Hs.26239	Human DNA sequence from clone RP11-438B2	1.9
		D14661	Hs.119	Wilms' tumour 1-associating protein	1.9 1.9
15		AK001440	Hs.131840	hypothetical protein FLJ10578	1.9
15		AW882645	Hs.88044	sprouty (Drasophila) homolog 1 (antagoni KIAA1116 protein	1.9
		NM_014652 AB037810	Hs.227602 Hs.18760	KIAA1389 protein	1.9
		R68351	18.10100	gb:yh99b03.r1 Soares placenta Nb2HP Homo	1.9
		A1272141	Hs.83484	SRY (sex determining region Y)-box 4	1.9
20		Al681270	Hs.99824	BCE-1 protein	1.9
		F08208	Hs.283844	similar to rat tricarboxylate carrier-li	1.9 1.9
		AK001690	Hs.16390	hypothetical protein FLJ10035	1.9
		AA350994 AA100012	Hs.20281 Hs.48827	KIAA1700 hypothetical protein FLJ12085	1.9
25		U73737	Hs.284289	vitiligo-associated protein VIT-1	1.9
		D20433		gb:HUMGS01407 Human promyelocyte Homo sa	1.9
		AA386192	Hs.193482	Homo sapiens cDNA FLJ11903 fis, clone HE	1.9
		AL039248	Hs.3094	KIAA0063 gene product	1.9 1.9
20		270200	Hs.246112	KIAA0788 protein	1.9
30		X54942	Hs.83758 Hs.171939	CDC28 protein kinase 2 ESTs	1.9
	134937 134506	AI251449 AW247364	Hs.84285	ubiquitin-conjugating enzyme E2I (homolo	1.9
	126469	BE384361	Hs.182885	ESTs, Weakly similar to JC5024 UDP-galac	1.9
	115261	AA938293	Hs.60088	hypothetical protein MGC11314	1.9
35	125198	W69474	Hs.323140	ESTs	1.9
	115317	AA303799	Hs.300141	ribosomal protein L39	1.9 1.9
	112342	AW410273		longevity assurance (LAG1, S. cerevisiae Homo sapiens cDNA: FLJ22664 fis, clone H	1.9
	117329 116353	AA524065 AB032966	Hs.93670 Hs.131728	KIAA1140 protein	1.9
40	114459	AW445217		ESTs	1.9
	133903	X63692	Hs.77462	DNA (cytosine-5-)-methyltransferase 1	1.9
	116083	AA455706	Hs.44581	heat shock protein hsp70-related protein	1.9
	130037	A1498631	Hs.111334	ferritin, light polypeptide	1.9 1.9
15	102273	BE391815	Hs.75981	ubiquitin specific protease 14 (tRNA-gua hypothetical protein IMAGE3510317	1.9
45	120452	AL022328 BE271922	Hs.104335 Hs.71243	ESTs, Weakly similar to zinc finger prol	1.9
	116432 115916	AI052731	Hs.91910	ESTs	1.9
	120827	AA382525	Hs.132967	Human EST clone 122887 mariner transposo	1.9
	129602	Al282193	Hs.198298	v-src avian sarcoma (Schmidt-Ruppin A-2)	1.9
50	105693	BE250951	Hs.181368	U5 snRNP-specific protein (220 kD), orth	1.9 1.9
	102316	U34301	11 00070	gb:Human nonmuscle myosin heavy chain II Human PAC clone RP3-515N1 from 22q11.2-q	1.9
	131422 128434	AW607731 AI190914	Hs.26670 Hs.143880	ESTs	1.9
	117086	AA581602		ESTs	1.9
55	102006	AL048967	Hs.172207	non-POU-domain-containing, octamer-bindi	1.9
	121335	AA404418		gb:zw37e02.s1 Soares_total_fetus_Nb2HF8_	1.9
	105905	AA401533	Hs.19440	ESTs	1.9 1.9
	125165	W45350	11- 20225	gb:zc81h08.s1 Pancreatic Islet Homo sapl	1.9
60	109875	H03260 AW38072	Hs.30385 3 Hs.73451	ESTs ESTs, Weakly similar to S55024 nebulin,	1.9
00	109152 126203	AK001035		B-cell CLL/lymphoma 11A (zinc finger pro	1.9
	122530	AW95974		adaptor-related protein complex 1, sigma	1.9
	124506	BE273688		heterogeneous nuclear ribonucleoprotein	1.9
	130525	AA361850		Human clone 137308 mRNA, partial cds	1.9
65	127226	AL036559		ribosomal protein \$23	1.9 1.9
	106465			topoisomerase-related function protein 4 ESTs	1.9
	106970 134275			cisplatin resistance-associated overexpr	1.9
	126825			gb:zl81c01.s1 Stratagene colon (937204)	1.9
70	132443			hypothelical protein FLJ20274	1.8
	104631			ESTs	1.8
	111468		Hs.205481	ESTs	1.8
	114317			succinate dehydrogenase complex, subunit	1.8 1.8
75	126158		Hs.16390 7 Hs.311002	hypothetical protein FLJ10035 Homo sapiens cDNA FLJ10705 fis, clone NT	1.8
13	113782 119229		1 NS.311002	gb:FB5C2 Fetal brain, Stratagene Homo sa	1.8
	105930		1 Hs.9880	peptidyl prolyl isomerase H (cyclophilin	1.8
	127245			gb:EST26810 Cerebellum II Homo sapiens c	1.8
	100967	BE01184	5 Hs.251064	high-mobility group (nonhistone chromoso	1.8
80	105149		8 Hs.8958	Homo sapiens cDNA FLJ12024 fis, clone HE	1.8 1.8
	104542		c	gb:F1-1179D 22 week old human fetal live gb:Homo sapiens full length insert cDNA	1.8
	124238 127155			gb:riomo sapians iun rangin inser conve gb:zi23e10.r1 Soares ovary tumor NbHOT H	1.8
	12/ 100	, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	-	2	

128554 AJ775986 Hs.71646 Hs.14570 Hs.14570 Hs.14570 Hs.14570 Hs.14570 Hs.17646
110223 AW274701 Hs.31040 ESTs 110389 AW000342 Hs.77646 Whome sagiens mRNAx CDNA DKF2p751M0223 (f gbthome sagiens clane FLBA217 mRNAx seque ESTs 110381 AF116322 Hs.268758 ESTs 112683 AF24400 hs.55075 KAAA010 gene product 110312 BE266985 hs.140720 SSK-3 binding protein FRA12 ls.2405 lb.236782 ls.236782 who for the same product line of the saging line of the sag
114899 A000342 https://doi.org/10.1003/14. https://doi.org
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11034 His52/2 his 26878 ESTS 12789 AAS68631 his 2556 KAA0319 protein 127891 AMS62485 his 140720 104249 AF0A231 his 24056 110619 AAC623591 his 26879 110619 AAC623591 his 26879 110619 AAC623591 his 26879 110619 AAC62369 his 268794 his 26879 110619 AF0A6586 his 19910 his 268794 127610 AMS66504 his 10910 his 268794 his 10920 his 268794 his 109303 AA1986504 his 109303 AA198657 his 26830 AM977893 his 268791 his 26879 his 268791
132693 2424/200 145.55075 143.64379 protein 145.2765 1
127684 AASB6831 hs. 342756 K3AA0379 protein C8727 AW629486 hs. 140720 hs. 242765 hs. 140720
127297 Wic23465 Rs.140720 SSK-3 blanding protein FRA72 1 12652 ES269699 Rs.235782 10312 ES259698 Rs.11896 Rs.2173 Rs.2207 Rs.2083 CDC-Pate Rises of 1 State Rises of 1 Rs.2207 Rs.2083 CDC-Pate Rises of 1 Rs.2173
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15 12652 AA26234 hs. 16648 STS. Weakly similar to 138022 hypothetic hypothetical protein FLJ20515 1 100739 Ms9287 hs. 2013 110335 Hz2868 hs. 1910 hs. 1910 hypothetical protein FLJ20515 1 1585 Hs. 1910 hypothetical protein FLJ20515 1 1585 Hs. 1910 hypothetical protein flags of 115867 hs. 18820 hs. 1910 hypothetical protein flags of 115867 hs. 18820 hs. 1910 hypothetical protein flags of 11586 hs. 1910 hypothetical protein flags of 11587 hypothetical protein flags of 11587 hypothetical protein flags of 11587 hypo
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129285 M83127 M5110121 SEC7 homolog 12923 AW972893 H5.78869 transcription elongation factor A (SII), 110459 AW373062 H5.83623 transcription elongation factor A (SII), 110590 AW372447 H5.28833 H57695 H5.268919 ESTs, Moderately similar to ALU1_HUMAN A 127303 AX366951 H5.28833 H57695
11959 R4979 hs. 271498 S271498 S
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15882 W92113 gb:zh48e01.r1 Soares_fetal_liver_spleen_ gb:ae32g02.s1 Gessler Wilms turnor Horno s 1
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111598 R11505 Hs.268912 ESTs 121643 AA640987 Hs.193767 ESTs 118761 AW799109 Hs.226755 ESTs 118761 AW799109 Hs.226755 ESTs 118761 AW799109 Hs.226755 ESTs 1188761 AW799109 Hs.29282 minsufin receptor substrate 2 1188803 AV248705 Hs.149321 ESTs 118803 AV248705 Hs.49321 ESTs 118803 AV248705 Hs.49321 ESTs 118762 AV85458 Hs.54900 Hs.22770 KIAA1545 protein 111122 R183753 Hs.16492 DKFZP564G2022 protein 111122 R183753 Hs.16492 DKFZP564G2022 protein 111623 AV65458 Hs.47061 Hs.27720 KIAA1545 protein 116654 Z26324 Hs.79204 ESTs, Weakly similar to 138022 hypothetic protein FLJ13044 Hs.22750 Hs.99486 hypothetical protein FLJ13044 Hs.22750 Hs.99486 hypothetical protein FLJ12785 120259 AW04786 Hs.192724 ESTs, Weakly similar to 138022 hypothetic protein FLJ12785 120259 AW04786 Hs.192742 Hs.268024 hs.10134 ESTs, Highly similar to 138022 hypothetic protein FLJ13785 Hs.268024 Hs.268
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114122 R46128 Hs. 12751 ESTs peptide:N-glycanase similar to yeast PNG 133047 AA310500 Hs. 63657 peptide:N-glycanase similar to yeast PNG 133089 L37368 Hs. 75104 RNA-binding protein S1, serine-rich doma phorbodin (similar to apolipoprotein B m 13498 BE299587 Hs. 85301 cacium binding protein P22 for apolipoprotein Hs. 60 131144 AA305255 Hs. 23528 Hs. PO2038 protein P22 for apolipoprotein S1, serine-rich doma phorbodin (similar to apolipoprotein B m 14 14 14 14 14 14 14 14 14 14 14 14 14
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104261 AW248364 Hs.5409 RNA polymerase I subunit 115507 AU83568 Hs.50801 hypothetical protein MGC10986 109073 T05003 Hs.10056 hypothetical protein FLJ14621 activator of S phase kinase 112657 AW844878 Hs.19769 hypothetical protein MGC4174 102504 R20215 125549 R20215 133797 AL133921 Hs.76272 RNA polymerase I subunit 11500186 1900186 1
115507 A1083668 Hs.50601 hypothetical protein MGC10986 1 109073 T05003 Hs.10056 hypothetical protein FLJ14621 1 115363 AA214618 Hs.152759 activator of S phase kinase 1 102567 AW844878 Hs.19769 hypothetical protein MGC4174 1 102560 A904738 Hs.76053 DEAD/H (Asp-Giu-Ab-Asp/His) box polypep 1 125549 R20215 gbyg18b09.r1 Soares Infant brain 1NIB H 1 133797 AL133921 Hs.76272 retinoblastoma-binding protein 2
115363 AA214618 Hs.152759 activator of S phase kinase hypothetical protein MGC4174 102950 Al904738 Hs.76053 DEAD/H (Asp-Glu-Ala-Asp/His) box polypep gb;yg18b09_r1 Soares infant brain 1NIB H retinoblastome-binding protein 2
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102960 Al904738 Hs.76053 DËAD/H (Asp-Gtu-Ala-Asp/His) box polypep 1 125549 R20215 gb:yg18b09.r1 Soares infant brain 1NIB H 1 133797 AL133921 Hs.76272 retinoblasioma-binding protein 2
125549 R20215 gb;yg18b09.r1 Soares Infant brain 1NIB H 1 133797 AL133921 Hs.76272 retinoblasioma-binding protein 2
133797 AL133921 Hs.76272 retinoblastoma-binding protein 2
70 125048 AW440068 Hs.59425 hypothetical protein FLJ23323 pb:H.sæpiens cyclin E gene.
123546 AA608817 Hs.112597 EST 1 124694 R06108 gbye94h05.s1 Soares fetal liver spleen 1
102406 U43177 (NONE)
130695 T97205 Hs.17998 ESTs. Weakly similar to 2109260A R cell
75 123951 AB012922 Hs.173043 metastasis-associated 1-fike 1
118533 N71861 Hs.49413 ESTs
123197 AA489250 gb:aa57h12.s1 NCI_CGAP_GCB1 Homo sapiens
125656 AW516428 Hs.78687 neutral sphingomyelinase (N-SMase) activ 1
100154 H50720 Ne R1892 KIAA0101 none conduct
80 106876 N52821 Hs.269412 ESTs, Moderately similar to ALU7_HUMAN A
8U 106876 N52821 Hs.269412 ESTs, Moderately similar to ALU7_HUMAN A 128339 AL121087 Hs.296406 KIAA0685 gene product 1
80 106876 N52821 Hs.269412 ESTs, Moderately similar to ALU7_HUMAN A

	100221	D28383		gb:Human mRNA for ATP synthase B chain,	1.8
	101741	NM_003199		transcription factor 4	1.8
	101701	NM_002436		membrane protein, palmitoylated 1 (55kD) ESTs	1.8 1.8
5	107119 134362	Al375499 U47742	Hs.27379 Hs.82210	zinc finger protein 220	1.8
•	127964	F06298		gb:HSC13F081 normalized infant brain cDN	1.8
	101437	M20681	Hs.7594	solute carrier family 2 (facililated glu	1.8 1.8
	106204	AA188734	Hs.21479 Hs.110802	ubinuclein 1 von Willebrand factor	1.8
10	112716 109779	AW590680 AB029396	Hs.3353	beta-1,3-glucuronyltransferase 1 (glucur	1.8
10	111369	AA535740	Hs.170263	tumor protein p53-binding protein, 1	1.8
	135204	AF067515	Hs.183418	cell division cycle 2-like 1 (PITSLRE pr	1.8 1.8
	105788	AB009698 AW862823	Hs.23965 Hs.168052	solute carrier tamily 22 (organic anion KIAA0421 protein	1.8
15	110997 111620	R14853	Hs.307478	EST, Weakly similar to 139058 hypotheti	1.8
	115618	H11695	Hs.322901	disrupter of silencing 10	1.8
	115904	Al167560	Hs.61297	ESTS FOTo Missister circiles to CMMSU entending	1.8 1.8
	107510 116435	BE613332 AA186761	Hs.132055 Hs.334812	ESTs, Weakly similar to GNMSLL retroviru hypothetical protein DKFZp586K0717	1.8
20	112399	R60920	Hs.296770	KIAA1719 protein	1.8
	127426	AA854756	Hs.124076	ESTs	1.8
	125175	W52355	Hs.303030	EST	1.8 1.8
	132972 125982	AA034365 R98091	Hs.288924	Homo sapiens cDNA FLJ11392 fis, clone HE ob:yr30e11.r1 Soares fetal liver spleen	1.8
25	115620	AA399997	Hs.211610	CUG triplet repeat, RNA-binding protein	1.8
	128115	Al435590	Hs.130168	ESTs	1.8
	106880	Al493206	Hs.32425	ESTs	1.7 1.7
	101199 104159	L22075 BE386983	Hs.1666 Hs.283685	guanine nucleotide binding protein (G pr hypothetical protein FLJ20396	1.7
30	101368	M13058	Hs.73952	proline-rich protein Haelfl subfamily 2	1.7
-	103646	AW248439	Hs.2340	junction plakoglobin	1.7
	130717	AA334274	Hs.18368	DKFZP564B0769 protein	1.7 1.7
	124981 124770	N25485 AA984414	Hs,330310 Hs.120429	maternal G10 transcript ESTs	1.7
35	126926	AA179472	Hs.832	ESTs, Highly similar to A41029 Integrin	1.7
	101636	BE392781	Hs.89474	ADP-ribosylation factor 6	1.7
	123553		Hs.111977	ESTs	1.7 1.7
	127172 130621		Hs.251278 Hs.16803	KIAA1201 protein LUC7 (S. cerevisiae)-like	1.7
40	116925		Hs.260603	ESTs, Moderately similar to A47582 B-ce	1.7
	108845			ESTs, Wealdy similar to phosphalidylseri	1.7
	128092		Hs.166229	ESTs	1.7 1.7
	128193		Hs.155020 Hs.19631	putative methyltransferase ESTs, Weakly similar to 138022 hypotheti	1.7
45	113965 106620		Hs.296317	KIAA1789 protein	1.7
	102926		Hs.239752	nuclear receptor subfamily 2, group F, m	1.7
	114964		Hs.8834	ring finger protein 3	1.7 1.7
	101800 130094		3 Hs.105806 1 Hs.167017	granulysin gamma-aminobutyric acid (GABA) B recepto	1.7
50	120112			Homo sapiens cDNA: FLJ21028 fis, clone C	1.7
•	109978		Hs.22528	ESTs	1.7
	121252			ESTs	1.7 1.7
	127768 125445		2 Hs.156187 Hs.7709	ESTs WW domain binding protein 1	1.7
55	100052		113.7705		1.7
	119863	AA081218		Homo sapiens cDNA FL/14206 fis, clone NT	1.7
	134333			teukemia-associated phosphoprotein p18 (1.7 1.7
	12354 ⁻ 13419 ⁻		1 Hs.112592 Hs.7979	ESTs KIAA0736 gene product	1.7
60	10330			qb:H.sapiens Fas, Apo-1 gene (promoter a	1.7
	11241		Hs.271510	ESTs, Moderately similar to ALU1_HUMAN A	1.7
	10059		Hs.146409	cell division cycle 42 (GTP-binding prot gb:ye25f01.s1 Stratagene lung (937210) H	1.7 1.7
	11361 10559		Hs.174151	aldehyde oxidase 1	1.7
65	12531		Hs.112461	ESTs, Weakly similar to 138022 hypotheti	1.7
	12595			hypothetical protein FLJ20207	1.7 1.7
	10510 13279		Hs.87016 1 Hs.7910	hypothetical protein FLJ22938 RING1 and YY1 binding protein	1.7
	11699		Hs.40535	ESTs	1.7
70	13333	5 BE25101	2 Hs.263812	nuclear distribution gene C (A.nidulans)	1.7
	12095			putative nuclear protein uncharacterized hypothalamus protein HTO	1.7 1.7
	10562 10618			ESTs	1.7
_	12566			ESTs	1.7
75	12758	5 AA60414	4 Hs.190632	ESTs	1.7
	11203			ribosomal protein L36 breakpoint cluster region	1.7 1.7
	10287 10803		Hs.234799 9 Hs.288840	PRO1575 protein	1.7
	12589			Homo sapiens mRNA; cDNA DKFZp564C2478 (f	1.7
80	11474	10 N70103		gb:za53e10.s1 Soares letal liver spleen	1.7 1.7
	12030		69 Hs.271838 Hs.78948	ESTs Rab geranylgeranyltransferase, beta subu	1.7
	10343 1161			ESTs, Wealdy similar to 138022 hypothet	1.7

	105260	AF174499	Hs.6764	blatere describitors C	1.7
	105269 125431	AW851639	Hs.75584	histone deacetylase 6 polymyositis/scleroderma autoantigen 2 (1.7
	133579	X75346	Hs.75074	mitogen-activated protein kinase-activat	1.7
_	105355	AL031447	Hs.26938	Homo saptens, clone IMAGE:4053044, mRNA,	1.7
5	129601	AB032964	Hs.115726	KIAA1138 protein	1.7
	113739	AA356599	Hs.173904	ESTs	1.7
	100840 122878	U04816 AAB47744	Hs.183418 Hs.99640	cell division cycle 2-like 1 (PITSLRE pr	1.7 1.7
	119495	BE144608	Hs.55533	ESTs ESTs	1.7
10	125669	R51308	Hs.333256	ESTs, Weakly similar to ALU8_HUMAN ALU	1,7
	109891	H04757	Hs.323176	EST8	1.7
	126884	U49436	Hs.286236	KIAA1856 protein	1.7
	132977	AA093322	Hs.301404	RNA binding motif protein 3	1.7
15	101396	BE267931	Hs.78996	proliferating cell nuclear antigen	1.7 1.7
13	104730 102205	AW139789 BE242291	Hs.16370 Hs.197540	Homo sapiens cDNA FLJ11652 fis, clone HE hypoxia-inducible factor 1, atpha subuni	1.7
	112945	AW138458	Hs.20787	Homo sapiens cDNA: FLJ21688 fis, clone C	1.7
	129902	AA076278	Hs.13277	hypothetical protein FLJ22054	1.7
•	107157	AW853745	Hs.286035	hypothetical protein FLJ22686	1.7
20	133229	AL137480	Hs.6834	KIAA1014 protein	1.7
	129912	AF155096	Hs.107213	hypothetical protein FLJ20585	1.7
	119811	AW137640	Hs.231444	Homo saptens, Similar to hypothetical pr	1.7 1.7
	126323 133134	N77584 AF198620	Hs.68644 Hs.65648	Homo saptens microsomal signel peptidase RNA binding motif protein 8A	1.7
25	115278	AK002163	Hs.301724	hypothetical protein FLJ11301	1.7
	133817	AW578716	Hs.7644	H1 histone family, member 2	1.7
	130753	AA205223	Hs.189	phosphodiesterase 4C, cAMP-specific (dun	1.7
	107463	AW952022	Hs.315164	hypothetical protein similar to actin re	1.7
30	121009	NM_001533	Hs.2730	heterogeneous nuclear ribonucleoprotein	1.7
30	125546 129991	H09950 R28386	Hs.179925	gb:ym01d12.r1 Soares infant brain 1NIB H ESTs, Weakly similar to ALU8_HUMAN ALU	1.7 1.7
	119015	N95490	Hs.29700	hypothetical protein FLJ20094	1.7
	100058	1150150	1020700	nyposiosaa pretan razzoo .	1.7
	116655	AF271732	Hs.68090	bridging integrator-3	1.7
35	119898	R93325	Hs.58690	ESTs	1.7
	105021	H07960	Hs.306044	CGI-05 protein	1.7
	102098	N25485	Hs.330310	maternal G10 transcript	1.7
	126730 113427	AA442429 T85105	Hs.15471	gb:zv70g02.r1 Soares_total_fetus_Nb2HF8_ ESTs	1.7 1.7
40	122317	T85253	Hs.290874	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.7
	130503	BE208491	Hs.295112	KIAA0618 gene product	1.7
	117348	N24157		gb:yx96b12.s1 Soares melanocyte 2NbHM Ho	1.7
	127033	AF169301	Hs.9098	sulfate transporter 1	1.7
15	128554	AW972147	Hs.101395	hypothetical protein MGC11352	1.7
45	124733	R20547	Hs.100830	ESTs	1.7 1.7
	106310 122638	R98185 AL137476	Hs.17240 Hs.123609	ESTs Homo sapiens mRNA; cDNA DKFZp434I0623 (f	1.7
	101075	L03532	Hs.79024	heterogeneous nuclear ribonucleoprotein	1,7
	126659	T16245		gb:NIB1005R Normalized Infant brain, Ben	1.7
50	127717	F12209	Hs.173380	CK2 Interacting protein 1; HQ0024c prote	1.7
	105441	N28522	Hs.8935	quinolinate phosphoribosyltransferase (n	1.7
	104188	AA478423	Hs.300870	Homo sapiens mRNA; cDNA DKFZp547M072 (fr	1.7
	134750	L29073	Hs.1139	cold shock domain protein A	1.7 1.7
55	106826 113511	BE253927 TB9578	Hs.24983 Hs.189740	hypothetical protein from EUROIMAGE 2021 ESTs	1.7
-	111070		Hs.171834	PCTAIRE protein kinase 1	1.7
	129091	AA056483	Hs.301463	Human Chromosome 16 BAC done CIT987SK-A	1.7
	129710	AJ277841	Hs.120963	ELG protein	1.7
60	132833	U78525	Hs.57783	eukaryotic translation initiation factor	1.7
60	125775	AW514585	Hs.29205	alpha integrin binding protein 63	1.7 1.7
	113675 100487	T81034 AU076640	Hs.14841 Hs.15243	ESTs nucleolar protein 1 (120kD)	1.7
	119302	T25725	NS.13243	gb:ESTDIR152 CD34+DIRECTIONAL Homo saple	1.7
	128245	AA993101	Hs.170486	ESTs	1.7
65	130322	NM_014247		PDZ domain containing guanine nucleotide	1.7
	135363	AW589601	Hs.119	Wilms' turnour 1-associating protein	1.7
	125181	R40815	Hs.12396	ESTs, Weakly similar to 2004399A chromos	1.7
	132347	BE271016	Hs.169850	ESTs, Weakly similar to T21554 hypotheti	1.7
70	127205	AW816490 AW946155	Hs.337508	ESTS	1.7 1.7
70	121880 125797	H03117	Hs.7750 Hs.111497	hypothetical protein AL133206 similar to mouse neuronal protein 15.6	1.7
	114601	AA075566	165.111451	gb:zm88f06.s1 Stratagene ovarian cancer	1.7
	126278	AA417302	Hs.63042	DKFZp564J157 protein	1.7
75	120964	AA398085	Hs.142390	ESTs	1.7
75	133634		Hs.234279	microtubule-associated protein, RP/EB fa	1.7
	107025		Hs.21255	ESTs, Wealthy similar to 138022 hypotheti	1.7 1.7
•	105638 135398		Hs.247817 Hs.287270	H2B histone family, member A ret proto-oncogene (multiple endocrine	1.7
	115794		Hs.112227	membrane-associated nucleic acid binding	1.7
80	102083		Hs.75117	Interleukin enhancer binding factor 2, 4	1.7
	100188	AW247090	Hs.57101	minichromosome maintenance deficient (S.	1.7
	130868		Hs.171917	hypothetical protein FLJ11085	1.7
	110493	A1247707	Hs.36915	ESTs	1.7

	115041 AA25	2457 Hs.86543	ESTs, Moderately similar to T00256 hypot 1.7
	128764 AW02	24282 Hs.104938	hypothetical protein MGC15906
	134065 X789		butyrate response factor 2 (EGF-response 1.7 interferon regulatory factor 1 1.7
5	101082 BE61 130945 U205		actin like protein
,	106974 AI817	7130 Hs.9195	Homo sapiens CDNA FLI13698 fis, clone PL 1.7 FCT. Woodky signifier to 130022 by profile fig. 1.7
	126752 Al073		ES1, Weakly Stillida: W DOOZZ Hypothesis
	133327 AL39 127005 T813		rupperlike arowth factor 2 (somatomedi 1.7
10		31959 Hs.5210	glia maturation factor, gamma
	116295 AA74	42596 Hs.91216	ESTs, Weakly similar to 2004399A chromos 1.7
	111587 Al12		ESTs 1.7
	104570 AW9		arachidonale 5-fipoxygenase
15	130430 W27		putative translation initiation factor
	119244 AW4	107564 Hs.275865	TIDOSONIAI DIOCENIO TO
		004380 Hs.23598 42676 Hs.73172	crowth factor independent 1 1.7
		42676 Hs.73172 39541 Hs.24956	hypothelical protein FLJ22056
20	116482 AW	207000 Hs.126857	Homo sapiens cDNA FLJ12936 fis, clone NT 1.7
		500131 Hs.171763	CD22 antigen ubiquitin specific protease 22 1.7
)28986 Hs.12064 283893 Hs.337079	FSTe
		30882 Hs.59368	ESTS 1.7
25	126295 Al2	B1459 Hs.270114	ESIS
	122528 AA	449804 Hs.292154	stromal cell protein
	Table 2B:		
	Pkey:		eset identifier number
30	CAT number.	Gene cluster nur	
	Accession:	Genbank access	Mil Dalineis
	Pkey C	AT number	Accession
0.5	108451 1	3766_27	AA079195 AA084955 AA126308 AA084956 AF086006 H64722 H65212 H66282
35		6919_1	
	115982 1	73_2	
			A1124782 AA889402 AA765804 AA765530 AA055698 AA554019 A1267366 AA456540 K35554 K1 264524 K1
40		1394292_1	F04405 BE173130
40		1852047_1 1692163_1	W45350 W45406 R07785 T85948 T86972
		1601238_1	H64450 H64464
	125499	1562851_1	H10543 R11878
45		1205826_1 356478_1	N95428 W24040 AW751366 H81987 H09950 R18413 AA570553 AW973425
40		1702179_1	R20215 R18767
	125761	1744008_1	R68351 R68364
		200358_1	AA284993 AA478122 AA477923 H41694 H45213
50		1583542_1 1766315_1	R98091 W92898
50	127245	226662_1	AA323958 AA370268
	127248	227560_1	AA364195 AA325029 AW962050 AA828125 AA834883 AA330555
	127262 126659	231725_1 1541209_1	T16245 R19694 F13545 H10299 T66048 T65279 H18006
55	127303	258778_1	AA366951 AA470999 AA469425
	127315	37938_1	AF116622 A114507 AA640834 AA377999
	126730	297653_1	AA442429 T19477 AA248884
	103898 126872	187213_3 142696_1	AWA50979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238036 BE011212 BE011333 BE011633
60			BE011368 BE011362 BE011215 BE011365 BE011363
	112540	1605263_1	R69751 R70467 H69771 H80879 H80878 AJ003322 AJ003324
	127705 121335	966283_2 279548_1	AA404418 Al217248
	120734	208882_1	AA299948 AA299949
65	114620	32062_8	AA642974 AA084223
	122652 123636	26401_30 genbank_AA609263	AA454641 AA609263
	100842	tigr_HT4398	U05597
~ 0	116548	genbank_D20433	D20433
70		genbank_AA610112 genbank_T74884	AA610112 T74884
	125032 123808	genbank_AA620552	AAG20552
	102316	entrez_U34301	U34301
75	102406	entrez_U43177	U43177 AF086215 W02702 AA284288 W25655
75	134076 104542	40321_1	R29657
	113119	genbank_T47910	T47910
	104799	genbank_AA029703	AA029703
80	127964	135151_1 genbank_AA346495	F06298 R18057 AA346495
80	120809 113610	genbank_T93279	T93279
	113947	genbank_W84768	
	101045	entrez_J05614	0.00
			07

	129969 117031	genbank_N57818	
	101447	genbank_H88353 entrez_M21305	
	124540	genbank_N63232	
5	124554	genbank N65961	
•	117348	genbank_N24157	
	117357	genbank_N24829	
	124577	genbank_R01073	
	124694	genbank_R06108	
10	103138	entrez, X65965	
	103305	entrez_X82279	
	103392	entrez_X94563	
	103403	entrez_X95406	
1.5	119229	genbank_T03229	
15	119302	genbank_T25725	
	126825	430458_1	AA100230 AA100274
	105225	genbank_AA211777	
	121292	genbank_AA401807	7
20	112853	genbank_T02843	T02843
20	121387	genbank_AA405854	
	114601 100221	genbank_AA075566 entrez_D28383	D28383
	123197	genbank_AA489250	026363 AA489250
	114740	379876_1	N70103 N70020 AW383189 Al207469 W00935 W00906 AA551569 Al343637 AA135199
25	123331	genbank_AA497013	(10100 1110020 A11000100 A1201 403 1100000 1100000 A100 1000 A100 1000 A100 1000
	107794	genbank_AA019255	
	100554	tigr_HT2241	M95923
	123423	genbank_AA598484	
	123474	genbank_AA599209	
30	109061	genbank_AA160896	

TABLE 3A: About 1346 Genes Up-regulated in Acute Lymphocytic Leukemia (ALL) Compared to Normal Adult Hernatopoletic Tissues

Table 3A lists about 1346 genes up-regulated in acute lymphocytic leukemia (ALL) compared to normal adult hernatopoletic tissues. These were selected from 35403 probesets on the Affymetrity/Eos Hu01 GeneChip array such that the ratio of "average" leukemia to "average" normal adult hernatopoletic tissues was greater than or equal to 3.0. The "average" leukemia level was set to the 85th percentile amongst various ALL samples. The "average" normal adult hernatopoletic tissues was greater than or equal to 3.0. The "average" leukemia level was set to the 85th percentile amongst various non-malignant hernatopoletic tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the tissues was subtracted from both the numerator and the demoninator before the ratio was evaluated. 35

Pkey: ExAcon: UnigenelD: Unigene Title: R1: unique cos probesel Identifier number
Unique Cos probesel Identifier number
Exemplar Accession number, Genbank accession number
Unigene number
Unigene gene title
Ratio of leukemia to hematopoletic tissues 40

45	Pkey	ExAcon	UnigenelD	Unigene Title	R1
	129498	AA449789	Hs.75511	connective tissue growth factor	57.88
	100458	S74019	Hs.247979	pre-B lymphocyte gene 1	49.45
	133774	X54079	Hs.76067	heat shock 27kD protein 1	48.42
	102564	U59423	Hs.79067	MAD (mothers against decapentaplegic, Dr	41,49
50	130650	AB040951	Hs.284208	DKFZP434N161 protein	35.88
-	132922	AF249745	Hs.6066	Rho quanine nucleotide exchange factor	35.74
	112254	AA852097	Hs.25829	ras-related protein	33.28
	106706	AB037810	Hs.18760	KIAA1389 protein	32.39
	101050	AU077324	Hs.1832	neuropentide Y	30.68
55	102455	U48705	Hs.75562	discoidin domain receptor family, member	26.81
	101838	BE243845	Hs.75511	connective tissue growth factor	25.46
	113374	179925	Hs.269165	ESTs, Weakly similar to ALU1_HUMAN ALU S	24.69
	134125	NM_014781	Hs.50421	KIAA0203 gene product	24.63
	106943	AW888222	Hs.9973	tensin	23.14
60	130069	Al754813	Hs.146428	collagen, type V, alpha 1	23.06
•	119073	BE245360	Hs.279477	ESTs	22.53
	130444	M12125	Hs.300772	tropomyosin 2 (beta)	21,96
	100420	D86983	Hs.118893	Melanoma associated gene	21.05
	114324	AF084481	Hs.26077	Wolfram syndrome 1 (wolframin)	18.95
65	101400	M15990	Hs.194148	v-yes-1 Yamaguchi sarcoma viral oncogene	18.46
•••	102759	NM_005100	Hs.788	A kise (PRKA) anchor protein (gravin)	17.88
	100893	BE245294	Hs.180789	S164 protein	16.75
	131689	AB012124	Hs.30696	transcription factor-like 5 (basic helix	16.60
	106410	AB037787	Hs.26229	neuroligin 2	16.51
70	101304	AA001021	Hs.6685	thyroid hormone receptor interactor 8	15.60
	131524	AB040927	Hs.301804	KIAA1494 protein	15.01
	107794	AA019255	110.001001	gb:ze56e10.s1 Soares reti N2b4HR Homo	14.78
	129213	AJ146494	Hs.109525	ESTs, Weakly similar to IRX2_HUMAN IROQU	14.76
	116068	AA328041	Hs.194329	hypothetical protein FLJ21174	14.24
75	134416	X68264	Hs.211579	melanoma cell adhesion molecule	14.06
	134545	Al902899	Hs.85155	butyrate response factor 1 (EGF-response	14.03
	114009	AJ248544	Hs.103000	KIAA0831 protein	13.93
	115110	AK001671	Hs.11387	KIAA1453 protein	13.75
	130107	AF112977	Hs.172887	phytanoyl-CoA hydroxylase (Refsum diseas	13.60
80	133558	X66945	Hs.748	fibroblast growth factor receptor 1 (tms	13.60
	100871	T85231	Hs.179661	tubulin, beta 5	13.50
	101462	AL035668	Hs.73853	bone morphogenetic protein 2	13.48
	120809	AA346495		gb:EST52657 Fetal heart II Homo saplans	13.33

	123340	AA504264	Hs.182937	peptidylprolyl isomerase A (cyclophilin	13.25
	103460	AA504264 Al021993	Hs.14331	S100 calcium-binding protein A13	13.25
	102460	U48959	Hs.211582	myosin, light polypeptide kise	13.14
_	100168	H73444	Hs.394	adrenomedullin	13.09
5	115844	Al373062	Hs.332938	hypothetical protein MGC5370	13.00
	130103	Y13492	Hs.149098	smoothelin	12.92 12.03
	102407 113632	AW602154 T94907	Hs.82143 Hs.188572	E74-like factor 2 (ets domain transcript ESTs	11.85
	118951	NM_000448	Hs.73958	recombition activating gene 1	11.73
10	100305	NM_004941	Hs.171872	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	11.63
	109737	AAQ55415	Hs.13233	ESTs, Moderately similar to A47582 B-cel	11.55
	122577	AA829725	Hs.334437	hypothetical protein MGC4248	11.49
	115147	AA745781	Hs.38399	hypothetical protein MGC2454	11.40 11.37
15	132303	BE177330	Hs.325093 Hs.76884	Horno sapiens cD: FLJ21210 fis, clone C inhibitor of D binding 3, domint neg	11.17
13	103176 108358	AL021154 MB1933	Hs.1634	cell division cycle 25A	11.15
	104584	AA704538	Hs.193777	ESTs	11.12
	106777	AF037261	Hs.33787	vinexin beta (SH3-containing adaptor mol	11.08
00	121054	AW976570	Hs.97387	ESTs	10.90
20	119400	T92767	** ******	gb:ye27d06.s1 Stratagene lung (937210) H	10.83 10.83
	126610	AI911353	Hs.191391	ESTs hydroxysteroid (17-beta) dehydrogese 1	10.80
	134555 131555	U34879 T47364	Hs.85279 Hs.278613	Interferon, alpha-inducible protein 27	10.79
	130979	NM_012446	Hs.169833	single-stranded-D-binding protein	10.70
25	113783	AL359588	Hs.7041	hypothetical protein DKFZp762B226	10.65
	123503	AW975051	Hs.293156	ESTs, Weakly similar to 178885 serine/th	10.60
	117031	H88353		gb:yw21a02.s1 Morton Fetal Cochlea Homo	10.45 10.44
	100752	T81309	Hs.251664	insulin-like growth factor 2 (somatomedi	10.36
30	102618 113089	AL037672 T40707	Hs.81071 Hs.270862	extracellular matrix protein 1 ESTs	10.33
50	132089	W22007	Hs.39122	hypothetical protein MGC15737	10.29
	101663	NM_003528	Hs.2178	H2B histone family, member Q	10.23
	104876	Al933128	Hs.25220	lika-glycosyltransferase	10.23
25	106370	AF039843	Hs.18676	sprouty (Drosophila) homolog 2	10.18
35	129406	AB018255	Hs.111138	KIAA0712 gene product	10.18 10.13
	115354 123077	AA281636 AA485229	Hs.334827 Hs.105649	ESTs ESTs	10.05
	131273	AW206008	Hs.283378	Homo sapiens cD: FLJ21778 fis, clone H	9.95
	126177	AW752782	Hs.129750	hypothetical protein FLJ10546	9.83
40	133699	BE501689	Hs.75617	collagen, type IV, alpha 2	9.80
	110855	AB007928	Hs.28169	KIAA0459 protein	9.65
	111826	R35975	11 404007	gb:yh91b07.s1 Soares placenta Nb2HP Homo	9.58 9.50
	126947	Z40778	Hs.191837	ESTs ESTs	9.48
45	116674 129087	A1768015 A1348027	Hs.92127 Hs.108557	hypothetical prolein PP1057	9.46
73	114837	BE244930	Hs.166895	ESTs	9.45
	120009	Al080491	Hs.93270	ESTs, Moderately similar to S65657 alpha	9.45
	112483	AW969785	Hs.285885	Homo sapiens cD FLJ11321 fis, done PL	9.40
50	103487	AA743603	Hs.172108	nucleoporin 88kD	9.30
50	105675	AL390083	Hs.271277	hypothetical protein from EUROIMAGE 3636	9.28 9.23
	129158 114394	NM_004413 T34462	Hs.109 Hs.103291	dipeptidase 1 (rel) neuritin	9.17
	133331	Y14487	Hs.738	ribosomal protein L14	9.11
	114787	AA156509	Hs.231892	ESTs, Weakly similar to S65657 alpha-1C-	9.10
55	125502	AW977181	Hs.194718	zinc finger protein 265	9.03
	132325	N37065	Hs.44856	hypothetical protein FLJ12116	9.01
	127968	AA830201	Hs.124347 Hs.306478	ESTs	9.00 8.93
	114605 114875	AL157423 AA235609	Hs.236443	Homo sapiens mR; cD DKFZp76100511 (f Homo sapiens mR; cD DKFZp564N1063 (f	8,93
60	129898	AI672731	Hs.13256	ESTs	8,89
•	106263	W21493	Hs.28329	hypothetical protein FLJ14005	8.89
	117130	AA748850	Hs.125830	bladder cancer overexpressed protein	8.88
	105553	AA256756	Hs.31178	ESTs	8.85
65	103657	Z73677	11- 047000	gb:H.sapiens gene encoding plakophilin 1	8.83 8.82
65	105831	AA329449	Hs.247302 Hs.289072	twisted gastrulation hypothetical protein FLJ22175	8.80
	106375 114518	AW872878 AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	8.75
	123433	AW450922	Hs.112478	ESTs	8.67
	134558	NM_001773	Hs.85289	CD34 antigen	8.67
70	115893	Al652127	Hs.48419	ESTs	8.67
	128621	AA032197	Hs.102558	Homo sapiens, clone MGC:5352, mR, comp	8.60
	122798	AW366286	Hs.145696	splicing factor (CC1.3)	8.58 8.55
	112554 129969	R71489 N57818	Hs.29196	EST gb:yv59d07.s1 Soares fetat liver spleen	8.53
75	131558	AA453208	Hs.28726	RAB9, member RAS oncogene family	8.45
	134027	Z97630	Hs.226117	H1 histone family, member 0	8.45
	134138	AB023169	Hs.7935	KIAA0952 protein	8.43
	120030	AI076355	Hs.58694	ESTs	8.43
80	101005	NM_005239	Hs.85146	v-ets avian erythroblastosis virus E26 o	8.33 8.33
90	115423	AI499516 AW242407	Hs.89303 Hs.73848	ESTs carcinoembryonic antigen-retated cell ad	8.30
	104946 131965	W79283	Hs.35962	ESTs	8.30
	126426	AA125984	- mayor Vita	gb:zn27h06.r1 Stratagene neuroepithelium	8.28

	108886	AW248434	Hs.91521	hypothetical protein	8.26
	107985	T40064	Hs.71968	Homo sapiens mR; cD DKFZp564F053 (fr	8.25
	114239	AL137667	Hs.267445	Homo septens mR; cD DKFZp434B231 (fr	8.23
5	124281 117099	A1333756 H93699	Hs.111801	arsete resistance protein ARS2	8.23
•	119432	AL120247	Hs.40109	gb;yv16a11.s1 Soares fetal liver spleen KIAA0872 protein	8.20 8.15
	115967	AI745379	Hs.42911	EST8	8.15
	132355	D87942	Hs.46328	fucosyltransferase 2 (secretor status in	8.13
10	108339 131694	AW151340	Hs.51615	ESTs, Weakly similar to ALU7_HUMAN ALU S	8.10
10	104897	NM_000246 N33937	Hs.3076 Hs.10336	MHC class II transactivator ESTs	8.05
	120266	AI807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	8.03 8.03
	130404	AJ672727	Hs.76753	endoglin (Osler-Rendu-Weber syndrome 1)	8.00
15	115729	AA417812	Hs.38775	ESTs	8.00
13	127216 131693	A1798703 AW963776	Hs.143702 Hs.110796	ESTs, Wealdy similar to S70029 probable SAR1 protein	7.95
	113107	AI821027	Hs.8429	ESTs	7.93 7.90
	122282	BE246331	Hs.98401	Homo sapiens mR full length insert cDN	7.90
20	111040	A1435502	Hs.14931	ESTs	7.90
20	127987 125317	Al022103 Z99348	Hs.124511 Hs.112461	ESTs ESTs, Wealdy similar to 138022 hypotheti	7.90
	105242	A1564857	Hs.27888	ESTs, Wealthy similar to serine/threonine	7.88 7.75
	100421	D86985	Hs.79276	KIAA0232 gene product	7.71
25	114359	NM_016929	Hs.283021	chloride intracellular channel 5	7.70
23	119772 124040	AJ250839 U23752	Hs.58241 Hs.32964	gene for serine/threonine protein kise	7.70
	134361	BE549343	Hs.82208	SRY (sex determining region Y)-box 11 acyl-Coenzyme A dehydrogese, very long	7.65 7.57
	105476	AL117352	Hs.120828	Human D sequence from clone RP5-876B10	7.55
20	113289	T66900	Hs.188446	ESTs	7.50
30	122707	NM_002039	Hs.239706	GRB2-associated binding protein 1	7.50
	130055 108766	AJ566248 AF145713	Hs.146355 Hs.61490	v-abl Abelson murine leukemia viral onco	7.49
	107957	Z36842	Hs.57548	schwannomin-interacting protein 1 ESTs	7.45 7.45
0.0	123116	AW190412	Hs.183738	FERM, RhoGEF (ARHGEF) and pleckstrin dom	7.38
35	123190	AA489212	Hs.105228	EST	7,38
	129574	AA026815	Hs.11463	UMP-CMP kise	7.38
	115274 102571	C01566 U60115	Hs.86671 Hs.239069	ESTs four and a half UM domains 1	7.35 7.34
	116845	AA649530	110120000	gb:ns44f05.s1 NCI_CGAP_Alv1 Homo sapiens	7.33
40	134851	AB011124	Hs.90232	KIAA0552 gene product	7.33
	101780	M82882	Hs.154365	E74-like factor 1 (ets domain transcript	7.28
	125042 118472	178906 AL 167646	Hs.269432	ESTs, Moderately similar to ALU1_HUMAN A	7.28
	108700	AL157545 AA121518	Hs.42179 Hs.193540	bromodomain and PHD finger containing, 3 ESTs, Moderately similar to 2109260A B c	7.25 7.23
45	109411	R98881	Hs.109655	sex comb on midleg (Drosophila)-like 1	7.23 7.20
	127692	Al021912	Hs.187983	ESTs	7.18
	128501	AL133572	Hs.199009	protein containing CXXC domain 2	7.18
	107727 118089	AA149707 Al762507	Hs.173091 Hs.47878	ubiquitin-like 3 ESTs	7.14
50	106025	AV653785	Hs.173334	ELL-RELATED R POLYMERASE II, ELONGATIO	7.12 7.10
	122111	AW593206	Hs.98785	Ksp37 protein	7.08
	119674	W60379	Hs.57773	ESTs	7.05
	126607 121545	W87425 AA412442	Hs.114688 Hs.98132	ESTs ESTs	7.05
55	113287	T66847	Hs.194040	ESTs, Weakly similar to I38022 hypotheti	7.05 7.03
	126672	AA255592	Hs.203631	ESTs, Weakly similar to attertively sp	7.00
	132087	H14486	Hs.3903	Cdc42 effector protein 4; binder of Rho	6.97
	118697	N22706	Hs.43234	ESTs	6.97
60	100295 101188	M74782 L20320	Hs.172689 Hs.184298	Interleukin 3 receptor, alpha (low affin cyclin-dependent kise 7 (homolog of Xe	6.95 6.95
	121481	AA411931	1 801 107 1000	gb:zu03g05.s1 Soares_testis_NHT Homo sap	6.95
	113003	AW292315	Hs.7215	ESTs	6.93
	101851	BE260964	Hs.82045	midkine (neurite growth-promoting factor	6.91
65	113529 132887	Al190741 AA195831	Hs.177415 Hs.273385	Finkel-Biskis-Reilly murine sarcoma viru	6.90
-	113560	T91015	Hs.268626	guanine nucleotide binding protein (G pr ESTs	6.90 6.85
	123440	AI733692	Hs.112488	ESTs	6.83
	130390	AA490770	Hs.182382	ESTs	6.83
70	133889	U48959	Hs.211582	myosin, light polypeptide kise	6.83
	113573 112453	R89379 R63899	Hs.15990 Hs.28455	ESTs ESTs	6.80 6.78
	125221	AA236115	Hs.120785	ESTs	6.78
	134081	AL034349	Hs.79005	protein tyrosine phosphatase, receptor t	6.77
75	127610	AA960867	Hs.150271	ESTs, Highly similar to unmed protein	6.75
, ,	105486 107796	AW449258 AA058848	Hs.6187 Hs.60797	ESTs ESTs	6.75 6.71
	132754	AJ752244	Hs.75309	eukaryotic translation elongation factor	6.71
	105806	AF206019	Hs.110347	REV1 (yeast homolog)- like	6.70
80	110837	H03109	Hs.108920	HT018 protein	6.65
55	117698 128994	N62293 AF205849	Hs.45107	ESTs Kruppel-like factor 2 (lung)	6.65 6.65
	129131	AB026436	Hs.107740 Hs.177534	dual specificity phosphatase 10	6.65 6.65
	108528	AA650558	Hs.325202	ESTs, Highly similar to GBAS_HUMAN GUANI	6.62
				100	

					6.61
	131009	AF169802	Hs.22142	cytochrome b5 reductase b5R.2	6.60
	129389	NM_012445	Hs.288126 Hs.129998	spondin 2, extracellular matrix protein enhancer of polycomb 1	6.59
	125278 124667	AI218439 W24320	Hs.102941	Homo sapiens cD: FLJ21531 fis, clone C	6.59
5	105640	AA001021	Hs.6685	thyroid hormone receptor interactor 8	6.58
•	106474	BE383668	Hs.42484	hypothetical protein FLJ10618	6.58 6.53
	105808	Al133161	Hs.286131	CGI-101 protein	6.52
	120087	AF186780	Hs.79219	RafGDS-tike gene; KIAA0959 protein spermidine/spermine N1-acetyltransferase	6.50
10	100514	AU076887	Hs.28491 Hs.74615	platelet-derived growth factor receptor,	6.50
10	108378 133350	Al368460 Al499220	Hs.71573	hypothetical protein FLJ10074	6.50
	115673	AA406341	Hs.269908	Homo sepiens cD FLJ11991 fis, clone HE	6.48
	133410	Y07847	Hs.73088	RAS-related on chromsome 22	6.48 6.46
	131281	AA251716	Hs.25227	ESTs	6.45
15	105510	Z42047	Hs.283978	Homo sapiens PRO2751 mR, complete cds crantofacial development protein 1	6.45
	128766	AW160432	Hs.296460 Hs.191797	ESTs, Weakly similar to S65657 alpha-1C-	6.43
	114530 120120	AA601038 BE547267	Hs.59791	hypothetical protein MGC13183	6.40
	120593	AA748355	Hs.193522	ESTs	6.40
20	125832	AA628600	Hs.117587	ESTs	6.38 6.38
	129637	NM_004606	Hs.1179	TATA box binding protein (TBP)-associate	6.33
	115302	AL109719	Hs.47578	ESTs hypothetical protein FLJ20689	6.30
	126137	AA312594	Hs.99115 Hs.131731	hypothetical protein FLJ11099	6.29
25	114465 125562	BE621056 Al494372	Hs.98968	hypothetical protein FLJ23058	6.29
23	127380	AF070554	Hs.15535	Homo sapiens clone 24582 mR sequence	6.26
	106956	R06428	Hs.226351	ESTs	6.25
	105962	AW880358	Hs.339808	hypothetical protein FLJ 10120	6.25 . 6.23
••	109416	BE268388	Hs.86945	ESTs, Weakly similar to A46010 X-linked	6.23
30	111116	AK002039	Hs.26243	Homo saplens cD FLJ11177 fis, clone PL ESTs	6.23
	127282	AA347158	Hs.185780 Hs.31137	protein tyrosine phosphatase, receptor t	6.21
	113074 101664	AK001335 AA436989	Hs.121017	H2A histone family, member A	6.20
•	103317	X83441	Hs.166091	ligase IV, D, ATP-dependent	6.20
35	133894	AW021236	Hs.180433	rTS bela protein	6.19
	109260	AW978515	Hs.131915	KIAA0863 protein	6.18 6.18
	112772	Al992283	Hs.35437	ESTs, Moderately similar to 138026 MLN 6	6.18
	132050	Al267615	Hs.38022 Hs.7246	ESTs ESTs	6.17
40	113009	T23699 AA535246	Hs.50852	ESTs	6.16
40	118835 125626	AX333246 AX338854	Hs.180789	S164 protein	6.15
	117086	AA581602	Hs.41840	ESTs	6.14
	101960	AL036287	Hs.194662	calponin 3, acidic	6.13 6.13
	104488	N56191	Hs.106511	protocadherin 17	6.13
45	127695	AA714731	Hs.291457	ESTs, Wealdy similar to heterogeneous ri Homo saplens cD FLJ12961 fis, clone NT	6.13
	127894	AL121053	Hs.5534 Hs.290240	ESTs, Moderately similar to ALU2_HUMAN A	6.10
	113595 120784	T92056 AW752101	Hs.16580	hypothetical protein FLJ11026	6.10
	115004	AA329340	Hs.4867	mannosyl (alpha-1,3-)-glycoprotein beta-	6.08
50	129740	BE165866	Hs.83623	nuclear receptor subfamily 1, group 1, m	6.05 6.04
	117483	N72185	Hs.44189	ESTs	6,03
	103815	BE245294	Hs.180789	S164 protein	6.03
	122040	AA847758	Hs.111030 Hs.119120	ESTs E3 ubiquitin ligase SMURF1	6.02
55	109638 112727	AW977747 T91029	Hs.15069	ESTs	6.01
"	120273	AA176688	Hs.269284	ESTs	6.00
	122127	AW207175	Hs.106771	ESTs	6.00
	126046	AA804957	Hs.119840	ESTs	5.99 5.98
60	119774	AB032977	Hs.6298	KIAA1151 protein Homo sapiens mR; cD DKFZp58610521 (f	5.98
60	106265	AA412176	Hs.236463 Hs.6763	KIAA0942 protein	5.98
	111987 123619	NM_015310 AA602964	HS.0705	gb:no97c02.s1 NCt_CGAP_Pr2 Homo sapiens	5.96
	128122	Al267491	Hs.160593	ESTs	5.95
	128473	T78277	Hs.100293	O-linked N-acetylghucosamine (Glcc) tr	5.95
65	102283	AW161552	Hs.83381	guarine nucleotide binding protein 11	5.94 5.93
	122468	AA448172	Hs.137687	ESTs, Highly similar to K6B1_HUMAN RIBOS	5.93
	101801	M86407	Hs.1216 Hs.23044	actinin, atpha 3 RAD51 (S. cerevisiae) homolog (E coli Re	5.92
	107059	BE614410 AA136569	Hs.10848	KIAA0187 gene product	5.90
70	108908 121470		Hs.324751	ESTs	5.90
, ,	131938		Hs.34956	neural polypyrimidine tract binding prot	5.89
	109613		Hs.27519	ESTs	5.89
	109384	AA219172	Hs.86849	ESTs	5.88 5.88
75	118559		Hs.49519	ESTs	5.86
75	102010		Hs.385 Hs.169119	fms-related tyrosine kise 3 ESTs, Weakly similar to T25731 hypotheti	5.85
	105921		U2.102112	gb:yv04a07.s1 Soares fetal liver spicen	5.85
	124298 120827		Hs.132967	Human EST clone 122887 mariner transposo	5.84
	103331		Hs.147996	protein kise, X-linked	5.82
80	135052	AL136653	Hs.93675	decidual protein induced by progesterone	5.80 5.78
	115219		Hs.269314	Homo sapiens cD FLJ14123 fis, clone MA	5.78
	121899		Hs.50421 Hs.9658	KIAA0203 gene product hypothetical protein FLJ11790	5.77
	135217	7 AA453880	FIS.3030	appointment protein a contract	

	122072	C14905		-b-014005 Cloutosh human and anluAD	5.77
	123973 112605	C14805 R79374	Hs.29852	gb:C14805 Clontech human aorta polyA+ mR ESTs	5.76
	110151	H18835	Hs.31608	hypothetical protein FLJ20041	5.75
_	129889	AA810932	Hs.131899	ESTs, Weatdy similar to T00370 hypotheti	5.75
5	102638	U67319	Hs.9216	caspase 7, apoptosis-related cysteine pr	5.73
	121501	AA470687	Hs.104772	ESTs	5.73
	124921	R93082	Hs.332635	ESTs	5.70
	109850	A1150548	Hs.23155	ESTs	5.70
10	120594	AW136478	Hs.5094	ring finger protein 10	5.70
10	126433 100455	AA325606 AW888941	U- 75700	gb:EST28707 Cerebellum II Homo sapiens c	5.70 5.69
	106565	NM_014892	Hs.75789 Hs.227602	N-myc downstream regulated KIAA1116 protein	5.6B
	120912	AA376690	Hs.187650	ESTs	5.68
	127209	AA305023	Hs.81964	SEC24 (S. cerevisiae) related gene famili	5.68
15	107606	AF207989	Hs.330425	Homo sapiens, Similar to G protein-coupl	5.67
	106597	AI091277	Hs.302634	frizzled (Drosophila) homolog 8	5.66
	102126	AW950870	Hs.78961	protein phosphatase 1, regulatory (inhib	5.65
	100064			AFFX control - TrpnX-3	5.63
20	108758	AA127395	Hs.222414	ESTs	5.63 5.61
20	101392 102211	NM_002507 BE314524	Hs.1827 Hs.78776	narve growth factor receptor (TNFR super putative transmembrane protein	5.60
	107427	W26975	Hs.46736	hypothetical protein FLJ23476	5.60
	135175	M91463	Hs.95958	solute carrier family 2 (facilitated glu	5.60
	111764	AI420368	Hs.290259	ESTs, Weakly similar to 138022 hypotheti	5.58
25	119405	T93865	Hs.91085	ESTs	5.58
	126464	A1990046	Hs.54780	transcription termition factor, R po	5.58
	133865	AB011155	Hs.170290	discs, large (Drosophila) homolog 5	5.58
	123255	AA830335	Hs.105273	ESTs	5.57 5.56
30	122861 112046	AA335721 AA383343	Hs.119394 Hs.22116	ESTs CDC14 (cell division cycle 14, S. cerevi	5.55
20	132906	BE613337	Hs.234896	geminin	5.55
	109001	AI056548	Hs.72116	hypothetical protein FLJ20992 similar to	5.55
	115816	BE042915	Hs.287588	Homo sapiens cD FLJ13675 fis, clone PL	5.55
·	128401	R01865	Hs.268586	ESTs	5.53
35	129296	Al051967	Hs.110122	ESTs	5.53
	120314	T10013	Hs.221040	HBS1 (S. cerevisiae)-like	5.51
	132815	AI815189	Hs.57475	sex comb on midleg homolog 1	5.50 5.50
	113983	W87415	Hs.55296	HLA-B associated transcript-1 ESTs, Moderately similar to altertivel	5.49
40	105002 132025	- AA224244 AA011117	Hs.182704 Hs.3745	milk fat globule-EGF factor 8 protein	5.49
40	110732	AW070838	Hs.174174	KIAA0601 protein	5.48
	112891	T03927	Hs.293147	ESTs, Moderately similar to A46010 X-lin	5.48
	126758	A1559444	Hs.293960	ESTs	5.48
	129426	AF077953	Hs.111323	Protein inhibitor of activated STAT X	5.47
45	103217	NM_001841	Hs.73037	canbinoid receptor 2 (macrophage)	5.46
	132261	U80743	Hs.306094	trinucleotide repeat containing 12	5.45
	105586	AA865118	Hs.191538	ESTs	5.43 5.43
	109454 113063	AA232255 W15573	Hs.295232 Hs.5027	ESTs, Moderately similar to A46010 X-lin ESTs, Wealdy similar to A47582 B-cell gr	5.43
50	134092	AA218558	Hs.7905	sorting nexts 9	5.41
50	119316	Al114630	Hs.208334	Homo sapiens cD: FLJ21874 fis, clone H	5.38
	108019	AI017773	Hs.249159	adrenergic, alpha-2A-, receptor	5.38
	109421	AW604652	Hs.332442	ESTs	5.38
	111929	AF027208	Hs.112360	prominin (mouse)-like 1	5.38
55	119718	W69216	Hs.92848	ESTs	5.38
	106154	BE540255	Hs.6994	Homo saplens cO: FLJ22044 fis, clone H	5.35 5.35
	108544 119580	W39433 AL079310	Hs.23971 Hs.92260	hypothetical protein DKFZp547N043 high-mobility group protein 2-like 1	5.35 5.35
	126777	AL157491	Hs.145211	Homo sapiens mR; cD DKFZp434K1111 (f	5.35
60	112944	H18063	Hs.13254	ESTs	5.34
- •	103149	NM_006201	Hs.171834	PCTAIRE protein kise 1	5.34
	132437	AA152106	Hs.4859	cyclin L ania-6a	5.33
	103860	AW976877	Hs.38057	ESTs	5.33
6 5	104865	179340	Hs.22575	B-cell CLL/lymphoma 6, member B (zinc fi	5.33
65	129914	NM_012421	Hs.13321	rearranged L-myc fusion sequence	5.33 5.31
	130309 116312	AF067804	Hs.15423 Hs.65403	hypothetical protein HDCMC04P hypothetical protein	5.30
	124191	BE379794 T96509	Hs.248549	ESTs, Moderately similar to S65657 alpha	5.28
	125583	AA195667	Hs.86022	ESTs	5.28
70	130591	N59646	Hs.169745	crumbs (Drosophila) homolog 1	5.28
	116355	AA789133	Hs.88650	ESTs	5.26
	115553	AJ275986	Hs.71414	transcription factor (SMIF gene)	5.26
	122802	A1687303	Hs.285529	G protein-coupled receptor 49	5.25
75	128495	NM_005904	Hs.100602	MAD (mothers against decapentaplegic, Dr	5.24 5.23
13	117667	U59305	Hs.44708	Ser-Thr protein kise related to the my ESTs, Weakly similar to ISHUSS protein d	5.23 5.22
	127890 134843	AA294934 AA428520	Hs.293902 Hs.90061	progesterone binding protein	5.21
	120968	AA528283	Hs.292737	ESTs	5.21
	102076	BE299197	Hs.179665	cyclin-dependent kise inhibitor 1A (p2	5,20
80	100934	J03019	Hs.99913	adrenergic, beta-1-, receptor	5.20
	112667	BE538516	Hs.15423	hypothetical protein HDCMC04P	5.20
	119304	AW249266	Hs.98493	X-ray repair complementing defective rep	5.20
	131868	AW408296	Hs.33532	zinc finger protein 151 (pHZ-67)	5.20
				100	•

	105914	AW245680	Hs.9701	growth arrest and D-damage-inducible,	5.18
	102258	NM_001546	Hs.34853	Inhibitor of D binding 4, domint neg	5.18 5.18
	103850	AA187101 T83909	Hs.213194	hypothetical protein MGC10895 gb:yd67f10.r1 Soares fetal liver spleen	5.18
5	112516 133640	AW246428	Hs.75355	ubiquitin-conjugating enzyme E2N (homolo	5.18
•	135180	D90070	Hs.96	phorbol-12-myristate-13-acetate-induced	5.18 5.18
	135309	Al564123	Hs.42500 Hs.89695	ADP-ribosylation factor-like 5 insufin receptor	5.17
	134801 133362	S76825 AK001519	Hs.7194	CGI-74 protein	5.17
10	135206	AB024703	Hs.96334	ring finger protein 11	5.15 5.15
	111480	R06453	Hs.19706	ESTs gb:yz33g08.s1 Morton Fetal Cochlea Homo	5.15 5.15
	118466	N66741 A1274906	Hs.166835	ESTs, Highly similar to 1814460A p53-ass	5.15
	125757 127140	A1273507	Hs.303966	ESTs	5.15
15	109223	AW000714	Hs.65818	ESTS	5.14 5.14
	103656	Z73497	Hs.247802 Hs.182447	Human D sequence from clone U240C2 on heterogeneous nuclear ribonucleoprotein	5.12
	133388 100511	AW245631 M76676	Hs.116840	ESTs	5.10
	101941	S77583		gb:HERVK10/HUMMTV reverse transcriptase	5.10 5.10
20	109937	A1084066	Hs.20072	myosin regulatory light chain Interactin ESTs, Weakly similar to ZN91_HUMAN ZINC	5.10
	122996 128242	A1436216 AA992626	Hs.191715 Hs.269755	ESTs, Moderalely similar to ALU5_HUMAN A	5.10
	112374	NM_016323	Hs.26663	cyclin-E binding protein 1	5.10
0.5	124506	BE273688	Hs.182447	heterogeneous nuclear ribonucleoprotein	5.10 5.09
25	104216	AB002313	Hs.3989 Hs.83484	plexin B2 SRY (sex determining region Y)-box 4	5.08
	135051 131629	Al272141 Z45794	Hs.238809	ESTs	5.08
	111722	R23924	Hs.23596	EST	5.07 5.06
20	107034	AF257770	Hs.20930	poly(rC)-binding protein 4 gb:yl14g03.s1 Soares breast 2NbHBst Homo	5.05
30	110243 125837	H26683 AW968123	Hs.333513	small inducible cytokine subfamily E, me	5.05
	130300	X58288	Hs.154151	protein tyrosine phosphatase, receptor t	5.05
	103967	AL120051	Hs.144700	ephrin-B1	5.04 5.03
35	112678	AJ418466	Hs.33665 Hs.101375	ESTs Homo sapiens mR; cD DKFZp434H205 (fr	5.03
33	124963 131379	F06600 AK001123	Hs.26176	hypothetical protein FLJ10261	5.03
	109451	N32264	Hs.44330	ESTs	5.02 5.02
	101396	BE267931	Hs.78996	proliferating cell nuclear antigen hypothetical protein DKFZp761H2024	5.01
40	131038	W87778 L25081	Hs.169388 Hs.179735	ras homolog gene family, member C	5.01
40	101208 104973	NM_015310	Hs.6763	KIAA0942 protein	4.99
	103141	X66113	Hs.75584	polymyositis/scleroderma autoantigen 2 (4.98 4.98
	111260	AB033035	Hs.51965	KIAA1209 protein ESTs, Weakly similar to unmed protein	4.98
45	128142 113857	T67162 AW243158	Hs.135127 Hs.5297	DKFZP564A2416 protein	4.96
73	105292	AF128542	Hs.166846	polymerase (D directed), epsilon	4,96 4,95
	114341	AF270491	Hs.28249	hepatocellular carcinoma-associated anti RAP2A, member of RAS oncogene family	4.95
	100615 103208	W32474 AW411340	Hs.301746 Hs.31314	retinoblastorna-binding protein 7	4.95
50	121121	AA399371	Hs.189095	similar to SALL1 (sal (Drosophila)-like	4.95 4.95
• •	125321	T86652	Hs.178294	ESTs lectin, galactoside-binding, soluble, 3	4.95 4.95
	101145	L13210	Hs.79339 Hs.129053	Homo sapiens NOTCH 1 (N1) mR, complete	4.93
	100551 126182	M73980 AA721331	Hs.293771	ESTs	4.93
55	127925	AA805151	Hs.3628	mitogen-activated protein kise kise	4.93 4.93
	133969	AA669112	Hs.78	GA-binding protein transcription factor, gb:EST66864 Fetal lung III Homo sapiens	4.92
	120873 125219	AA358015 A1804331	Hs.99423	ATP-dependent R helicase	4.91
	102790	BE245277	Hs.154196	E4F transcription factor 1	4.90 4.90
60	129486	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain transcription elongation factor 8 (SIII)	4.89
	130381	L47345 AA310393	Hs.155202 Hs.190044	ESTs	4.88
	132389 100260	D38491	Hs.322478	KIAA0117 protein	4.88
	109585	N59650	Hs.27252	ESTs	4.88 4.88
65	111603	R11529	Hs.20634	EST gb:zr59b02.s1 Soares_NhHMPu_S1 Homo sapi	4.88
	120514 130314	AA258335 NM_014674	Hs.154332	KIAA0212 gene product	4.86
	108958	AF142482	Hs.203846	TEA domain family member 3	4.86 4.85
70	126603	W86610	Hs.185736	ESTs	4.85
70	100406	A1962060 AV660717	Hs.118397 Hs.47144	AE-binding protein 1 DKFZP586N0819 protein	4.84
	116238 105288		Hs.3585	ESTs, Weakly similar to AF126743 1 DJ	4.83
	118753	AA346206	Hs.50471	ESTs, Wealdy similar to T14267 Xin prote	4.82 4.81
75	113070		Hs.6298	KIAA1151 protein ESTs	4.80
75	107908 119678		Hs.42826 Hs.6106	R binding motif protein 4	4.80
	100415		Hs.75822	TGFB1-induced anti-apoptotic factor 1	4.79 4.79
	128360	F12374	1). 400000	gb:HSC39B101 normalized infant brain cDN	4.78 4.78
80	133101		Hs.180952 Hs.296323	dyctin 4 (p62) serum/glucocorticoid regulated kise	4.78
80	103507 107666		Hs.60418	EST	4.78
	108030) Al378523	Hs.62011	ESTs	4.78 4.78
	131479	D86181	Hs.273	galactosylceramidase (Krabbe disease)	7.10
				103	

	133140	AF180681	Hs.6582	Rho quanine exchange factor (GEF) 12	4.78
	134654	AK001741	Hs.8739	hypothetical protein FLJ 10879	4.78
	108288	AB037742	Hs.24336	KIAA1321 protein	4.76
_	101524	NM_000448	Hs.73958	recombition activating gene 1	4.75
5	113095	AA828380	Hs.126733	ESTs	4.75
	114924	AI338053	Hs.87329	HSPC072 protein	4.75
	127543	AK000787	Hs.157392	Homo saplens cD FLJ20780 fis, clone CO	4.75
	115866	AW062629	Hs.52081	KIAA0867 protein	4.75
10	101382	AU076772	Hs.1279	complement component 1, r subcomponent	4.74
10	126509 127930	R47400 AA809672	Hs.23850 Hs.123304	ESTs ESTs	4.74 4.73
	127824	AI911516	Hs.127811	ESTs	4.73
	110049	H12449	Hs.31159	EST, Weakly similar to ALUB_HUMAN IIII A	4.73
	127115	H77859	Hs.65450	reticulon 4	4.73
15	104727	N81203	Hs.20047	zinc finger protein, subfamily 2A (FYVE	4.72
	127532	AJ003429		gb:AJ003429 Selected chromosome 21 cD	4.71
	127304	AI741577	Hs.99962	proteoglycan 2, bone marrow (tural kil	4.70
	105409	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8	4.70
20	114969	AW162998	Hs.24684	KIAA1376 protein	4.70
20	115125 118348	AA193588	Hs.85888	ESTS	4.70 4.70
	123130	AW408586 AA487200	Hs.91052	ESTs, Moderately similar to ALU5_HUMAN A gb:ab19f02.s1 Stratagene lung (937210) H	4.70 4.70
	130881	AA809875	Hs.25933	ESTs	4.70
	132074	AA478486	Hs.3852	KIAA0358 protein	4.70
25	106897	AF039023	Hs.167496	RAN binding protein 6	4.69
	131121	AA120865	Hs.23136	ESTs	4.69
	116046	BE395293	Hs.94491	hypothetical protein FLJ20297	4.68
	112868	AW388359	Hs.10667	ESTs	4.68
20	116877	AA708958	Hs.168732	ESTs	· 4.68
30	131241	BE501914	Hs.24654	Homo saplens cD FLJ11640 fis, clone HE	4.68
	132027 133323	AF151020 BE336654	Hs.181444	hypothetical protein H3 histone family, member A	4.68 4.68
	114269	AA176769	Hs.70937 Hs.23450	mitochondrial ribosomal protein S25	4.67
	122713	Al089443	Hs.99436	ESTs	4.67
35	133571	BE515037	Hs.177556	melanoma antigen, family D, 1	4.66
	134453	Al272141	Hs.83484	SRY (sex determining region Y)-box 4	4.66
	115510	BE299339	Hs.72249	three-PDZ containing protein similar to	4.66
	115322	L08895	Hs.78995	MADS box transcription enhancer factor 2	4.66
40	129315	NM_014563	Hs.174038	spondyloepiphyseal dysplasia, late	4.65
40	104674	Al935962	Hs.26289	ESTs	4.65
	106276	AA625947	Hs.25750	ESTs ESTs	4.65 4.65
	108216 120376	AA524743 AA227469	Hs.44883	gb:zr18a07.s1 Stratagene NT2 neurol pr	4.65
	121743	AA397636		gb:zt79e09.r1 Soares_testis_NHT Homo sap	4.65
45	128011	AI347067	Hs.124636	ESTs	4.65
	123454	AA868510	Hs.112496	ESTs	4.64
	103409	NM_004454	Hs.43697	ets variant gene 5 (ets-related molecule	4.64
	120484	AA253170	Hs.96473	EST	4.63
50	127046	AA321948	Hs.293968	ESTs	4.63
50	133184	AA001021	Hs.6685	thyroid hormone receptor interactor 8	4.63 4.62
	123184	BE247767	Hs.18166	KIAA0870 protein	4.62 4.61
	106627 115475	AK000706 AB033085	Hs.15125 Hs.40193	hypothetical protein FLJ20699 hypothetical protein KIAA1259	4.61
	119468	AI911535	Hs.6657	hypothetical protein bK1048E9.5	4.59
55	133662	BE409053	Hs.299629	peroxisomal long-chain acyl-coA thioeste	4.58
	113941	AA531016	Hs.22399	hypothetical protein FLJ14824	4.58
	131590	R46277	Hs.250638	Homo sapiens mR full length insert cDN	4.58
	128795	AA531287	Hs.105805	ESTs	4.58
60	116480	C14088	Hs.169476	glyceraldehyde-3-phosphate dehydrogese	4.58 4.58
UU	111713	C75253	Hs.220950 Hs.18190	ESTs EST	4.56 4.57
	113721 111657	AF143885 R07364	Hs.268667	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.56
	102009	BE245149	Hs.82643	protein tyrosine kise 9	4.55
	135242	Al583187	Hs.9700	cyclin E1	4.55
65	127580	BE548749	Hs.148016	ESTs	4.55
	109785	AB011131	Hs.12376	piccolo (presyptic cytomatrix protein)	4.53
	109700	F09609		gb:HSC33H092 normalized infant brain cDN	4.53
	124882	A1698652	Hs.101539	ESTs	4.53
70	131765	AW381270	Hs.194110	hypothetical protein PRO2730	4.53 4.52
70	115684	NM_006577 Al903474	Hs.284284	ESTs, Highly similar to beta-1,3-N-acety fibromodulin	4.52 4.52
	102034 109776	AI903474 R43665	Hs.230 Hs.12257	ESTs	4.52 4.50
	111650	R16722	Hs.124246	ESTs	4.50
	132993	AB023154	Hs.62264	KIAA0937 protein	4.49
75	129017	AA115333	Hs.107968	ESTs	4.49
	132902	A1936442	Hs.59838	hypothetical protein FLJ10808	4.48
	114814	AB006622	Hs.182536	KIAA0284 protein	4.48
	120839	AA348913	11- 4400	gb:EST55442 Infant adrel gland II Homo	4.48
80	101434	AV650066	Hs.1430	coagulation factor XI (plasma thrombopla	4.48 4.48
ov.	102018 104619	U03398 AA001635	Hs.1524 Hs.287414	tumor necrosis factor (ligand) superfami transcriptiol intermediary factor 1 ga	4.48
	106716	AA931198	Hs.238928	HT002 protein; hypertension-related calc	4.48
	126020	H79863	Hs.114243	ESTs	4.48

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					4.47
	119899	A1057404	Hs.58698	ESTs	4.46
	115582	AW245047	Hs.136164	cutaneous T-cell lymphoma-associated tum	4.46
	125695	W22529	Hs.30942	ephrin-B2 putative small membrane protein NID67	4.45
_	105715	BE621800	Hs.29444	ESTs, Weakly similar to HZHU hemoglobin	4,45
5	117169	R87866	Hs.95120 Hs.30942	ephrin-B2	4.45
	102757	AW955454	NS.30342	gb:ob39a05.s1 NCI_CGAP_GCB1 Homo sapiens	4.45
	120637 131579	AA811804 N62922	Hs.29088	ESTs	4.45
	135287	U82670	Hs.9786	zinc finger protein 275	4.45
10	112540	R69751		gb:yi40a10.s1 Soares placenta Nb2HP Homo	4.45
10	125724	AL360190	Hs.295978	Homo sapiens mR full length insert cDN	4.44
	115498	AA291070	1,5,200	gb:zs46a08.s1 NCI_CGAP_GCB1 Homo sapiens	4.43
	102263	U29171	Hs.75852	casein kise 1, delta	4.43
	124312	H94647	Hs,102329	ESTs	4.43
15	112366	AF035318	Hs.12533	Homo sapiens clone 23705 mR sequence	4.43
10	115955	AF263613	Hs.44198	intracellular membrane-associated calciu	4.43
	103562	NM_002702	Hs.2815	POU domain, class 6, transcription facto	4.42
	100169	AL037228	Hs.82043	D123 gene product	4.40 4.40
	108928	AA143802	Hs.71781	ESTs	4.40
20	125908	AF265555	Hs.250646	baculoviral IAP repeat-containing 6	4.40 4.40
	126996	BE161065	Hs.167531	methylcrotonoyl-Coenzyme A carboxylase 2	4.40
	129512	T88845	Hs.112200	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.40
	134570	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	4.40
	135073	W55956	Hs.94030	Homo sapiens mR; cD DKFZp586E1624 (f	4.40
25	105011	BE091926	Hs.16244	mitotic spindle coited-coil related prot	4,40
	128793	AB011125	Hs.105749	KIAA0553 protein	4.38
	107292	BE166479	Hs.4789	Homo sapiens serologically defined breas	4,38
	126144	H84455	Hs.40639	ESTs retinoic acid receptor, beta	4.38
20	130783	X07282	Hs.171495	purinergic receptor P2X, ligand-gated io	4.38
30	135192	U83993	Hs.321709	small inducible cytokine subfamily A (Cy	4.37
	100284	D43767	Hs.66742	KH-type splicing regulatory protein (FUS	4.36
	117269	N21621	Hs.91142	R polymerase I subunit	4.35
	104261	AW248364	Hs.5409	hypothetical protein	4.35
25	108609	BE409857	Hs.69499	gb:HUM184E05B Human fetal brain (TFujiwa	4.35
35	126319	D81689	Hs.193942	ESTs	4.35
	127445	AA906286	Hs.19192	cyclin-dependent kise 2	4.35
	130772	BE270640	Hs.184389	ESTs	4.35
	134625	AA977638	Hs.166563	replication factor C (activator 1) 1 (14	4.35
40	135397 128070	L14922 AA886944	Hs.303908	ESTs	4.35
40	135046	A1494054	Hs.93589	hypothetical protein DKFZp564B1162	4.33
	101881	NM_004957	Hs.754	folylpolyglutamate synthase	4.33
	129838	AB007863	Hs.185140	KIAA0403 protein	4.33
	130974	NM_003528	Hs.2178	H2B histone family, member Q	4.33
45	107763	AA018220	Hs.106730	chromosome 22 open reading frame 3	4.32
	129818	T71092	Hs.172572	hypothetical protein FLJ20093	4.31
	129407	AL137597	Hs.11114	hypothetical protein dJ1181N3.1	4.30
	110846	BE277343	Hs.297875	endoplasmic reticulum chaperone SIL1, ho	4.30
	111433	R01452	Hs.40193	hypothetical protein KIAA1259	4.30 4.30
50	114860	AL157545	Hs.42179	bromodomain and PHD finger containing, 3	4.30
	115853	AW978561	Hs.191548	ESTs	4.30
	116165	Al184751	Hs.75874	pregncy-associated plasma protein A	4.30
	126911	AA428049	Hs.1501	syndecan 2 (heparan sulfate proteoglycan	4.30
~ ~	131230	NM_005865	Hs.274407	protease, serine, 16 (thyrnus)	4.29
55	100349	D64110	Hs.77311	BTG family, member 3 acetyl-Coenzyme A acytransferase 2 (mit	4.29
	100175	BE258769	Hs.32500		4.29
	105335	AW291165	Hs.25447	ESTs ESTs	4.28
	122507	BE567620	Hs.99210 Hs.7395	hypothetical protein FLJ23182	4.28
60	105397	AAB14807	Hs.75497	Homo sapiens cD: FLJ22139 fis, clone H	4.28
UU	133674	AW851121	Hs.8679	cytosolic acyl coenzyma A thioester hydr	4.28
	102826	NM_007274 NM_006680	Hs.2838	malic enzyme 3, DP(+)-dependent, mitoc	4.28
	103272	R38635	Hs.12328	KIAA 1005 protein	4.28
	111887	N85785	Hs.181165	eukaryotic translation elongation factor	4.28
65	120336 133736	D49958	Hs.75819	glycoprotein M6A	4.28
Ų,	130356	AF127577	Hs.155017	nuclear receptor interacting protein 1	4.27
	119830	AW054922	Hs.53478	Homo sapiens cD FLJ12366 fis, clone MA	4.27
	106758	AB014564	Hs.22616	KIAA0664 protein	4.25
	109709	F09749	Hs.187405	ESTs	4.25
70	110463		Hs.165067	ESTs	4.25
, 0	124472		Hs.102670	EST	4.25
	109770		Hs.248420	ESTs, Moderately similar to A47582 B-cel	4.24
	131487		Hs.27373	Homo sapiens mR; cD DKFZp564O1763 (f	4.23
	107216		Hs.211579	metanoma cell adhesion molecute	4.23
75	123562		Hs.190065	ESTs	4.23
. •	125986		Hs.205555	ESTs	4.23
	126221		Hs.172965	ESTs	4.23 4.23
	127092	T26985		gb:NIBT065H01R Infant brain, LLNL array	4.23 4.23
	132349		Hs.181286	serine protease inhibitor, Kazal type 1	4.23 4.22
80	118946	N92834		gb:zb67f03.s1 Soares_fetal_lung_NbHL19W	4.22 4.21
	101531		Hs.576	fucosidase, alpha-L-1, fissue	4.21
	105322		Hs.16346	ESTs, Weakly similar to S57447 HPBRII-7	4.20
	104219	AB002323	Hs.7720	dynein, cytoplasmic, heavy polypeptide 1	7.20

	102825	BE262386	Hs.7137	clones 23667 and 23775 zinc finger prote	4.20
	103571	A1675749	Hs.21,1608	nucleoparin 153kD	4.20
	106942	AA995351	Hs.31314	retinoblastoma-binding protein 7	4.20
-	112685	R87650	Hs.33439	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.20
5	123107	AA225048	Hs.104207	ESTs	4.20
	132659	Z75190	Hs.54481	low density tipoprotein receptor-related	4.20
	130084 114553	Al929377 BE219860	Hs.173724 Hs.22505	creatine kise, brain	4.19 4.18
	129628	U38945	Hs.1174	hypothetical protein FLJ 10159 cyclin-dependent kise Inhibitor 2A (me	4.18 4.18
10	102266	U29725	Hs.3080	mitogen-activated protein kise 7	4.18
	110637	AI241470	Hs.268982	ESTs	4.18
	127520	T51239		gb:yb20d12.s1 Stratagene fetal spleen (9	4.18
	130322	NM_014247	Hs.154545	PDZ domain containing guanine nucleotide	4.17
15	104768	D82319	Hs.11056	RALBP1 protein	4.17
13	123360 133110	AA532718 AA808177	Hs.178604 Hs.65228	ESTs ESTs	4.17 4.16
	130923	H96115	Hs.21293	UDP-N-acteylglucosamine pyrophosphorylas	4.16
	109878	BE620775	Hs.4866	Homo sapiens cD FLJ14387 ffs, clone HE	4.16
	119265	BE539706	Hs.285363	ESTs	4.16
20	124214	H58608	Hs.151323	ESTs	4.15
	106193	AA057478	Hs.23272	ESTs	4.15
	105169	BE245294	Hs.180789	S164 protein	4.15
	132304 131600	AA610002 NM_004377	Hs.44296 Hs.29331	hypothetical protein FLJ22324 camiltine palmitoyltransferase I, muscle	4.15 4.14
25	131365	M93415	Hs.26014	activin A receptor, type II	4.14
	121993	AW297880	Hs.98661	ESTs	4.14
	110779	Al391472	Hs.12561	ESTs, Highly similar to C212_HUMAN 28.3	4.13
	126383	AB032977	Hs.6298	KIAA1151 protein	4.13
20	104446	AF084555	Hs.7351	cyclic AMP phosphoprotein, 19 kD	4.13
30	131475 128933	AA992841 NM_002050	Hs.27263 Hs.334695	KIAA1458 protein	4.13 4.12
	113141	Al493276	Hs.9187	GATA-binding protein 2 ESTs	4.12
	134833	L20965	Hs.89901	phosphodiesterase 4A, cAMP-specific (dun	4.11
	106461	Al630759	Hs.17481	Homo saplens clone 24606 mR sequence	4.10
35	128056	A1990131	Hs.276973	potassium large conductance calcium-acti	4.10
	114757	AW970579	Hs.291031	ESTs	4.10
	134653	AI765883	Hs.87385	ESTs	4.09
	100472 103102	D90084 X61177	Hs.1023 Hs.68876	pyruvate dehydrogese (lipoamide) alpha interleukin 5 receptor, alpha	4.08 4.08
40	106779	BE276013	Hs.172364	Homo sapiens mR for FL100086 protein,	4.08
	133615	M62843	Hs.75236	ELAV (embryonic lethal, abnormal vision,	4.08
	130178	U20982	Hs.1516	insulin-like growth factor-binding prote	4.07
	124659	A1680737	Hs.289068	Homo sapiens cO FLJ11918 fis, clone HE	4.07
15	127861	AW295020	Hs.198529	ESTs	4.07
45	112129	AB037715	Hs.183639	hypothetical prolein FLJ10210	4.07
	100918 124677	AK001335 R01073	Hs.31137	protein tyrosine phosphatase, receptor t gb:yeB4c03.s1 Soares fetal liver spteen	4.06 4.05
	102722	F13271	Hs.79981	Human clone 23560 mR sequence	4.05
	111117	AB037721	Hs.173871	KIAA1300 protein	4.05
50	122506	AA449120	Hs.99209	ESTs	4.05
	126392	AI356294	Hs.3280	caspase 6, apoptosis-related cysteine pr	4.05
	130760	AW379130	Hs.18953	phosphodiesterase 9A	4.05
	104220	AB002324	Hs.301094	KIAA0326 protein	4.05
55	112774 111128	R95770 AW505364	Hs.35455 Hs.19074	ESTs LATS (large tumor suppressor, Drosophila	4.04 4.04
55	113146	BE151985	Hs.5722	hypothetical protein FLJ23316	4.04
	124940	AF068845	Hs.103804	heterogeneous nuclear ribonucleoprotein	4.03
	105498	H68279	Hs.24937	transformer-2 alpha (htra-2 alpha)	4.03
60	112631	R82040		gb:yj06b06.s1 Soares placenta Nb2HP Homo	4.03
60	118244	N62516	Hs.48556	ESTs	4.03
	118720 129232	N73515 R98881	Hs.109655	gb:za49d07.s1 Soares fetal liver spleen sex comb on midleg (Drosophila)-like 1	4.03 4.03
	134192	H01345	Hs.24139	Homo sapiens cD: FLJ23137 fis, done L	4.03
	131893	BE336886	Hs.3416	adipose differentiation-related protein	4.02
65	116793	T77781		gb:yd20a11.s1 Soares fetal liver spleen	4.02
	125674	AL036166	Hs.323378	coated vesicle membrane protein	. 4.01
	116640	X89984	Hs.211563	B-cell CLL/lymphoma 7A	4.01
	105057	AA134233	Hs.336942	Homo sapiens cD: FLJ21488 fis, clone C	4.00
70	105158 116245	AW976357 AB033107	Hs.234545 Hs.42796	hypothetical protein NUF2R KIAA1281 protein	4.00 4.00
70	119946	AA932283	Hs.58925	ESTs	4.00
	121975	AA740679	Hs.98631	ESTs	4.00
	132037	AA352702	Hs.332541	Homo sapiens, Similar to RIKEN cD 2700	4.00
75	133669	NM_006925	Hs.166975	splicing factor, arginine/serine-rich 5	4.00
75	109468	NM_015310	Hs.6763	KIAA0942 protein	3.99
	106829	AW959893	Hs.27099	hypothelical protein FLJ23293 similar to	3.99
	134682 105966	AW882645 AA142984	Hs.88044 Hs.5344	sprouty (Drosophila) homolog 1 (antagoni adaptor-related protein complex 1, gamma	3.98 3.98
	100448	AF234887	Hs.57652	cadherin, EGF LAG seven-pass G-type rece	3.98
80	102589	AU076728	Hs.8867	cysteine-rich, angiogenic inducer, 61	3.98
	104146	AW880614	Hs.146381	R binding motif protein, X chromosome	3.98
	111465	Al968256	Hs.15470	putative ring zinc finger protein NY-REN	3.98
	126499	AK001779	Hs.110445	CGI-97 protein	3.98

	134388	AW405434	Hs.82575	small nuclear ribonucleoprotein polypept	3.98
	105564	BE616694	Hs.288042	hypothetical protein FLJ14299	3.97
	115206	AW183695	Hs.186572	ESTs	3.96
5	103853	AF272390	Hs.111782	myosin 5C	3.96 3.96
	110542 106797	H58373 Al768801	Hs.332938 Hs.169943	hypothetical protein MGC5370 Homo sapiens cD FLJ13569 fis, clone PL	3.96
	130589	AL110226	Hs.16441	DKFZP434H204 protein	3.95
	122788	AI828638	Hs.99514	hypothetical protein FLJ20574	3.95
10	104518	H20816	Hs.112423	Homo sapiens mR; cO DKFZp586I1420 (f	3.95
10	130640	NM_004753	Hs.17144	short-chain dehydrogese/reductase 1	3.95
	110847	N30169	Hs.279807	ESTs, Weakly similar to 2004399A chromos	3.95
	116156 122096	AA461045 AA431162	Hs.50701 Hs.98690	ESTs ESTs	3.95 3.95
	122160	AI769281	Hs.97439	ESTs	3.95
15	123930	AA740878	Hs.112982	ESTs	3.95
	126280	Z19417		gb:HSB26B122 STRATAGENE Human skeletal m	3.95
	126547	U47732	Hs.84072	transmembrane 4 superfamily member 3	3.95
	134757	AA913267	Hs.211576	IL2-inducible T-cell kise	3.95
20	117296	AL133427	Hs.42506	Homo saplens mR full length insert cDN	3.95
20	112261 112268	AL050297 W39609	Hs.300861 Hs.22003	ESTs, Highly similar to T08701 hypotheti solute carrier family 6 (neurotransmitte	3.95 3.94
	131844	Al419294	Hs.324342	ESTs	3.94
	101607	X60111	Hs.1244	CD9 antigen (p24)	3.94
	121613	AA416879	Hs.193195	ESTs, Wealdy similar to 2109260A 8 cell	3.93
25	115815	AW905328	Hs.180842	ribosomal protein L13	3.93
	125684	AW589427	Hs.158849	Homo sapiens cD: FLJ21663 fis, clone C	3.93
	126783	AA083531	11- 400200	gb:zn09d10.s1 Stratagene hNT neuron (937	3.93
	129201 128954	H18359 AA346839	Hs.109390 Hs.209100	ESTs DKFZP434C171 protein	3.93 3.92
30	122939	AA477141	113.203100	gb:zu37g06.s1 Soares ovary tumor NbHOT H	3.92
•	130348	AB032957	Hs.210850	KIAA1131 protein	3.92
	125847	AW161885	Hs.249034	ESTs	3.91
	120452	AL022328	Hs.104335	hypothetical protein IMAGE3510317	3.91
35	123143	AA487595	41. 000045	gb:aa95e02.s1 Stratagene fetal reti 93	3.91
33	105729	H46612	Hs.293815 Hs.21103	Homo sapiens HSPC285 mR, partial cds	3.91 3.90
	106605 126714	AW772298 AF114491	Hs.137354	Homo saplens mR; cD DKFZp564B076 (fr egf-like module containing, mucin-like,	3.90
	121611	M31669	Hs.1735	inhibin, beta B (activin AB beta polypep	3,90
40	120468	AW967675	Hs.96487	ESTs, Highly similar to S08228 ribosomal	3.90
	101356	AW878229	Hs.80642	sigl transducer and activator of trans	3.89
	133668	L77964	Hs.271980	mitogen-activated protein kise 6	3.89
	109114	BE622787	Hs.84045	hypothetical protein FLJ20288	3.88
	115134 107850	AW968073 AA022910	Hs.194331 Hs.295446	ESTs, Highly similar to A55713 inositol ESTs, Moderately similar to 810024C cyto	3.88 3.88
45	130907	AA322866	Hs.21107	neuroligin	3.88
••	101879	AA176374	Hs.243886	nuclear autoantigenic sperm protein (his	3.88
	104267	AF043244	Hs.278439	nucleolar protein 3 (apoptosis repressor	3.88
	112232	BE253927	Hs.24983	hypothetical protein from EUROIMAGE 2021	3.88
50	113248	T63857		gb:yc16e01.s1 Stratagene lung (937210) H	3.88
50	114044	BE327427	Hs.79953	ESTs	3.88 3.88
	115414 129598	AA662240 N30436	Hs.283099 Hs.11556	AF15q14 protein Homo saplens cD FLJ12566 fis, clone NT	3.88
	102134	AL036967	Hs.2324	protamine 2	3.87
	106310	R98185	Hs.17240	ESTs	3.87
55	116470	Al272141	Hs.83484	SRY (sex determining region Y)-box 4	3.86
	110947	AW298410	Hs.21475	ESTs	3.85
	115839	BE300266	Hs.28935	transducin-like enhancer of split 1, hom	3.85
	103534 105209	AW970672	Hs.9247	protein kise, AMP-activated, alpha 1 c KIAA0980 protein	3.85 3.85
60	103203	AB023197 AA127017	Hs.227743 Hs.71052	ESTs	3.85
•	110565	A)884970	Hs.4983	ESTs	3.85
	110799	AI089660	Hs.323401	dpy-30-like protein	3.85
	117068	H91257	Hs.41391	EST	3.85
65	130956	NM_001135	Hs.2159	aggrecan 1 (chondroitin sulfate proteogl	3.85
65	102273	BE391815	Hs.75981	ubiquitin specific protesse 14 (tR-gua	3.85
	112960 114414	AL110209 AW152166	Hs.6770 Hs.182113	LCAT-like lysophospholipase ESTs	3.84 3.84
	109665	AA249439	Hs.27027	hypothetical protein DKFZp762H1311	3.84
	106208	AK001674	Hs.22630	cofactor required for Sp1 transcriptio	3.84
70	122311	NM_014913	Hs.131915	KIAA0863 protein	3.84
	124271	AW293223	Hs.8928	hypothetical protein FLJ20291	3.83
	106650	AL049951	Hs.22370	Homo sapiens mR; cD DKFZp56400122 (f	3.83
	112167	N99591	Hs.25587	ESTs, Weakly similar to T00329 hypotheti	3.83
75	122354 111462	AL157579 R05296	Hs.153610	KIAA0751 gene product gb:ye91e08.s1 Soares fetal liver spleen	3.83 3.81
13	128109	AW269421	Hs.128093	go:yes reos.s r Soares rerai liver spieen ESTs	3.81
	127003	AW816515	Hs.173540	ATPase, Class V, type 10D	3.81
	109210	AA669722	Hs.272137	ESTs	· 3.81
00	132543	BE568452	Hs.5101	protein regulator of cytokinesis 1	3.80
80	106827	AA457456	Hs.11408	hypothelical protein FLI20435	3.80
	124232	H63391	Hs.339677	ESTs, Weakly similar to 138022 hypotheti	3.80
	126039 128022	AL137523 AW195569	Hs.181102 Hs.125906	p30 DBC protein ESTs	3.80 3.80
		A11130003	1 12.12.000	word	3.00

				AA M. D. A	3.79
	132005	AA149707	Hs.173091	ubiquitin-lika 3	3.79
	131392	AA235153	Hs.26320	TRABID protein	3.79
	131775	AB014548	Hs.31921	KIAAD648 protein	3.79
5	126257	N99638	·	gb:za39g11.r1 Soares fetal liver spleen gb:zw75c05.s1 Soares_testis_NHT Homo sap	3.79
5	121950 116067	AA429515 AA454827	Hs.293637	ESTs	3.78
	104658	AA360954	Hs.27268	Homo sapiens cD: FLJ21933 fis, clone H	3.78
	104493	AW960427	Hs.79059	transforming growth factor, beta recepto	3.77
	100163	W44671	Hs.124	gene predicted from cO with a complete	3.77
10	116223	AF045458	Hs.47061	unc-51 (C. elegans)-like kise 1	3.77
	120586	AL031778	Hs.797	nuclear transcription factor Y, alpha	3.76
	128764	AW024282	Hs.104938	hypothetical protein MGC15906	3.75
	111574	AI024145	Hs.188526	ESTs	3.75
4.5	117396	W20128	Hs.296039	ESTs	3.75
15	119052	R10889		gb:yf38d02.s1 Soares fetal liver spleen	3.75 3.75
	121806	AA424313	Hs.98402	ESTs	3.75 3.75
	122410	AA446854	Hs.271004	ESTs, Weakly similar to I38022 hypotheti	3.75
	126638	AA649257	Hs.188602	ESTs ESTs	3.75
20	127879	AA768098	Hs.189079 Hs.196029	Homo sapiens mR for KIAA1657 protein,	3.75
20	121095 103430	AA320134 BE564090	Hs.20716	translocase of inner mitochondrial membr	3.74
	101230	AW504300	Hs.295605	mannosidase, alpha, class 2A, member 2	3.74
•	100200	H94688	Hs.173737	ras-related C3 botulinum toxin substrate	3.73
	106913	AI219346	Hs.86178	M-phase phosphoprotein 9	3.73
25	110975	H17012	Hs.14633	ESTs	3.73
	117314	N32498	Hs.42829	ESTs	3.73
	118737	AA199686		gb:zq75g09.r1 Stratagene hNT neuron (937	3.73
	124169	BE079334	Hs.271630	ESTs	3.73
20	124580	N68420	Hs.107992	ESTS	. 3.73 3.73
30	125747	NM_002884	Hs.865	RAP1A, member of RAS oncogene family	3.73 3.72
	124879	R73588	Hs.101533	ESTs	3.72
	128527	AA504583	Hs.101047	transcription factor 3 (E2A immunoglobul opsin 1 (cone pigments), long-wave-sensi	3.72
	103644	M13305 N90344	Hs.247787 Hs.149436	kinesin family member 58	3.71
35	106044 127867	C18530	113, 175750	gb:C18530 Human placenta cD (TFujiware	3.71
55	133828	T28472	Hs.7655	U2 small nuclear ribonucleoprotein auxil	3.71
	107387	D86983	Hs.118893	Melanoma associated gene	3.71
	104160	AA455706	Hs.44581	heat shock protein hsp70-related protein	3.71
	106098	BE278344	Hs.7970	DKFZP4348027 protein	3.70
40	133691	M85289	Hs.211573	heparan sulfate proteoglycan 2 (perlecan	3.70
	120717	AA904681	Hs.154434	ESTs, Weakly similar to unknown [H.sapie	3.70
	119263	T15977		gb:182328 Infant brain, Bento Soares Hom	3.70
	102305	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)	3.70
	106566	8E298210		gb:601118016F1 NIH_MGC_17 Homo sapiens c	3.70
45	110708	N33878	Hs.306117	KIAA0306 protein	3.70 3.70
	114357	R41677	Hs.6107	Homo sapiens cD FLJ14839 fis, clone OV	3.70
	115285	AW972872	Hs.293736	ESTs ninein (GSK3B interacting protein)	3.70
	123034	AL359571	Hs.44054 Hs.153326	EST	3.70
50	126396 132597	T06298 Y11192	Hs.5299	aldehyde dehydrogese 5 family, member	3.70
50	105823	A1559444	Hs.293960	ESTs	3.70
	102644	T59816	Hs.173311	C18B11 homolog (44.9kD)	3.70
	133513	AF136407	Hs.7446	chromosome 6 open reading frame 5	3.70
	116450	A1654450	Hs.47274	Homo sapiens mR; cD DKFZp564B176 (fr	3.69
55	104596	AF067804	Hs.15423	hypothetical protein HDCMC04P	3.69
	133579	X75346	Hs.75074	mitogen-activated protein kise-activat	3.68
	124556	N29317	Hs.236463	Homo sapiens mR; cD DKFZp586I0521 (f	3.68
	120534	AI635113	Hs.270366	ESTs, Weakly similar to 178885 serine/th	3.68
~	103156	BE259039	Hs.129953	Ewing sarcoma breakpoint region 1	3.68 3.68
60	134992	AA464444	Hs.5831	tissue inhibitor of metalloproteise 1	3.68
	106730	BE467313	Hs.260/0/	ESTs EST	3.68
	120880	AA360240	Hs.97019	gb:ee62f01.s1 Stratagene lung carcinoma	3.68
	123731	AA609839	Hs.251928	nuclear pore complex interacting protein	3.67
65	126973 103646	W46653 AW248439	Hs.2340	junction plakoglobin	3.67
05	116333	AF155827	Hs.203963	hypothetical protein FLJ10339	3.67
	120922	AA481003	Hs.97128	ESTs	3.67
	127407	AW089514	Hs.279681	heterogeneous nuclear ribonucleoprotein	3.67
	106578	AA836381	Hs.315111	nuclear receptor co-repressor/HDAC3 comp	3.67
70	123000	AI584156	Hs.105640	Homo sapiens, ctone IMAGE:4139775, mR,	3.67
	101464	AA852431	Hs.51299	DH dehydrogese (ubiquinone) fizvopro	3.67
	101397	M26380	Hs.180878	lipoprotein lipase	3.67
	131135	NM_016569	Hs.267182	TBX3-iso protein	3.66
	106112	AL117518	Hs.3686	KIAA0978 protein	3.66
75	123974	NM_015678	Hs.3821	neurobeachin	3.66
	127742	AW293496	Hs.180138	ESTs	3.66 3.66
	112908	BE281000	Hs.3530	TLS-associated serine-arginine protein 2	3.66 3.65
	131802	AL137406	Hs.296356	Homo saplens mR; cD DKFZp434M162 (fr	3.65
0Λ	135162	AJ187925	Hs.95667	F-box protein 30 eukaryotic translation elongation factor	3.65
80	124984	BE313210	Hs.223241	hypothetical protein	3.65
	118844	AL035364	Hs.50891 Hs.114191	ESTs	3.65
	125429 125596	A1023654 R25698	No.114131	gb:yg44h11.r2 Soares infant brain 1NiB H	3.65
	123330	112000		100	

	125792	AA496205	Hs.193700	Homo sapiens mR; cD DKFZp586I0324 (f	3.65
	126965	Al470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	3.65
	130776	AF167706	Hs.19280	cysteine-rich motor neuron 1	3.65
_	131949	AK000010	Hs.258798	hypothetical protein FLJ 20003	3.65
5	116612	C14904	Hs.45184	Homo sapiens cD FLJ12284 fis, done MA	3.65
	123749	AA609949	Hs.112790	EST	3.65
	134203	AA161219	Hs.799	diphtheria toxin receptor (heparin-bindi	3.64 3.64
	133605	AL038165	Hs.75187	translocase of outer mitochondrial membr calcitonin gene-related peptide-receptor	3.64
10	109235 125447	Al381800 Al582222	Hs.300684 Hs.128686	ESTs	3.63
10	122942	Al277829	Hs.111862	KIAA0590 gene product	3.63
	122748	AA458822	Hs.193815	ESTs	3.63
	103840	AW975861	Hs.47367	KIAA1785 protein	3.63
	105333	AA234831	Hs.246112	KIAA0788 protein	3.63
15	108807	Al652236	Hs.49376	hypothetical protein FLJ20644	3.63
	114699	AA127386		gb:zn90d09.r1 Stratagene lung carcinoma	3.63
	126040	Z28444	Hs.24119	Homo saplens mR; cD DKFZp586G2222 (f	3.63
	131028	A1879165	Hs.2227	CCAAT/enhancer binding protein (C/EBP),	3.63
20	131710	NM_015368	Hs.30985	pannexin 1	3.63 3.62
20	100164	AW372032	Hs.173714	MORF-related gene X Homo sapiens cD FLJ11953 fis, clone HE	3.62
	120837 131089	BE149656 Z42645	Hs.306621 Hs.22870	Homo sapiens of real 1965 its, cone ric Homo sapiens mR full length insert cDN	3.62
	126428	AA412436	Hs.301985	ESTs	3.62
	129148	AW501216	Hs.108945	KIAA0515 protein	3.61
25	102337	Al814663	Hs.170133	forkhead box O1A (rhabdomyosarcoma)	3.61
	104520	AI702384	Hs.76925	hypothetical protein FLJ14981	3.60
	112954	AA928953	Hs.6655	Homo sapiens EST from clone 208499, full	3.60
	125197	AF086270	Hs.278554	heterochromatin-like protein 1	3.60
	128124	AI125748	Hs.130194	ESTs	3.60
30	129553	AW015763	Hs.113065	ESTs	3.60
	123998	AA203429	Hs.79474	tyrosine 3-monooxygese/tryptophan 5-mo	3.60
	128835	AK001731	Hs.106390	Homo sapiens mR; cD DKFZp586H0924 (f	3,59 3.59
	129226	BE222494	Hs.180919	inhibitor of D binding 2, domint neg Homo sapiens, Similar to complement comp	3.59
35	135131	AI582743	Hs.94953 Hs.185807	Homo sapiens, Similar to PRO0478 protein	3.58
33	128955 100225	AA775076 D28539	Hs.167185	glutamate receptor, metabotropic 5	3.58
	101572	AA437199	Hs.656	cell division cycle 25C	3.58
	102277	U31099	Hs.158326	prostaglandin D2 receptor (DP)	3.58
	103667	Z80788	Hs.247815	H4 histone family, member L	3.58
40	112373	AW963357	Hs.7847	ESTs	3.58
	119284	AL041224	Hs.65379	ESTs	3.58
	125422	AA903229	Hs.153717	ESTs	3.58
	126381	M76665	Hs.275215	hydroxysteroid (11-beta) dehydrogese 1	3.58
ic	129168	Al132988	Hs.109052	chromosome 14 open reading frame 2	3.58
45	123133	AA487264	Hs.154974	Homo sapiens mR; cD DKFZp667N064 (fr	3.57
	128789	AW368576	Hs.139851	caveolin 2	3.57 3.57
	104172	AA476418	11- 0000	gb:zx02a12.s1 Soares_total_fetus_Nb2HF8_	3.57 3.57
	134263	AW973443	Hs.8086	R (guanine-7-) methyltransferase solute carrier family 7 (catlonic amino	3.57
50	101759 104942	M80244 NM_016348	Hs.184601 Hs.10235	chromosome 5 open reading frame 4	3.56
50	123443	BE244537	Hs.167382	triuretic peptide receptor A/guanylate	3.56
	110707	AI239832	Hs.15617	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.55
	106787	AI492261	Hs.32450	ESTs	3.55
	112940	AK001757	Hs.281348	hypothetical protein FLJ10895	3.55
55	115301	T11832	Hs.127797	Homo sapiens cD FLJ11381 fis, clone HE	3.55
	125978	N66843	Hs.35608	ESTs	3.55
	128002	Al985897	Hs.125293	ESTs	3.55
	119847	H81136	Hs.334604	Homo sapiens mR for KIAA1870 protein,	3.55
60	134595	NM_002401	Hs.29282	mitogen-activated protein kise kise	3.55 3.54
60	121309	AA293834 AA811286	Hs.97312 Hs.192837	ESTs ESTs, Weakly similar to ALU5_HUMAN ALU S	3.54
	122679 106061	AA511200 AA565356	Hs.13250	ESTs	3.54
	127207	AA377165	Hs.44833	ESTs	3.54
	129563	AF119664	Hs.27299	transcriptiol regulator protein	3.54
65	105951	R48700	Hs.20733	Homo sapiens cD: FLJ22356 fis, clone H	3.53
	115643	AA404276	Hs.123253	hypothetical protein FLJ22009	3.53
	130473	U11690	Hs.1572	faciogenital dysplasia (Aarskog-Scott sy	3.53
	104246	AF016032	Hs.201377	lysosomal	3.53
	120562	BE244580	Hs.302267	hypothetical protein FLJ10330	3.53
70	101211	AA355357	Hs.283429	SMC (mouse) homolog, X chromosome	3.53
	100774	J05581	Hs.89603	mucin 1, transmembrane	3.53
	108407	AA075519	Un 45467	gb:zm87h09.s1 Stratagene ovarian cancer ESTs, Wealdy similar to S37482 finger pr	3.53 3.53
	113538	Al554947	Hs.15167 Hs.5635	ESTs, weakly similar to 53/462 triger pr	3.53
75	113876 110731	A1799751 NM_014899	Hs.188006	KIAA0878 protein	3.52
13	125845	AK001440	Hs.131840	hypothetical protein FLJ10578	3.51
	112945	AW138458	Hs.20787	Homo sapiens cD: FLJ21686 fis, clone C	3.51
	131586	NM_012296	Hs.30687	GRB2-associated binding protein 2	3.51
	125413	Al887951	Hs.74566	dihydropyrimidise-like 3	3.51
80	129360	AJ000534	Hs.110708	sarcoglycan, epsilon	3.50
	128819	R38007	Hs.77578	ubiquitin specific protease 9, X chromos	3.50
	101973	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	3.50
	103616	NM_002647	Hs.32971	phosphoinositide-3-kise, class 3	3.50

	105535	AJ459519	Hs.297681	serine (or cysteine) proteise inhibito	3.50
	118767	AI038653	Hs.50500	ESTs	3.50
	126634	AW361109	Hs.43627	SRY (sex determining region Y)-box 22	3.50
5	130851 134353	R66282 AL138201	Hs.20247 Hs.82120	ESTs, Weakly similar to \$65657 atpha-1C-	3.50
•	111394	AA412227	Hs.16131	nuclear receptor subfamily 4, group A, m hypothetical protein FLJ12876	3.50 3.50
	102696	BE540274	Hs.239	forkhead box M1	3.49
	113037	R17268	Hs.259873	exol transport of sypiic vesicles	3.49
10	111028 131688	H59346 Al935413	Hs.30151	ESTs, Weakly similar to I38022 hypotheti	3.49
10	115613	AW136951	Hs.30692 Hs.173946	p21 (CDKN1A)-activated kise 2 hypothetical protein FLJ10486	3.49 3.48
	116975	H81076	Hs.269001	ESTs	3.48
	100210	D26361	Hs.3104	KJAA0042 gene product	3.48
15	110147 115600	H18700 AA081395	Hs.268799	ESTs	3.48
13	119088	R39261	Hs.42173 Hs.90790	Homo saplens cD FLJ10366 fis, clone NT Homo saplens cD: FLJ22930 fis, clone K	3.48
	120347	AA211068	Hs.120247	nuclear fragile X mental retardation pro	3.48 3.48
	122702	AI220089	Hs.99439	ESTs	3.48
20	125552	H09701	Hs.278366	ESTs, Weakly similar to 138022 hypotheti	3.48
20	126461 128572	Al381659	Hs.267086	ESTs	3.48
	118397	AA933022 BE139479	Hs.256583 Hs.161492	interleukin enhancer binding factor 3, 9 ESTs	3.48
	127999	AW978827	Hs.69851	nucleolar protein family A, member 1 (H/	3.47 3.47
25	132066	AI929392	Hs.181195	DJ (Hsp40) homolog, subfamily B, membe	3.47
25	105693	BE250951	Hs.181368	U5 snRNP-specific protein (220 kD), orth	3.47
	128874 119984	H06245	Hs.106801	ESTs, Weakly similar to PC4259 femilin	3.45
	104000	AA230228 AI146527	Hs.59197 Hs.80475	ESTs	3.46
	101488	BE547216	Hs.181128	polymerase (R) !! (D directed) polyp ELK1, member of ETS oncogene family	3.46 3.46
30	101045	J05614		gb:Human proliferating cell nuclear anti	3.46
	120149	AA227609	Hs.94834	ESTs	3.46
	107025	AA825523	Hs.21255	ESTs, Weakly similar to 138022 hypotheti	3.45
	101716 102899	AF050658 AI815559	Hs.2563 Hs.75730	tachykinin, precursor 1 (substance K, su	3.45
35	123075	AW293133	Hs.101340	sigt recognition particle receptor (d ESTs, Weakly similar to A42442 integrin	3.45 3.45
	124695	AA594979	Hs.239307	tyrosyl-tR synthetase	3.45
	127669	N28989	Hs.22891	solute carrier family 7 (cationic amino	3.45
	129793	AW207000	Hs.126857	Homo sapiens cD FLJ12936 fis, clone NT	3.44
40	120095 110915	AA693774 BE092285	Hs.59601 Hs.29724	ESTs	3.44
-10	130542	1)64675°	Hs.179825	hypothetical protein FLJ13187 RAN binding protein 2-like 1	3.43 3.43
	100488	BE273749	Hs.752	FK506-binding protein 1A (12kD)	3.43
	115027	AA743331	Hs.272572	hemoglobin, alpha 2	3.43
45	119298	NM_001241	Hs.155478	cyclin T2	3.43
45	126486 130021	Al065133 M24470	Hs.152316	hypothetical protein PRO0971	3.43
	127166	AW954605	Hs.1435 Hs.263395	guanosine monophosphate reductase sema domain, transmembrane domain (TM),	3.43 3.42
	114988	AA251089	1323000	gb:zs04f05.s1 NCI_CGAP_GC81 Homo sapiens	3.42
50	133817	AW578716	Hs.7644	H1 histone family, member 2	3.41
50	133562	M60721	Hs.74870	H2.0 (Drosophila)-like homeo box 1	3.41
	105610 129007	AA280072 AK001521	Hs.99872	fetal Alzheimer antigen	3.41
	100662	Al368680	Hs.107882 Hs.816	hypothetical protein FLJ10659 SRY (sex determining region Y)-box 2	3.41 3.41
	120159	R60781	Hs.92927	putative 47 kDa protein	3.41
55	134966	AW402389	Hs.920	modulator recognition factor I	3.41
	100369	D79988	Hs.115778	KIAA0166 gene product	3.41
	104260 100134	AF008192 AA305746	Hs.194283 Hs.49	putative GR6 protein	. 3.40
	116015	AA338648	Hs.50334	macrophage scavenger receptor 1 testes development-related NYD-SP22	3.40 3.40
60	119251	T15753	Hs.65250	EST 22	3.40
	127176	BE387162	Hs.280858	ESTs, Highly similar to A35661 D excis	3.40
	123422	AA598484	11- 440042	gb:ae38f04.s1 Gessler Wilms tumor Homo s	3.39
	123094 105289	AA761073 AB020638	Hs.146847 Hs.103000	TRAF family member-associated NFKB activ KIAA0831 protein	3.39
65	111219	N68836	Hs.19247	ESTs, Moderately similar to ALUC_HUMAN!	3.39 3.38
	127963	Al299013	Hs.87779	Homo saciens cD: FLJ23087 fis, clone L	3.38
	109412	BE543313	Hs.209473	hypothetical protein FLJ10520	3.38
	118794	AW517051	Hs.118210	ESTs	3.38
70	112040 111180	R43286 Al798851	Hs.283108	gb:yg17e11.s1 Soares infant brain 1NIB H hemoglobin, gamma G	3.38
	117329	AA524065	Hs.93670	nemogroom, gamma G Homo sapiens cD: FLJ22664 fis, clone H	3.38 3.38
	104371	AI288896	Hs.194081	ESTs, Weakly similar to 138022 hypotheti	3.38
	109265	AA195285	Hs.85982	ESTs	3.38
75	109557	AW452405	Hs.6427	ESTs	3.38
, ,	120753 120970	AA312551 AA398118	Hs.230157 Hs.97579	ESTs ESTs, Wealthy similar to A46010 X-linked	3.38
	127094	F13215	Hs.287849	ESTs, Weakly similar to A45010 X-linked ESTs, Weakly similar to T22074 hypotheti	3.38 3.38
	127746	A1239495	Hs.120189	ESTs	3.38
90	123553	Al494291	Hs.111977	ESTs	3.37
80	130652	M31669	Hs.1735	inhibin, beta 8 (activin AB beta polypep	3.37
	135101 121799	U82275 A1885670	Hs.94498 Hs.124027	leukocyte immunoglobulin-like receptor, SELENOPHOSPHATE SYNTHETASE; Human selen	3.37 3.37
	112278	Z41698	Hs.26039	Homo sepiens cD FLJ13937 fis, clone Y7	3.37 3.38

				Name against a D CI (4040C Co. along 544	3,36
	113401	AA610175	Hs.179647	Homo sapiens cD FLJ12195 fis, clone MA	3.36
	109292	AW975746	Hs.188662	KIAA1702 protein	3.36
	135026	N92165	Hs.93231 Hs.46914	ESTs ESTs, Weakly similar to A46010 X-linked	3.35
5	118210 123476	N49233 AA384564	Hs.108829	ESTs	3.35
,	111076	N59129	Hs.20851	ESTs	3.35
	111520	AI985369	Hs.301134	ESTs	3.35
	133383	BE313555	Hs.7252	KIAA1224 protein	3.35
	103731	AA070545		gb:zm70c03.r1 Stratagene neuroepithelium	3.35
10	110828	AK002114	Hs.23495	hypothetical protein FLJ11252	3.35
	112520	R68654	Hs.30814	ESTs	3.35
	115725	AW899053	Hs.76917	F-box only protein 8	3.35
	125867	H13331	Hs.123721	ESTs	3.35 3.35
15	127719	AI242163	Hs.22670	chromodomain helicase D binding protei	3.35
15	129863	BE379765	Hs.129872	sperm associated antigen 9 spectrin, alpha, erythrocytic 1 (ellipto	3.35
	130816	M61877	Hs.1985 Hs.173094	Homo sapiens mR for KIAA1750 protein,	3.35
	130888 133377	AL044315 AJ131245	Hs.7239	SEC24 (S. cerevisiae) related gene famil	3.35
	118986	AF148713	Hs.125830	bladder cancer overexpressed protein	3.35
20	101723	U34304	10.12000	gb:Human nonmuscle myosin heavy chain II	3.34
20	134693	N70361	Hs.8854	Human transcription unit PVT gene, exons	3.34
	102856	M26150	Hs.248177	H3 histone family, member L	3.34
	105593	AA279341	Hs.174151	aldehyde oxidase 1	3.34
	134748	L34059	Hs.89484	cadherin 4, type 1, R-cadherin (retil)	3.34
25	109149	AA831179	Hs.40065	hypothetical protein MGC4825	3.33
	115026	AA251972	Hs.188718	ESTs	3.33 3.33
	103546	Z14244	Hs.75752	cytochrome c oxidase subunit VIIb	3.33
	111189	N67603	Hs.272130	ESTs, Weakly similar to S65824 reverse t	3.33
20	127076	A1422951	Hs.146162	ESTs tubulin, beta polypeptide	3.33
30	124949	AI903210	Hs.336780 Hs.269818	ESTs, Weakly similar to Z195_HUMAN ZINC	3.33
	111012 113412	A1077389 AW628660	Hs.44131	KIAA0974 protein	3.33
	116351	AL133623	Hs.82501	similar to mouse Xm1 / Dhm2 protein	3.33
	121633	AA417011	Hs.98175	EST	3.33
35	124591	N69243	Hs.192974	hypothetical protein FLJ12735	3.33
-	130225	AB021179	Hs.15299	HMBA-inducible	3.33
	131945	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	3.33
	132581	AK000631	Hs.52256	hypothetical protein FLJ20624	3.33
40	105726	NM_012068	Hs.9754	activating transcription factor 5	3.32
40	101867	M96132		gb:Human MHC class II HLA-DR-beta-1*0901	3.32 3.32
	105004	BE616023	Hs.25298	KIAA1813 protein	3.32
	100288	AL039103	Hs.153834	pumilio (Drosophila) homolog 1 ESTs, Weakly similar to ALU1_HUMAN ALU S	3.32
	118349	N63786	Hs.94149 Hs.78853	uracil-D glycosylase	3.30
45	103352	H09366	ns.76000 Hs.12450	protocadherin 9	3.30
43	107436 109062	W27720 AA160941	FIS. 12400	gb:zq40d12.s1 Stratagene hNT neuron (937	3.30
	110379	Al300505	Hs.33130	Homo sapiens cD: FLJ23486 fis, clone L	3.30
	111221	AB037782	Hs.15119	KIAA1361 protein	3.30
	117903	AA768283	Hs.47111	ESTs	3.30
50	123265	AA491209		gb:aa47a08.s1 NCI_CGAP_GCB1 Homo saplens	3.30
	128226	AJ284940	Hs.289082	GM2 ganglioside activator protein	3.30
	111945	R40663	Hs.124944	ESTs	3.30
	126214	AW748336	Hs.168052	KIAA0421 protein	3.30 3.30
<i>E E</i>	121073	H46199	Hs.112184	DKFZP586J0619 protein	3.30
55	102083	T35901	Hs.75117	Interlaukin enhancer binding factor 2, 4 membrane metallo-endopeptidase (neutral	3.30
	100992	NM_007289	Hs.1298	growth arrest-specific 6	3.30
	134021	L13720 R26867	Hs.78501	gb:yh52e01.s1 Soares placenta Nb2HP Homo	3.29
	126452	A1798425	Hs.42710	ESTs	3.29
60	117195 127663	AK000452	Hs.10340	hypothetical protein FLJ20445	3.29
00	113677	Z70200	Hs.246112	KIAA0788 protein	3.28
	132398	AA876616	Hs.16979	ESTs, Weakly similar to A43932 mucin 2 p	3.28
	109533	AL043979	Hs.259729	KIAA0596 protein	3.28
	102915	X07820	Hs.2258	matrix metalloproteise 10 (stromelysin	3.28
65	104348	H05405	Hs.19221	hypothetical protein DKFZp566G1424	3.28
	113047	A1571940	Hs.7549	ESTs	3.28
	113203	AA743563	Hs.10305	ESTs	3.28 3.28
	114503	AL040600	Hs.188083	ESTs	3.28 3.28
70	122100	AA431220	Hs.41086	pleckstrin homology domain-containing, f ESTs	3.28
70	123073	AA485061	Hs.105652 Hs.167473	phosphoglucomutase 5	3.28
	130253	Al078570 W56119	Hs.155103	eukaryotic translation initiation factor	3.28
	130365 130762	D84371	Hs.1898	paraoxose 1	3.28
	132360	AW893660	Hs.46440	solute carrier family 21 (organic anion	3.28
75	110763	A1928445	Hs.92254	syptotagmin-like 2	3.27
, _	103437	AV655598	Hs.184211	peptidase (mitochondrial processing) bet	3.27
	114840	AA447591	Hs.87359	ESTs, Highly similar to RB18_HUMAN RAS-R	3.27
	106888	AA020964	Hs.24734	oxysterol binding protein	3.27
00	129896	BE295568	Hs.13225	UDP-Gal:betaGlcc beta 1,4- galactosylt	3.26
80	113459	T80206	Hs.14716	ESTs	3.26
	134332	D86962	Hs.81875	growth factor receptor-bound protein 10	3.26 3.26
	117048	H89732	Hs.230113	EST hypothorical cratain EL 120436	3.26 3.26
	109249	AA194730	Hs.268189	hypothetical protein FLJ20436	3.20

	134663	W73428	Hs.8750	uncharacterized bone marrow protein BM04	3.26
	114440	AL046511	Hs.106525	hypothetical protein FLJ 12567	3.25
	102196	BE266830	Hs.75238	chromatin essembly factor 1, subunit B (3.25
5	109581	R45584	Hs.23025	ESTs, Wealty similar to ALU5_HUMAN ALU S	3.25
3	120814	AW867796	Hs.96860	ESTs, Weakly similar to 138022 hypotheti	3.25
	122391 122553	AA446316 AA451884	Hs.191622 Hs.190121	ESTs ESTs	3.25 3.25
	124755	R38087	Hs.267690	KIAA1228 protein	3.25 3.25
	130943	U20760	Hs.272429	calcium-sensing receptor (hypocalciuric	3.25
10	115185	BE299677	Hs.105461	hypothetical protein FLJ20357	3.25
	114297	AA149707	Hs.173091	ubiquitin-like 3	3.25
	106657	AW854339	Hs.33476	hypothetical protein FLJ11937	3.25
	124320	H95749	Hs.102342	EŜT	3.25
4.0	124087	H08773	Hs.288590	Homo sapiens cD FLJ11454 fis, clone HE	3.24
15	110705	AB007902	Hs.32168	KIAA0442 protein	3.24
	106508	AI205785	Hs.30348	ESTs	3.24
	112538	AA908813	11 400004	gb:og77h06.s1 NCI_CGAP_Ov8 Homo sapiens	3.24
	100130	NM_000304	Hs.103724	peripheral myelin protein 22	3.24
20	106017 113921	AA477956 AW976530	Hs.26268 Hs.28355	ESTs	3.24 3.23
20	121520	AA412163	Hs.164785	ESTs	3.23
	129255	A1961727	Hs.109804	H1 histone family, member X	3.23
	125069	H81306	Hs.194485	ESTs	3.23
	119863	AA081218	Hs.58608	Homo sapiens cD FLJ14205 fis, clone NT	3.23
25	111273	N70934		gb:za33f06.s1 Soares fetal liver spleen	3.23
	102971	X16609	Hs.183805	ankyrin 1, erythrocytic	3.23
	103937	AA934063	Hs.13836	ESTs, Weakly similar to 138022 hypotheti	3.23
	121770	NM_015902	Hs.278428	progestin induced protein	3.23
20	128972	AA528140	Hs.107515	ESTs, Weakly similar to T00329 hypotheti	3.23
30	132528	T78736	Hs.50758	SMC4 (structural maintence of chromoso	3.23
	134835	L04569	Hs.89925	calcium channel, voltage-dependent, L ty	3.23
	103158	BE242587	Hs.118651	hematopoletically expressed homeobox KIAA0978 protein	3.22 3.22
	118405 104631	AL117518 AA002064	Hs.3686 Hs.18920	ESTs	3.22
35	114253	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.22
55	134607	A1675881	Hs.86538	ESTs	3.22
	135114	AW340493	Hs.175043	ancient conserved domain protein 4	3.22
	120191	BE407106	Hs.65907	Homo sapiens, clone IMAGE:3959816, mR,	3.22
	105029	Al122691	Hs.13268	ESTs	3.21
40	128550	AA418276	Hs.170142	ESTs	3.21
	119873	A1660149	Hs.44865	lysosomal	3.21
	130115	T47294	Hs.149923	X-box binding protein 1	3.21
	133916	AL039185	Hs.77558	thyroid hormone receptor interactor 7	3.21
45	120259	AW014786	Hs.192742	hypothetical protein FLJ12785	3.21
43	110721	H97678	Hs.31319	ESTs	3.21 3.21
	130062 100265	AL049415 D38521	Hs.278679 Hs.112396	a disintegrin and metalloproteise doma KIAA0077 protein	3.20
	100203	AB001025	Hs.9349	ryanodine receptor 3	3.20
	122275	AA437124	Hs.187247	ESTs	3.20
50	127099	AA347668		gb:EST54026 Fetal heart II Horno sapiens	3,20
	134321	BE538082	Hs.8172	ESTs, Moderately similar to A46010 X-lin	3.20
	132809	AF036144	Hs.5734	meningloma expressed antigen 5 (hyaluron	3.20
	101125	AJ250562	Hs.82749	transmembrane 4 superfamily member 2	3.20
	128339	AL121087	Hs.296406	KIAA0685 gene product	3.19
55	117121	H95044	Hs.321386	EST	3.19
	124760	AW408586	Hs.91052	ESTs, Moderately similar to ALU5_HUMAN A	3.19
	132232	Al522273	Hs.42640	ESTs	3.19
	125919	W26713 AB018352	Hs.256972 Hs.105399	ESTs KIAA0809 protein	3.19 3.19
60	123324		Hs.119	Wilms' tumour 1-associating protein	3.19
00	100157 101447	D14661 M21305	113.113	gb:Human alpha satellite and satellite 3	3.19
	124345	NM_014487	Hs.120766	nucleolar cysteine-rich protein	3.18
	122583	NM_012447	Hs.20132	stromal antigen 3	3.18
	128961	AL133014	Hs.107387	CGI-20 protein	3.18
65	111321	Al569766	Hs.13205	ESTs	3.18
	134977	AL044963	Hs.306121	leukocyte receptor cluster (LRC) encoded	3.18
	131535	N22120	Hs.75277	hypothetical protein FLJ13910	3.18
	109950	H08200	Hs.268770	ESTs, Wealdy similar to 2004399A chromos	3.18
70	129875	AA181018	Hs.13056	hypothetical protein FLJ13920	3.18
70	101654	M60298	Hs.733	erythrocyte membrane protein band 4.2	3.18
	104732	AL079294	Hs.29952	Homo sapiens mR full length insert cDN	3.18
	106867	AB037744	Hs.34892	KIAA1323 protein ribosomal protein L24	3.18 3.18
	108301	AA069728 Al432389	Hs.184582 Hs.161465	noosomas protein 1,24 ESTs	3.18
75	118042 120900	AA830712	Hs.291931	ESTs	3.18
, ,	129312	T97579	Hs.110334	ESTs, Weakly similar to 178885 serine/th	3.18
	116291	AW410377	Hs.41502	hypothetical protein FLJ21276	3.17
	110672	AW612890	Hs.191178	ESTs	3.17
	115665	BE072425	Hs.44579	hypothetical protein FLJ20199	3.17
80	127581	AK000680	Hs.266175	phosphoprotein associated with GEMs	3.17
	129584	AV656017	Hs.184325	CGI-76 protein	3.16
	108830	AA131743	Hs.193352	ESTs	3.16
	124443	Al857519	Hs.302031	zinc finger protein, subfamily 1A, 4 (Eo	3.16

				h atherical acatoin El 110955	3.16
	106290	AW961393	Hs.16364 Hs.99512	hypothetical protein FLJ10955 ESTs	3.16
	122787 133112	Al209093 T15465	Hs.182231	thyrotropin-releasing hormone	3.16
	116435	AA185761	Hs.334812	hypothetical protein DKFZp586K0717	3.16 3.16
5	109121	BE389387	Hs.49767	DH dehydrogese (ubiquinone) Fe-S pro Thy-1 cell surface antigen	3.15
	126721	AW579621	Hs.125359 Hs.79474	tyrosine 3-monooxygese/tryptophan 5-mo	3.15
	102526 100512	AA203429 D13317	Hs.78915	GA-binding protein transcription factor,	3.15 3.15
	105299	AF098951	Hs.194720	ATP-binding cassette, sub-family G (WHIT	3.15
10	117842	A1984505	Hs.161121	ESTs dickkopf (Xenopus laevis) homolog 2	3.15
	123049	BE047680	Hs.211869 Hs.102897	CGI-47 protein	3.15
	128639 130343	AW582962 AB040914	Hs.278628	KIAA1481 protein	3.15 3.15
	115706	AB004849	Hs.50748	chromosome 21 open reading frame 18	3.15 3.15
15	120673	AW968634	Hs.105093	ESTs ESTs	3.15
	132116	AW960474	Hs.40289 Hs.123178	translocase of inner mitochondrial membr	3.15
	116217 104926	AU076474 BE298808	Hs.33363	DKFZP434N093 protein	3.14 3.14
	105297	NM_015905	Hs.183858	transcriptiol intermediary factor 1	3.14
20	125343	A1475495	Hs.304101	ESTs, Weakly similar to ALU7_HUMAN ALU S disrupter of silencing 10	3.14
	115618	H11695 AA830185	Hs.322901 Hs.269680	ESTs	3.13
	124893 105461	BE539071	Hs.69388	hypothetical protein FLJ20505	3.13 3.13
	126165	AI741816	Hs.125897	ESTs Homo sapiens mR; cD DKFZp566M063 (fr	3.13
25	105212	AA205334	Hs.324278	small inducible cytokine A1 (I-309, homo	3.13
	101628	M57506 Al300077	Hs.72918 Hs.61590	ESTs	3,13
	107951 109166	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	3.13 3.13
	117299	N75768		gb:yw30b07.r1 Morton Fetal Cochtea Horno ESTs, Moderately similar to ICE4_HUMAN C	3.13
30	119694	AA041350	Hs.57847 Hs.164515	EST, Weakly similar to AF090930 1 PRO047	3.13
	124840	R56146 AW979155	Hs.298275	amino acid transporter 2	3.13
	127433 128337	Al123529	Hs.166592	ESTs	3.13 3.13
	134053	AW628686	Hs.78851	KIAA0217 protein KIAA0305 gene product	3.13
35	134475	NM_014733	Hs.83790 Hs.104925	ectodermal-neural cortex (with BTB-like	3.12
	128761 124971	BE300341 T23800	Hs.151001	hypothetical protein FLJ14728	3.12
	128314	T87479	Hs.291797	ESTs	3.12 3.12
	134695	AB036829	Hs.178347	SKIP for skeletal muscle and kidney enri transposon-derived Buster1 transposase-I	3.12
40	131333	BE244603	Hs.25726 Hs.55565	ankyrin repeat domain 3	3.12
	119781 131824	AJ278016 U28838	Hs.32935	TATA box binding protein (TBP)-associate	3.11
	124595	AW194851	Hs.111801	arsete resistance protein ARS2	3.11 3.11
	116115	AL042355	Hs.70202	WD repeat domain 10 MADS box transcription enhancer factor 2	3.11
45	129415	Al907084	Hs.111243 Hs.191185	ESTs	3.10
	111552 134861	T97939 NM_000937	Hs.171880	polymerase (R) II (D directed) polyp	3.10
	104971	BE311926	Hs.15830	hypothetical protein FLJ12691	3.10 3.10
	126536	AA156151		gb:zo48c06.r1 Stratagene endothelial cel	3.10
50	128246	Al990612	Hs.214818	DMRT-like family C2 ESTs	3.10
	106412 107902	AA453734 AA026627	Hs.10198 Hs.61358	ESTs	3.10
	112495	Al346487	Hs.28739	ESTs	3.09 3.09
	131870	NM_014874	Hs.3363	KIAA0214 gene product MAGE1 protein	3.09
55	105301	AW352357	Hs.7457 Hs.112708	ESTs, Moderately similar to ZN91_HUMAN Z	3.09
	123670 116474	Al189844 AW160774	Hs.159154	tubulin, beta, 4	3.09
	112064	AL049390	Hs.22689	Homo sapiens mR; cD DKFZp586O1318 (f	3.09 3.08
	130525	AA361850	Hs.322149	Human cione 137308 mR, partial cds retinoic acid induced 1	3.08
60	120398	AL133649	Hs.110953 Hs.3382	protein phosphatase 4, regulatory subuni	3.08
	102735 124748	AF111106 R34617	15,000	ohyti85h12.s1 Soares placenta Nb2HP Homo	3.08 3.08
	120755		Hs.190745	Homo saplens cD: FLJ21326 fis, clone C	3.08
~~	118895	BE304917	Hs.31097	hypothetical protein FLJ21478 hypothetical protein similar to actin re	3.08
65	107463		Hs.315164 Hs.25793	ESTs	3.08
	114290 119005		Hs.125316	ESTs, Weakly similar to S33990 finger pr	3.08 3.08
	125676		Hs.151973	hypothetical protein FLJ23511	3.08
=-	127766	AA723659	Hs.290607	EST KIAA0410 gene product	3.07
70			Hs.55075 Hs.239370	DKFZP7271051 protein	3.07
	106812 125654		Hs.9004	chondroitin sulfate proteoglycan 4 (meta	3.07
	111836		Hs.25119	ESTs, Weakly similar to YEXO_YEAST HYPOT	3.06 3.06
	101682	AF043045	Hs.81008	filamin B, beta (actin-binding protein-2 ESTs	3.06
75			Hs.268774 Hs.44656	ESTs	3.06
	11759 11073		Hs.7589	ESTs, Wealdy similar to A46010 X-linked	3.06
	13433		Hs.81964	SEC24 (S. cerevisiae) related gene famil	3.06 3.06
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10	128025	T64877	No 100470	gb:EST35034 Embryo, 6 week, subtracted (3.05	
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43191			Hs.2868	peripheral myelin protein 2	99.0	11.8	
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42734		0044	Hs.127792 Hs.176977	delta (Drosophila)-like 3	53.5	2.5	
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41295			Hs.75090	KIAA0282 protein	49.5	3.1	
44700		296968	Hs.157539	EST8	46.3 43.7	3.0	
43687		65204	Hs.47448	ESTs	45.7 39.8	3,2 10.8	
43355		5544	Hs.289048	ESTs	39.7	4.3	
425842	2 AI58	7490	Hs.159623	NK-2 (Drosophila) homolog B	39.3	4.3 26.2	
407034	4 U84	540		gb:Human dystrobrevin isoform DTN-3 (DTN	39.1	39.1	
43172			Hs.2839	Norrie disease (pseudoglioma)	38.4	3.7	
453392			Hs.32964	SRY (sex determining region Y)-box 11	37.5	22.1	
447197				gb:yh88b01.s1 Soares placenta Nb2HP Homo	37.5	13.9	
43941			Hs.12825	ESTs	35.4	3.1	
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449539			Hs.58446	ESTs	33.6	33.6	
408562		6323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	32.8	5.9	
431019 427540			Hs.2714	forkhead box G18	32.4	17.0	
425057		26434	Hs.20976 Hs.96944	ESTs	32.1	2.0	
43194		00106	Hs.272227	ESTS	31.0	2.3	
416829		13805	Hs.80220	Homo saplens cDNA FLJ20099 fis, clone CO catenin (cadherin-associated protein), d	30.8	30.8	
420807		80627	Hs.57846	ESTs	30.4	2.2	
444190		8918	Hs.10526	cysteine and glycine-rich protein 2	30.4	30.4	
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451678		74181	Hs.26799	DKFZP564D0764 protein	28.8	3.0	
439979	9 AW6	00291	Hs.6823	hypothetical protein FLJ10430	27.7	3.2	
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411078		2020	Hs.182364	ESTs, Weakly similar to 25 kDa trypsin i	26.0	26.0	
407808			Hs.289109	dimethylarginine dimethylaminohydrolase	25.8	2.2	
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421659			Hs.106511	protocadherin 17	25.0	3.3	
430132			Hs.234149	hypothetical protein FLJ20647	24.7	24.7	
433332 452744		7347 7652	Hs.127809	ESTS	24.6	24.6	
419271			Hs.30504 Hs.238532	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	23.8	23.8	
447397			Hs.18442	ESTs E-1 enzyme	23.6	5.5	
439039			Hs.48713	ESTs	23.1	3.2	
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451099			Hs.25954	Interleukin 13 receptor, alpha 2	22.2 22.0	2.0 7.6	
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435706			Hs.7045	GL004 protein	19.7	19.7	
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416892 442562			Hs.80409	growth arrest and DNA-damage-inducible.	19.6	19.6	
439451			Hs.34789	ESTs	19.4	19.4	
426320			Hs.278554 Hs.169300	heterochromatin-like protein 1	19.1	17,4	
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452106			Hs.21342	ESTs	18.6	18.6	
431173			Hs.294068	ESTs	18.6 18.6	10.3	
422583			Hs.118578	H.sapiens mRNA for ribosomal protein L18	18.5	18.6 18.5	
419088			Hs.77496	small nuclear ribonucleoprotein polypegt	18.5	18.5	
443547			Hs.23767	Homo saplens cDNA FLJ12666 fis, clone NT	18.5	5.1	
451592		5416	Hs.213897	ESTs	18.4	18.4	
450313	3 A1031		Hs.24809	hypothetical protein FLJ10826	18.3	18.3	

	400544	A D040250	U= 440440	VIA ACTAE anno product	18.2	4.7
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	418027			hypothetical protein	18.0	8.2
_	414117			proteolipid protein (Pelizaeus-Merzbache	18.0 17.8	18.0 17.8
5	429418 432527		Hs.99283 Hs.102754	ESTs ESTs	17.7	4.2
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10	436476		Hs.53631	ESTs, Wealdy similar to enhancer-of-spli	17.4 17.3	2.1 18.8
10	445133 446659	AW157646 Al335361	Hs.153506 Hs.226376	ESTs, Weakly similar to AF150755 1 micro ESTs	17.2	2.8
	409049	Al423132	Hs.146343	ESTs	17.2	3.8
	443672	AA323362	Hs.9667	butyrobetaine (gamma), 2-oxoglutarate di	17.2 17.0	11.0 6.3
15	407748	AL079409	Hs.38176 Hs.143237	KIAA0606 protein; SCN Circadian Oscillat ESTs	16.9	16.9
13	438527 417791	Al969251 AW965339	Hs.111471	ESTs	16.8	10.5
	417355	D13168	Hs.82002	endothelin receptor type B	16.4	16.4
	427897	NM_017413		apelin; peptide ligand for APJ receptor	16.3 16.2	4.2 4.4
20	419721	NM_001650 AA411101	Hs.288650 Hs.221750	aquaporin 4 ESTs	16.1	3.9
20	427701 432435	BE218886	Hs.282070	ESTs	16.1	5.7
	426809	BE313114	Hs.29706	ESTs	16.0	10.0 15.9
	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	15.9 15.7	15.7
25	400859 409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	15.6	15.6
23	420092	AA814043	Hs.88045	ESTs	15.6	5.4
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	422365	AF035537	Hs.115521	REV3 (yeast homolog)-like, catalytic sub ESTs	15.2	15.2
30	449611 414922	AI970394 D00723	Hs.197075 Hs.77631	glycine cleavage system protein H (amino	15.2	5.6
50	405238				15.1	2.8
	429007	D80642		gb:HUM092E098 Human fetal brain (TFujiwa	15.0 14.9	3.5 7.1
	409638 445888	AW450420 AF070564	Hs.21335 Hs.13415	ESTs Homo sapiens clone 24571 mRNA sequence	14.8	5.7
35	416737	AF154335	Hs.79691	LIM domain protein	14.7	4.2
-	429163	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	14.6	3.0 2.6
	436870	AW204219	Hs.43679	ESTs	14.6 14.6	3.5
	443181 436281	AI039201 AW411194	Hs.54548 Hs.120051	ESTs ESTs	14.5	8.5
40	449448	D60730	Hs.57471	ESTs	14.4	4.8
	422564	AI148006	Hs.222120	ESTs	14.4 14.3	14.4 2.4
	448243	AW369771	Hs.77496	small nuclear ribonucleoprotein polypept ESTs	14.3	14.2
	428748 452576	AW593206 AB023177	Hs.98785 Hs.29900	KIAA0960 protein	14.1	8.1
45	452461	N78223	Hs.108106	transcription factor	14.1	12.8
	449670	F07693	Hs.23869	Homo sapiens mRNA; cDNA DKFZp434K2172 (f	14.1 14.0	14.1 2.3
	436637 429597	AI783629	Hs.26766 Hs.2442	ESTs a disintegrin and metalloproteinase doma	13.9	
	419078	M93119	Hs.89584	insulinoma-associated 1	13.9	2.9
50	410889	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	13.9	
	452355	N54926	Hs.29202	G protein-coupled receptor 34	13.9 13.9	
	421452 430290	Al925946 Al734110	Hs.104530 Hs.136355		13.8	
	430387	AW372884		nuclear cap binding protein subunit 2, 2	13.6	
55	415875	AA894876	Hs.5687	protein phosphatase 1B (formerly 2C), ma	13.5 13.5	
	416795 422025	AI497778 BE348774	Hs.168053 Hs.122554		13.3	
	400992	DESTOTA	113.122351	2515	13.3	5.5
60	41,3174	AA723564	Hs.191343		13.1 13.1	
60	425187	AW014486		ESTs ESTs, Weakly similar to hypothetical pro	13.	
	456965 419852	AW131888 AW503756		hypothetical protein dJ551D2.5	13.0	2.4
	409327	L41162	Hs.53563	collagen, type iX, alpha 3	12.5	
CE	439519	AA837118		6 ESTs hypothetical protein FLJ20729	12.9 12.1	
65	436299 446657	AK000767 Al335191	Hs.5111 Hs.260702		12.	
	423073	BE252922			12.	
	424278	AK000723			12.	
70	451996	AW51402	1 Hs.24551) ESTs	12. 12.	
70	400860 439579	AF086400	1	gb:Homo sapiens full length insert cDNA	12.	4 12.4
	408312	AF263613	Hs.44198	intracellular membrane-associated calciu	12.	
	419948	AB041035			12 12	
75	427304 419498	AA761526 AL036591			12	
13	428137	AA421792		. <u></u>	12	.2 12.2
	432683	AW99544	1 Hs.10475	ESTs	12	
	408622	AA056060			12 12	
80	453884 441440	AA355925 AJ807981			12	.0 3.6
55	414217	Al309298	Hs.27989	8 Homo sapiens cDNA: FLJ23165 fis, clone L	12	.0 62.7
	410227	AB00928			11 11	
	439444	Al277652	Hs.54576	ESTs		10.3

			11. 400ccn	EST-	11.7	9.0
	433309			ESTs ESTs	11.6	9.7
	439170 417160			protecilpid protein (Pelizaeus-Merzbache	11.5	7.2
	424668			cryptochrome 1 (photolyase-like)	11.5	5.8
5	410611		Hs.20924	KIAA1628 protein	11.5	28.2
	437124			ESTs	11.5 11.3	11.5 11.3
	418858			Homo sapiens cDNA: FLJ22489 fis, clone H	11.3	2.8
	423600		Hs.29076 Hs.201603	Homo saplens cDNA: FLJ21841 fis, clone H ESTs, Highly similar to hypothetical pro	11.3	11.3
10	429393 431103		Hs.44	pleiotrophin (heparin binding growth fac	11.3	3.4
10	452092		Hs.27842	hypothetical protein FLJ11210	11.3	11.7
	431701		Hs.14658	ESTs	11.3	2.6
	429399	AA452244	Hs.16727	ESTs	11.2	22
1.5	408988	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	11.2 11.1	27.8 11.1
15	442671	A1005668	Hs.134779	EST	11.1	11.1
	402524	A ADDE4 43	Hs.125719	ESTs	11.1	11.1
	415558 422390	AA885143 AW450893	Hs.121830	ESTs. Weakly similar to KIAA0924 protein	11.0	8.8
	418475	A1858732	Hs.30443	sentrin/SUMO-specific protease	11.0	6.1
20	458809	AW972512	Hs.20985	sin3-associated polypeptida, 30kD	11.0	5.6
	410297	AA148710	Hs.159441	ESTs	11.0	3.3
	444017	U04840	Hs.214	neuro-oncological ventral antigen 1	11.0	11.0 3.3
	437814	AJ088192	Hs.135474	ESTs, Weakly similar to DDX9_HUMAN ATP-D	10.9 10.8	8.0
25	427194	AA399018	Hs.250835	ESTs gb:EST383453 MAGE resequences, MAGL Homo	10.8	10.0
23	432060	AW971364 Al026838	Hs.30120	ESTs	10.8	10.8
	453861 408829	NM_006042		heparan sulfate (glucosamine) 3-O-sulfot	10.6	3.3
	416913	AW934714	110.10001	gb:RC1-DT0001-031299-011-a11 DT0001 Homo	10.6	3.4
	418049	AA211467	Hs.190488	hypothetical protein FLJ10120	10.6	10.6
30	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	10.6	27.2
	425264	AA353953	Hs.20369	ESTs, Weakly similar to gonadotropin ind	10.5	2.0 10.5
	434408	AI031771	Hs.132586	ESTs	10.5 10.5	6.2
	451697	AW449774	Hs.257208	ESTs ESTs, Moderately similar to gonadotropin	10.3	10.3
35	436754	AI061288	Hs.133437 Hs.182185	ESTs	10.3	2.9
33	410298 412766	A1693821 BE544475	Hs.54347	ESTs	10.3	10.3
	450689	Al369275	Hs.243010	ESTs, Moderately similar to RTCO_HUMAN G	10.3	10.3
	408331	NM_007240		dual specificity phosphatase 12	10.3	4.5
	442007	AA301116	Hs.142838	Homo sapiens cDNA: FLJ23444 fis, clone H	10.3	10.3
40	410386	W26187	Hs.3327	Homo sapiens cDNA: FLJ22219 fis, clone H	10.2	2.1 10.1
	440684	Al253123	Hs.127356	ESTs, Highly similar to NEST_HUMAN NESTI	10.1 10.0	10.0
	420892	AW975076	Hs.172589	nuclear phosphoprotein similar to S. cer	9.9	15.8
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein ESTs, Moderately similar to ALU2_HUMAN A	9.7	23.2
45	419972	AL041465 AK002135	Hs.294038 Hs.3542	hypothetical protein FLJ11273	9.6	6.5
40	433730 434851	AA806164	Hs.116502	ESTs	9.5	6.5
	436306	AA805939	Hs.117927	ESTs	9.5	4.7
	453331	AI240665	Hs.8895	ESTs	9.2	5.8
	414429	R51494	Hs.71818	ESTs	9.0	6.2 18.1
50	424998	U58515	Hs.154138	chitinase 3-like 2	8.9 8.9	3.6
	446936	H10207	Hs.47314	ESTs	8.8	3.8
	410276	A1554545	Hs.68301 Hs.35861	ESTs DKFZP586E1621 protein	8.8	3.8
	453857 448321	AL080235 NM 00588	3 Hs.20912	adanomatous polyposis coli lika	8.8	2.0
55	414783	AW069569		zinc finger protein 6 (CMPX1)	8.7	3.0
55	441079	AW150697			8.7	2.2
	437517	AI927675	Hs.99858	ribosomal protein L7a	8.6	4.5
	409062	AL157488	Hs.50150	Homo sapiens mRNA; cDNA DKFZp564B182 (fr	8.6 8.6	12.2 10.4
C 0	420630	AL133101	Hs.99508	Homo sapiens mRNA; cDNA DKFZp43400921 (f	8.5	11.5
60	409260	AW242407		ESTs	8.4	4.6
	442343	AA992480 AA180363			8.4	7.2
	416439 428054	A1948688	Hs.266619		8.2	9.2
	421633	AF121860			8.2	2.6
65	433285	AW975944			8.1	3.3
	433226	AW503733	3 Hs.9414	KIAA1488 protein	8.0	13.4 2.5
	424800	AL035588			8.0 7.9	4.8
	425681	AB018297			7.9 7.9	3.7
70	445034	AW293371			7.6	6.4
70	435020 446985	AW505070 AL038704			7.5	7.8
	446619	AU076643		secreted phosphoprotein 1 (osteopontin,	7.5	3.9
	418522	AA605038		Homo sapiens cDNA: FLJ21950 fis, clone H	7.5	2.2
	439864	AJ720078	Hs.29199		7.4	6.9
75	419723	AL120193			7.4 7.3	3.5 22.1
	447896	AJ436124	Hs.29406	9 ESTs, Wealdy similar to ORF2 contains a	7.3 7.3	40.8
	404210	A\44374F	D Um 44646	1 ESTs	7.2	11.8
	436671 439231	AW13715 AW58193			7.2	2.5
80	439231	BE20757			7.1	6.4
50	459290		46 Hs.34853		7.0	6.7
	423869	BE40930		2 C1q-related factor	7.0	4.9
	414825	X06370	Hs.77432	epidermal growth factor receptor (avian	6.9	6.4

			11 61076	tria samundana muhtijisinikavin l	6.9	8.6
	420018 428600	U56387 AW863261	Hs.15036	proprotein convertase subtilisin/kexin t ESTs, Highly similar to AF161358 1 HSPC0	6.9	7.7
	438380	T06430	Hs.6194	chondroitin sulfate proteoglycan BEHAB/b	6.9 6.8	3.1 7.0
5	402604 417022	NM_014737	Hs.80905	Ras association (RalGDS/AF-6) domain fam	6.8	2.5
•	405239	U89281	Hs.11958	oxidative 3 alpha hydroxysteroid dehydro	6.B 6.6	2.9 2.6
	433577 434629	AW007080 AA789081	Hs.8817 Hs.4029	ESTs glioma-amplified sequence-41	6.6	13.9
	413886	AW958264	Hs.103832	ESTs, Weakly similar to TRHY_HUMAN TRICH	6.6 6.5	2.2 13.7
10	451460	A1797550 A1022650	Hs.209652 Hs.8117	ESTs erbb2-interacting protein ERBIN	6.5	15.6
	442145 437273	AL137451	Hs.120873	ESTs, Highly similar to hypothetical pro	6.5	2.4
	418365	AW014345	Hs.161690	ESTs	6.4 6.4	12.8 4.3
15	421684 449458	BE281591 AI805078	Hs.106768 Hs.208261	hypothetical protein FLJ10511 ESTs	6.4	2.3
13	426413	AA377823		gb:EST90805 Synovial sarcoma Homo sapien	6.3 6.3	13.2 10.9
	426423 417709		Hs.169833 Hs.82426	single-stranded-DNA-binding protein KIAA0247 gene product	6.3	23.3
	448499	D87434 BE613280	Hs.250655	prothymosin, alpha (gene sequence 28)	6.2	2.9
20	444880	AW118683	Hs.154150	ESTs	6.2 6.2	19.4 12.7
	432715 444864	AA247152 AW965446	Hs.200483 Hs.46637	ESTs, Weakly similar to KIAA1074 protein ESTs, Weakly similar to cDNA EST yk289g5	6.2	4.1
	407792	A1077715	Hs.39384	putative secreted ligand homologous to f	6.2 6.1	3.4 2.6
25	431962	AL049385	Hs.272251 Hs.143460	Homo sapiens mRNA; cDNA DKFZp586M1418 (f protein kinase C, nu	6.1	14.6
23	424232 436443	AB015982 AW138211	Hs.128746	ESTs	6.1	2.8
	433647	AA603367	Hs.222294	ESTs	6.1 6.1	15.0 3.4
	449961	AW265634 AW080932		ESTs heterogeneous nuclear protein similar to	6.1	6.1
30	448704 408393	AW015318	Hs.23165	ESTs	6.1	21.6 2.2
	450693	AW450461		ESTs Cbp/p300-interacting transactivator, wit	6.1 6.0	2.4
	407846 445817	AA426202 NM 00364	Hs.40403 2 Hs.13340	histone acetyltransferase 1	6.0	10.9
	440650	R44692	Hs.6640	ESTs	6.0 6.0	2.1 2.4
35	417675	A1808607	Hs.3781 Hs.68318	similar to murine leucine-rich repeat pr hypothetical protein FLJ20344	6.0	3.6
	411083 407910	N41340 AA650274		fibronectin leucine rich transmembrane p	6.0	6.0
	402855			at a decrease and homeohouse 1	6.0 6.0	2.6 11.6
40	445594 418791	AW058463 AA935633		zinc-fingers and homeoboxes 1 ESTs	5.9	6.7
40	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	5.9 5.9	2,3 11.8
	435677	AA694142		ESTs ESTs	5.9	7.5
	430334 452834	A1824719 A1638627	Hs.47557 Hs.105685	ESTs	5.9	2.6
45	427315	AA179949		Homo sapiens mRNA; cDNA DKFZp564N0763 (f	5.8 5.8	3.1 2.0
	428250 418506	AW80920 AA084248		DKFZP566F2124 protein G protein-coupled receptor 39	5.8	2.5
	417115	AW95279	2 Hs.1066	small nuclear ribonucleoprotein polypept	5.8 5.8	16.0 3.8
50	436758	AW97716		ESTs hypothetical protein FLJ10773	5.7	5.1
50	446332 423943	AK001639 AF163570		polymerase (DNA-directed) kappa	5.7	11.1
	428180	AI129767		Homo saplens cONA: FLJ21929 fis, clone H	5.6 5.6	7.1 2.2
	424343 417318	AW95636 AW95393		ESTs, Highly similar to JN0902 pituitary ESTs	5.6	25.0
55	423582	BE00083	1 Hs.23837	Homo saplens cDNA FLJ11812 fis, clone HE	5.6 5.4	4.1 3.5
	427472 434701	AA52253 AA46047		transposon-derived Buster3 transposase-l KiAA0742 protein	5.4	21.2
	434707	R60704	Hs.234434	hairy/enhancer-of-split related with YRP	5.3	2.7 4.1
60	411019	AW99309		Homo sapiens cDNA FLJ12540 fis, clone NT Homo sapiens NY-REN-62 antigen mRNA, par	5.3 5.3	2.4
00	424939 424028	AK00005 AF05508			5.3	2.7
	444534	AW2716	26 Hs.42294	ESTs	5.3 5.2	2.1 3.8
	426171 431843	AI128606 AA51642			5.2	6.2
65	438204	A)58964	5 Hs.12869) ESTs	5.2 5.2	5.8 8.4
	424635	AA42068			5.2 5.2	2.4
	436223 450649	AK00188 NM_001	429 Hs.29772		5.2	15.3
70	441689	Al12370	5 Hs.10693	2 ESTs	5.2 5.1	2.2 3.3
70	443392 416179	AI05582 R19015		MAD (mothers against decapentaplegic, Dr	5.1	16.7
	452167	N75238	Hs.13075	Homo sagiens cDNA: FLJ23013 fis, clone L	5.1 5.0	18.7 2.4
	434001	AW9509		serine (or cysteine) proteinase inhibito 1 ESTs, Weakly similar to dJ37E16.2 [H.sap	5.0 5.0	3.9
75	458435 433586	Al41871 T85301	io FIS. 14412	gb:yd78d06.s1 Soares fetal liver spleen	5.0	28
	452040	AW973	242 Hs.29369		5.0 5.0	4.5 4.3
	404029 421141	AW117	261 Hs.1259	4 ESTs	5.0	21
•	402605				4.9 4.9	4.2 2.5
80					4.9	2.4
	416404 435615			potassium voltage-gated channel, KQT-lik	4.9	7.2
	448425			O1 ESTs	4.9	4.9
				4.1		

	445773 448451	H73456 AW015994	Hs.13299	Homo saplens mRNA; cDNA DKFZp761M0111 (f qb:UI-H-Bl0p-abh-g-09-0-UI.s1 NOL_CGAP_S	4.9 4.9	29 22
	444838	AV651680	Hs.208558	ESTs	4.8	6.7
_	452438	BE514230	Hs.29595	JM4 protein	4.8	2.7
5	443898	AW804296	Hs.9950	Sec61 gamma	4.8	7.2
	452776	AA194540	Hs.13522	ESTs	4.8	3.4
	426108	AA622037	Hs.166468	programmed cell death 5	4.8	16.7
	416774 427704	A1005169 AW971063	Hs.28274 Hs.292882	Homo sapiens cDNA: FLJ22049 fis, clone H ESTs	4.8 4.8	3.2 23.8
10	433588	A1056872	Hs.133386	ESTs ESTs	4.8	12.8
10	410108	AA081659	Hs.191098	KIAA1479 protein	4.7	2.1
	433556	W56321	Hs.111460	Homo sagiens cDNA: FLJ21715 fis, clone C	4.7	11.2
	418962	AA714835	Hs.271863	ESTs	4.7	2.2
4 -	404049				4,7	3.0
15	436222	Al208737	Hs.122810	Homo sapiens cDNA FLJ11489 fs, clone HE	4.7	3.3
	425234	AW152225	Hs.165909	ESTs	4.7	3.1
	426490 426514	NM_001621 BE616633	Hs.170087 Hs.301122	aryl hydrocarbon receptor bone morphogenetic protein 7 (osteogenic	4.7 4.7	9.1 2.7
	428722	U76456	Hs.190787	tissue inhibitor of metalloproteinase 4	4.6	6.7
20	451989	AF169797	Hs.27413	adaptor protein containing pH domain, PT	4.6	13.4
	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	4.6	18.4
	422488	AI679968	Hs.152060	ESTs	4.6	7.7
	428862	NM_000346		SRY (sex-determining region Y)-box 9 (ca	4.6	4.6
25	413724	AA131466	Hs.23767	Homo sapiens cDNA FLJ12666 fis, clone NT	4.5	11.9
25	442495	AJ184717		gb:qd64b01.x1 Soares_testis_NHT Homo sap	4.5 4.5	4.5 11.6
	403549 456209	W60633	Hs.297792	ESTs	4.5	5.1
	421181		Hs.184585	LIM domain only 2 (rhombotin-like 1)	4.5	10.6
	439566	AF086387	15.10-1000	gb:Homo sepiens full length insert cONA	4.4	2.6
30	446329	NM_013272	Hs.14805	solute carrier family 21 (organic anion	4.4	17.2
	446488	AB037782	Hs.15119	KIAA1361 protein	4.4	8.4
	426110	NM_002913	Hs.166563	replication factor C (activator 1) 1 (14	4.4	2.5
	427413	BE547647	Hs.177781	superoxide dismutase 2, mitochondrial	4.4	14.3
25	424340	AA339036	Hs.7033	ESTs	4.4	3.9
35	421552	AF026692	Hs.105700	secreted trizzled-related protein 4	4.3 4.3	31.1 6.1
	422033 434476	AW245805 AW858520	Hs.110903 Hs.271825	claudin 5 (transmembrane protein deleted ESTs	4.3	4.5
	420582	BE047878	Hs.99093	Homo sapiens chromosome 19, cosmid R2837	4.3	3.6
	419904	AA974411	Hs.18672	ESTs	4.3	17.1
40	407939	W05608		gb:za85e07.r1 Soares_fetal_lung_NbHL19W	4.3	9.0
•	425836	AW955696	Hs.94842	ESTs	4.3	3.2
	426304	AA374532	Hs.297985	ESTs	4.3	6.6
	439653	AW021103	Hs.6631	hypothetical protein FLJ20373	4.3 4.3	23 25
45	424723	BE409813	Hs.152337 Hs.166146	protein arginine N-methyltransferase 3(h Homer, neuronal immediate early gene, 3	4.2	4.1
73	426064 409509	BE387014 AL036923	Hs.127006	ESTs	4.2	16.4
	424391	BE550112	Hs.112712	ESTs	4.2	3.8
	425248	AW957442	Hs.252766	ESTs	4.2	11.1
	418259	AA215404	Hs.137289	ESTs	4.2	19.3
50	445525	BE149866	Hs.14831	ESTs	4.2	3.1
	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity la, re	4.2 4.2	34.8 3.0
	430935	AW072916	Hs.115654	ESTs ESTs, Wealdy similar to ORF2 (M.musculus	4.2 4.2	2.4
	442233 416959	AW967149 D28459	Hs.28439 Hs.60612	ubiquitin-conjugating enzyme E2A (RAD6 h	4.1	15.3
55	437097	N45312	Hs.46506	ESTs	4.1	15.6
• •	428189	AA424030	Hs.46627	ESTs	4.1	3.6
	434963	AW974957	Hs.288719	Homo sapiens cDNA FLJ12142 fis, clone MA	4.1	12.2
	425500	AB011541	Hs.158200	EGF-like-domain, multiple 4	4.1	2.8
60	435177	AI018174	Hs.42936	ESTS	4.1 4.1	2.1 4.1
UU	418357 419086	Z44718	Hs.301010 Hs.89591	ESTs, Highly similar to AF159851 1 Rho G Kalimann syndrome 1 sequence	4.1	4.1
	436557	W15573	Hs.5027	ESTs	4.0	21
	425588	F07396	Hs.46751	ESTs	4.0	2.2
	423905	AW579960			4.0	3.6
65	437095	D14661	Hs.119	Wilms' tumour 1-associating protein	4.0	10.0
•	425332	AA633306	Hs.127279		4.0	10.9
	431556	AF016028	Hs.260039		4.0	3.8
	427209	H06509	Hs.92423	KIAA1566 protein	4.0 4.0	3.1 2.2
70	435468 416773	AW362803 AK000340	Hs.166271 Hs.79828	ESTs hypothetical protein FLJ20333	4.0	2.6
70	440483	AI200836	Hs.150386		4.0	2.5
	444821	AA053564	Hs.12040	STE20-like kinase	4.0	10.4
	433873	AW156913		ESTs, Weakly similar to KIAA0987 protein	4.0	2.3
	420028	AB014680	Hs.8786	carbohydrate (chondroitin 6/keratan) sul	3.9	2.8
75	445706	AW807631			3.9	3.8
	424530	AI632083	Hs.28511	ESTs	. 3.9	22
	446851	AW007332		Homo sapiens cDNA: FLJ22053 fis, clone H SWI/SNF related, matrix associated, acti	3.9 3.9	16.0 4.5
	424720 409456	M89907 U34962	Hs.152292 Hs.54473	cardiac-specific homeo box	3.9	8.0
80	420439	AW270041			3.9	7.9
	447340	AW961327		ESTs	3.9	2.1
	430887	N66801	Hs.260287	ESTs, Wealdy similar to ALU7_HUMAN ALU S	3.9	2.5
	409361	MM_00598	2 Hs.54416	sine oculis homeobox (Drosophila) homolo	3.9	4.6

	426509	M31166		pentaxin-related gene, rapidly induced b	3.9	4.0
	410079	U94362		glycogenin 2 ESTs, Wealdy similar to ALU5_HUMAN ALU S	3.9 3.9	18.3 3.0
	426818 435232	AA554827 NM_001262		cyclin-dependent kinase inhibitor 2C (p1	3.8	4.0
5	427228	AA115770		small nuclear ribonucleoprotein 70kD pol	3.8	7.9
	443801	AW206942		ESTs	3.8	3.4
	450746	D82673		general transcription factor II, i, pseu spindle pole body protein	3.8 3.8	2.2 6.5
	443837 435760	Al984625 AF231922		chromosome 21 open reading frame 62	3.8	2.2
10	426757	AW205640	Hs.158206	ESTs	3.7	3.1
	443101	Al268936	Hs.129872	sperm surface protein	3.7	2.4
	440118	AB040893	Hs.6968	KIAA1460 protein	3.7 3.7	3.5 22.5
	410612 435869	AW502698 AF255910	Hs.118152 Hs.54650	ESTs vascular endothelial junction-associated	3.7	4.2
15	433208	AW002834	Hs.24095	ESTs	3.7	16.0
	432357	AA452506	Hs.274412	similar to yeast Up/3, variant A	3.7	26
	413916	N49813	Hs.75615	apolipoprotein C-II	3.7 3.7	5.4 3.2
	429766 437470	AA612710 AL390147	Hs.146140 Hs.134742	ESTs hypothetical protein DKFZp547D065	3.7	6.4
20	438459	T49300	Hs.35304	Homo sapiens cDNA FLJ13655 fis, clone PL	3.7	10.7
	420361	N92054	Hs.206910	ESTs	3.7	18.7
	408819	AW163483	Hs.48320	DKFZP566B1346 protein	3.7 3.7	8.8 2.3
	411960	R77776 BE301930	Hs.18103 Hs.5010	ESTs Homo sapiens clone 24672 mRNA sequence	3.7	2.2
25	435923 440145	AW021433	Hs.250863	ESTs	3.7	3.8
20	453740	AL120295		gb;DKFZp761M067_s1 761 (synonym; hamy2)	3.6	3.0
	440975	AW499914	Hs.7579	hypothetical protein FU10402	3.6 3.6	2.0 12.4
	443135	Al376331	Hs.156103 Hs.227699	ESTs ESTs, Weakly similar to Yhr217cp (S.cere	3.6	2.7
30	419687 451029	A1638859 AA852097	Hs.25829	ras-related protein	3.6	2.9
50	414512	AL044336	Hs.6831	golgi resident protein GCP60	3.6	10.5
	410853	H04588	Hs.30469	ESTs	3.6	23.9 3.6
	419900	A1469960	Hs.170698	ESTs protein tyrosine phosphatase, non-recept	3.6 3.6	7.5
35	429673 428290	AA884407 Al932995	Hs.211595 Hs.183475	Homo sapiens clone 25061 mRNA sequence	3.6	9.6
33	444381	BE387335	Hs.283713	ESTs, Weakly similar to CA54_HUMAN COLLA	3.6	4.9
	442104	L20971	Hs.188	phosphodiesterase 4B, cAMP-specific (dun	3.6 3.6	2.1 2.8
	441269	AW015206		ESTs ESTs	3.5	4.6
40	447961 447735	W32791 AA775268	Hs.170405 Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L	3.5	2.1
40	437580	AA761075	Hs.293567	ESTs	3.5	3.5
	447710	A1420523	Hs.161282	ESTs	3.5	3.5
	436446	AW016809		ESTs ESTs, Moderately similar to ALUB_HUMAN A	3.5 3.5	2.2 4.1
45	448412 409712	Al219083 AA167385	Hs.42532 Hs.13583	ESTs, Moderately Siliplan to ALOO_HOMAN A	3.5	3.8
73	404048	74101000	1 10.10000	25.0	3.5	3.2
	440516	S42303	Hs.161	cadherin 2, type 1, N-cadherin (neuronal	3.5	5.1
	409342	AU077058		BRCA1 associated RING domain 1	3.5 3.5	10.6 3.8
50	456508 426101	AA502764 AL049987	Hs.123469 Hs.166361	ESTs, Weakly similar to AF208855 1 8M-01 Homo sapiens mRNA; cDNA DKFZp564F112 (fr	3.5	32.2
50	436252	ALD49301	Hs.120969	Homo sapiens cDNA FLJ11562 fis, clone HE	3.5	4.6
	433854	AA610649		gb:np95c03.s1 NCI_CGAP_Thy1 Homo sapiens	3.5	3.5
	408495	W68796	Hs.237731	ESTs	3.5 3.5	6.1 5.1
55	418801 422493	AA228366 AW474183		ESTs ESTs	3.5	15.2
33	422493	D50402	Hs.182611	solute carrier family 11 (proton-coupled	3.5	2.4
	414591	AI888490	Hs.55902	ESTs	3.5	8.3
	439627	BE621702		Homo sapiens cDNA: FLJ21841 fis, done H	3.5 3.5	30.2 3,1
60	44,4969 435370	A1203334 A1964074	Hs.160628 Hs.225838		3.5	3.0
00	443228	W24781	Hs.293798		3.4	4.6
	414612	BE274552	2 Hs.76578	protein inhibitor of activated STAT3	3.4	5.0
	437410	AW02334		ESTs	3.4 3.4	2.7 12.9
65	444172 428484	BE147740 AF104032			3.4	2.8
05	437860	AA333063			3.4	4.0
	428776	AW01663		ESTs, Highly similar to R29144 1 [H.sapi	3.4	2.5
	409493	AA38619			3.4 3.4	3.4 6.3
70	432559	AW45294		ESTs liver-expressed antimicrobial peptide	3.4 3.4	6.1
70	451455 444153	AJ937227 AK00161		hypothetical protein FLJ10748	3.4	2.6
	422872	BE32678		S ESTs	3.4	2.2
	414761	AU07722	8 Hs.77256	enhancer of zeste (Drosophila) homolog 2	3.4	2.6
75	416131	L03532	Hs.79024	heterogeneous nuclear ribonucleoprotein	3.4 3.4	9.5 3.4
75	408576	NM_0035 BE22188	542 Hs.46423 0 Hs.26855	H4 historie family, member G 5 5'-3' exoribonuclease 2	3.4 3.4	21.2
	431770 426030	BE24393			3.4	2.1
	422573	AW29798	85 Hs.28777	H2A histone family, member L	3.4	3.7
00	436865	AW8803			3.4 3.4	7.6 2.9
80	442091	AW77049			34	5.5
	418699 434577	BE53963 R37316	9 Hs.17303 Hs.17976		3.4	3.9
	430314	AA36960			3.4	16.8

	447279	AA325308	Hs.18016	Homo sapiens mRNA; cDNA DKFZo586H0324 (f	3.3	3.0
	410020	T86315	Hs.728	ribonuclease, RNase A family, 2 (liver,	3.3	5.8
	447272	NM_014827	Hs.17969	KIAA0663 gene product	3.3	13.4
5	407656 435354	AW747986 AA678267	Hs.37443 Hs.117115	Homo saplens mRNA; cDNA DKFZp43482119 (f ESTs	3.3 3.3	2.3 5.5
•	443884	N20617	Hs.226627	leptin receptor	3.3	8.6
	444984	H15474	Hs.12214	Homo sapiens clone 23716 mRNA sequence	3.3	2.0
	431053	S40369	Hs.249141	Glutamate receptor subunit	3.3	2.4
10	424682 457972	AW604804 AJ419060	Hs.151717 Hs.47448	KIAA0437 protein . ESTs	3.3 3.3	13.7 4.2
10	424762	AL119442	Hs.183684	eukaryotic translation initiation factor	3.3	3.2
	438566	AW014493	Hs.126727	ESTs	3.3	10.8
	447796	AW953622	Hs.223025	RAB31, member RAS oncogene family	3.3	4.2
15	426751	W92744	Hs.22664	ESTs nucleolar protein (KKE/D repeat)	3.3 3.3	2.6 3.9
13	436251 452688	BE515065 AA721140	Hs.5092 Hs.49930	ESTs, Weakly similar to B34087 hypotheti	3.3	4.9
	416359	AL042210	Hs.16493	hypothetical protein DKFZp762N2316	3.3	4.2
	424090	X99699	Hs.139262	XIAP associated factor-1	3.3	2.9
20	434987	AW975114	Hs.293273	ESTS	3.3	2.2
20	428642 420372	NM_014899 AW960049	Hs.188006 Hs.293660	KIAA0878 protein ESTs, Weakly similar to A49618 probable	3.3 3.3	5.7 5.5
	422224	NM_013982		neuregulin 2	3.2	3.0
	432482	L19267	Hs.275924	dystrophia myotonica-containing WD repea	3.2	2.7
25	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	3.2	20
23	428418 416728	Al368826 AB024597	Hs.30654 Hs.79658	ESTs caseln kinase 1, epsilon	3.2 3.2	24 28
	416224	NM_002902		reticulocalbin 2, EF-hand calclum bindin	3.2	22
	429803	W81489	Hs.223025	RAB31, member RAS oncogene family	3.2	4.3
20	431387	A1878854	Hs.252229	v-maf musculoaponeurotic fibrosarcoma (a	3.2	2.8
30	404171 435575	AF213457	Hs.44234	biggarian encontes avenarend an municid	3.2 3.2	35.8 2.6
	435575	AW367884	Hs.169832	triggering receptor expressed on myeloid zinc finger protein 42 (myeloid-specific	3.2	3.8
	445070	NM_000677		adenosine A3 receptor	3.2	7.6
25	407047	X65965		gb:H.saplens SOD-2 gene for manganese su	3.2	82.0
35	446006	NM_004403 X54232		deafness, autosomal dominant 5	3.2 3.2	2.2 4.3
	430890 439807	AA376417	Hs.2699 Hs.173501	glypican 1 Homo sapiens mRNA for FLJ00008 protein,	3.2	23
	430412	AW341754	Hs.189305	ESTs	3.2	2.0
40	442807	AL049274	Hs.8736	Homo saplens mRNA; cDNA DKFZp564H203 (fr	3.2	2.7
40	420253	A1656055	Hs.96200	neighbor of A-kinase anchoring protein 9	3.2	2.9
	436042 423422	AF284422 AC005175	Hs.119178 Hs.128425	cation-chloride cotrans porter-interactin NY-REN-24 antigen	3,2 3,2	4.6 4.0
	413020	R98736	16.120120	gb:yr31h09.r1 Soares fetal liver spleen	3.2	4.1
45	452877	Al250789	Hs.32478	ESTs	3.2	4.0
45	418113	Al272141	Hs.83484	SRY (sex determining region Y)-box 4	3.1	9.0
	421097 450219	Al280112 Al826999	Hs.125232 Hs.224624	Homo sapiens cDNA FLJ13266 fis, clone OV ESTs	3.1 3.1	2.0 23.7
	434256	Al378817	Hs.191847	ESTs	3.1	3.4
	421407	T82331	Hs.127453	ESTs	3.1	3.9
50	451198	AW964541	Hs.11500	Homo saplens cDNA: FLJ21127 fis, clone C	3.1	3.9
	445664	AW968638	Hs.237691	ESTS	3.1 3.1	7.9 6.0
	411089 458050	AA456454 AA834708	Hs.118637	Homo sapiens cDNA FLJ13365 ffs, clone PL gb;od99d04.s1 NCI_CGAP_Ov2 Homo sapiens	3.1	4.4
	454140	AB040888	Hs.41793	hypothetical protein FLJ10474	3.1	2.7
55	417270	AA429615	Hs.98593	Homo saplens cDNA: FLJ23233 fis, clone C	3.1	2.4
	427951	AI826125	Hs.43546 Hs.9683	ESTS	3.1 3.1	2.3 7.2
	443693 413367	A1344782 NM_006517		protein-kinase, interferon-inducible dou solute carrier family 16 (monocarboxylic	3.1	2.6
	429402	AF116571	Hs.201671	SRY (sex determining region Y)-box 13	3.1	6.5
60	447752	M73700	Hs.347	lactotransferrin	3.1	19.4
	408949	AF189011	Hs.49163	putative ribonuclease III	3.1	3.7
	418039 447343	R06859 AA256641	Hs.193172 Hs.236894	ESTs ESTs, Highly similar to LRP1_HUMAN LOW-D	3.1 3.1	3.8 2.2
	424441	X14850	Hs.147097	H2A histone family, member X	3.1	3.2
65	435163	AA668884	Hs.19155	ESTs	3.1	21
	428712	AW085131	Hs.190452	KIAA0365 gene product	3.1	2.7
	434542 439147	AA769310	Hs.61260 Hs.234983	hypothetical protein FLJ13164 ESTs	3.1 3.1	14.3 2.7
	428147 415825	AW629965 Y18024	Hs.78877	inositol 1,4,5-trisphosphate 3-kinase B	3.1	2.5
70	422170	Al791949	Hs.112432	anti-Mullerian hormone	3.1	8.1
	448801	N57423	Hs.179898	HSPC055 protein	3.0	2.0
	413542	BE295928	Hs.75424	Inhibitor of DNA binding 1, dominant neg	3.0	18.3
	431562 410274	AI884334 AA381807	Hs.11637 Hs.61762	ESTs hypoxia-inducible protein 2	3.0 3.0	39 30
75	458962		Hs.25180	purine-rich element binding protein A	3.0	3.0
	436277	R88520	Hs.120917	ESTs	3.0	2.7
	453288	AW583292			3.0	3.0
	447471 442554	AF039843 AW467376	Hs.18676 Hs.129640	sprouty (Drosophila) homolog 2 ESTs	3.0 3.0	4.1 4.7
80	441466	AW673081		EST8	3.0 3.0	3.0
	420297	A1628272	Hs.88323	ESTs	3.0	8.1
	445101	T75202	Hs.12314	Homo sapiens mRNA; cDNA DKFZp586C1019 (f	3.0	18.7
	453405	A1567972	Hs.49919	ESTs	3.0	9.6

				2 Consideration of the Al	3.0	9.3
	434521 447948	NM_002267 AI620923	Hs.46679	karyopherin alpha 3 (importin alpha 4) ESTs	3.0	10.1
	445756	AA290690	Hs.288493	ESTs	3.0	3.5
_	413243	AA769266	Hs.193657	ESTS	3.0 3.0	5.9 2.2
5	422845 419409	AA317841 AW297831	Hs.301838 Hs.143792	ESTs, Weakly similar to ALU1_HUMAN ALU S ESTs	3.0	2.1
	446441	AK001782	Hs.15093	hypothetical protein	3.0	21
	427150	BE616183	Hs.173737	ras-related C3 botulinum toxin substrate	3.0	4.1
10	421043	BE379455	Hs.89072	ESTs	3.0 3.0	3.0 4.1
10	427239 433312	BE270447 Al241331	Hs.174070 Hs.131765	ubiquitin carrier protein ESTs	3.0	11.0
	415102	M31899	Hs.77929	excision repair cross-complementing rode	3.0	6.0
	414702	1.22005	Hs.76932	cell division cycle 34	3.0	3.3
1.5	428673	AW601325	Hs.274472	high-mobility group (nonhistone chromoso	3.0 3.0	15.8 2.1
15	422676	D28481	Hs.1570 Hs.279635	histamine receptor H1 ESTs	3.0	23
	451693 412420	BE220445 AL035668	Hs.73853	bone morphogenetic protein 2	3.0	10.5
	424005	AB033041	Hs.137507	KIAA1215 prolein	3.0	3.9
20	440769	BE561793		gb:601346842F1 NIH_MGC_8 Homo sapiens cD	3.0 3.0	5.1 2.3
20	428832	AA578229	Hs.238272	gb:nl22b12.s1 NCI_CGAP_HSC1 Homo sapiens inositol 1,4,5-triphosphate receptor, ty	3.0	6.3
	430293 450883	AI416988 NM_001348		death-associated protein kinase 3	3.0	5.6
	407879	AA045464	Hs.6557	ESTs	2.9	7.0
25	426167	AF039023	Hs.167496	Homo sapiens cDNA FLJ11120 fis, clone PL	2.9 2.9	2.6 3.9
25	435281 432339	AB020699	Hs.4864 Hs.25945	KIAA0892 protein ESTs	2.9	2.9
	432339	AW411259 R71264	Hs.16798	ESTs	2.9	9.7
	408083	BE383668	Hs.42484	hypothetical protein FLJ10618	2.9	4.4
	427729	AB033100	Hs.300646	Homo sapiens cDNA FLJ11744 fis, clone HE	2.9	3.1
30	422072	AB018255	Hs.111138	KIAA0712 gene product	2.9 2.9	2.9 3.6
	435904	AF261655 BE382685	Hs.8910 Hs.158549	1,2-alpha-mannosidase IC ESTs	2.9	3.6
	440100 448356	AL120837	Hs.20993	high-glucose-regulated protein 8	2.9	13.9
	428005	AW302245	Hs.181390	casein kinase 1, gamma 2	2.9	3.7
35	403019	AA834626	Hs.66718	RAD54 (S.cerevisiae)-like	2.9	5.8
	419175	AW270037	Hs.179507	KIAA0779 protein	2.9 2.9	2.3 2.3
	433592 413922	NM_004642 A1535895	Hs.221024	deleted in oral cancer (mouse, homolog) ESTs	2.9	2.8
	428593	AW207440		degenerative spermatocyte (homolog Droso	29	3.3
40	441789	D52059	Hs.7972	KIAA0871 protein	2.9	21
	459107	AA811881	Hs.28505	ubiquitin-conjugating enzyme E2H (homolo	29 29	2.8 3.0
	448560	BE613183	Hs.23213	ESTs Shooklast arough factor 11	2.9	3.3
	425304 434846	AA463844 AW295389	Hs.31339 Hs.119768	fibroblast growth factor 11 ESTs	29	5.1
45	408146	R45621	Hs.81057	ESTs, Moderately similar to CL3BC [R.nor	2.9	5.1
•-	446644		2 Hs.15791	transmembrane 7 superfamily member 1 (up	2.9	2.8
	446808	AA703226	Hs.16193	Homo sapiens mRNA; cDNA DKFZp586B211 (fr	29 29	8.5 2.2
	433017 429500	Y15067 X78565	Hs.279914 Hs.289114		2.9	4.5
50	42 <i>5</i> 300 444706	AK000398	Hs.11747	hypothetical protein FLJ20391	2.9	3.6
•	407925	BE002320		Homo sapiens cDNA FLJ14030 fis, clone HE	2.9	2.1
	431730	AF208856	Hs.268122		2.9 2.8	2.5 2.1
	447118 453496	AB014599 AA442103		KIAA0699 protein solute carrier family 2 (facilitated glu	2.8	7.4
55	425227	H84455	Hs.40639	ESTs	2.8	2.3
-	456534	X91195	Hs.100623	phospholipase C, beta 3, neighbor pseudo	2.8	76.2
	421465	AK001020			28 28	6.1 34.0
	409095	AW337273 Z99348	2 Hs.293656 Hs.112461		2.8	2.1
60	424066 432945	AL043683			2.8	11.9
00	414079	H19184	Hs.205230	ESTs .	2.8	21
	414359	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	2.8 2.8	3.9 4.9
	438890	AA827756			2.8	5.2
65	430354 458367	AA954810 AA088470		p53-responsive gene 6	2.8	4.4
0.5	412014	A1620650		ESTs	2.8	4.8
	428727	AF078847	Hs,19135		2.8	6.7
	447942	F12628	Hs.15547		2.8 2.8	2.2 3.5
70	426432 439189	AF001601 AI951185			2.8	2.5
70	446756	AW02848			2.8	4.1
	432148	AW50491			2.8	26
	405649		_		2.8	3.8
75	414473	BE30269		gb:ba74c02.y1 NiH_MGC_20 Homo sapiens cD 1 ESTs	2.8 2.8	2.4 2.1
13	443839 448804	AW13983 AW51221			2.8	2.7
	426825	AL13341		vimentin	2.8	25.0
	417528	H47315	Hs.27519		2.8	11.6
٥٥	453657	W23237	Hs.29616		2.8 2.8	3.2 6.7
80	432714	Y12059 AW2754	Hs.27867 30 Hs.39504		2.6 2.7	27
	441072 441297	AW4030		ubiquitin-conjugating enzyme E2E 1 (homo	2.7	2.2
	443849	BE56606		ASB-3 protein	2.7	3.0
				100	_	

	408243	Y00787	Hs.624	interleukin 8	27	3.8
	446243	BE296396	Hs.14512	Homo sapiens cDNA FLJ11761 fis, clone HE	2.7	3.3
	432238	AL133057	Hs.274135	Homo sapiens mRNA; cDNA DKFZp434K1815 (f	2.7 2.7	3.0 3.1
5	433944 411400	AL117518 AA311919	Hs.3686 Hs.69851	KIAA0978 protein GAR1 protein	2.7	16.0
,	436840	AW450376	Hs.130803	ESTs, Highly similar to T00367 hypotheti	27	4.1
	428281	AA194554	Hs.183434	ATPase, H+ transporting, lysosomal (vacu	2.7	3.2
	426340	Z97989	Hs.169370	FYN oncogene related to SRC, FGR, YES	2.7	2.0
10	408320	AI125867	Hs.20734	ESTs	2.7	4.7
10	422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38	27	2.2
	436440	A1471862	Hs.196008	Homo sapiens cDNA FLJ11723 fis, clone HE	27 27	4.7 2.1
	408912 419304	AB011084 Al271326	Hs.48924 Hs.146101	KIAA0512 gene product ESTs	27	3.4
	415045	AA321559	Hs.38270	Homo sapiens cDNA: FLJ20984 fis, clone C	2.7	2.3
15	441872	BE567100	Hs.154938	hypothetical protein MDS025	2.7	2.3
	422343	A1628633		gb:ty77d05.x1 NCI_CGAP_Kid11 Homo sapien	2.7	2.5
	415539	AJ733881	Hs.72472	ESTs	2.7	2.7
	443823	BE089782	Hs.9877	hypothetical protein	27	4.7
20	419881	AA329340	Hs.44649	ESTS	2.7 2.7	3.3 5.5
20	429155 431319	8E242291 AA873350	Hs.197540	hypoxia-inducible factor 1, alpha subuni gb:oh64h02.s1 NCI_CGAP_Kid5 Homo saplens	27	65.9
	430219	X99209	Hs.235887	HMT1 (hnRNP methyltransferase, S. cerevi	27	3.1
	421016	AA504583	Hs.101047	transcription factor 3 (E2A Immunoglobul	2.7	5.2
	417259	AW903838	Hs.81800	chondroltin sutfate proteoglycan 2 (vers	2.7	10.7
25	431747	AW979134	Hs.10700	hypothetical protein	2.7	29
	408085	N25929	Hs.42500	ADP-ribosylation factor-like 5	2.7	7.8
	426218	AF119043	Hs.168005	transcriptional intermediary factor 1 ga	2.7 2.7	4.5 4.6
	434845	BE267057	Hs.4200	hypothetical protein R32184_1 ESTs	2.7	2.3
30	451644 428408	N23235 W74437	Hs.30567 Hs.188757	Homo sapiens mRNA; cDNA DKFZp564M113 (fr	2.7	5.7
30	446627	AI973016	Hs.15725	hypothetical protein SBBI48	27	2.9
	450167	AA446404	Hs.24563	NTF2-related export protein 1	2.7	9.9
	408821	AL050385	Hs.48332	NIMA (never in mitosis gene a)-related k	2.7	2.1
	452068	W76412	Hs.57877	ESTs	2.7	2.1
35	431129	AL137751	Hs.263671	Homo sapiens mRNA; cDNA DKFZp434l0812 (f	2.7	6.2
	429025	Al399910	Hs.4842	ESTs	2.7	2.9
	421114	AW975051	Hs.293156	ESTs	2.7 2.7	8.8 3.0
	428755	D87454	Hs.192966	KIAA0265 protein mesoderm specific transcript (mouse) hom	27	5.7
40	416391 414283	AI878927 AW960011	Hs.79284 Hs.154993	ESTs	2.7	5.9
40	425262	D87119	Hs.155418	GS3955 protein	2.7	3.7
	447726	AL137638	Hs.19368	Homo septens mRNA; cDNA DKFZp434J065 (fr	2.7	14.3
	424623	AW963062	Hs.165809	ESTs	2.7	5.6
	444772	AW450800	Hs.176859	ESTs	2.7	2.7
45	428419	U49436	Hs.286236	eukaryotic translation initiation factor	2.7	4.6
	441049	W88920	Hs.29341	hypothetical protein FLJ22376	2.7	4.5
	412758	Y07818	Hs.74566	dihydropyrimidinase-like 3	2.6 2.6	5.1 3.2
	447720	AL038765	Hs.161304	ESTs hypothetical protein	2.6	3.0
50	419708 445502	AK000753 AW379160	Hs.92374 Hs.12813	DKFZP434J214 protein	26	5.0
50	437370	AL359567	Hs.161962	Homo sapiens mRNA; cDNA DKFZp547D023 (fr	2.6	2.9
	444147	AB002306	Hs.10351	KIAA0308 protein	2.6	6.8
	433193	AB040881	Hs.32580	Homo sapiens cDNA FLJ13122 fis, clone NT	2.6	3.2
	445439	BE243084	Hs.12719	regulator of nonsense transcripts 1	2.6	3.9
55	450309	W61348	Hs.4864	KIAA0892 protein	26	3.8
	422092	AB007883	Hs.111373	KIAA0423 protein	2.6 2.6	2,3 5.5
	424118 407618	BE269041 AW054922	Hs.140452 Hs.53478	cargo selection protein (mannose 6 phosp Homo sapiens cDNA FLJ12366 fis, clone MA	26	2.9
	446493	AK001389	Hs.15144	hypothetical protein DKFZp5640043	2.6	3.2
60	442878	AI868648	Hs.22315	ESTs	2.6	4.7
	448771	BE315511	Hs.296244	SNARE protein	2.6	5.0
	416611	AA568308	Hs.192789	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.6	7.7
	409348	AI401535	Hs.146090	ESTs	2.6	3.5
65	439349	AI660898	Hs.195602		2.6 2.6	3.2 7.9
03	428433	AA521410	Hs.41371 Hs.204169	ESTs ESTs	2.6	3.0
	436565 438662	BE547674 AA223599	Hs.6351	cleavage and polyadenylation specific fa	26	26
	429362	T25833	Hs.200478		2.6	2.3
	459035	AW291109			2.6	2.6
70	451814	AA847992	Hs.137003	ESTs	2.6	19.1
	452331	AA598509		H.sapiens mRNA for pur alpha extended 3	26	2.2
	438461	AW075485			26	21
	424362	AL137646	Hs.146001		2.6 2.6	4.9 3.7
75	423699	H41850 BE563042	Hs.131846		26	2.5
, 5	441226 444940	AK002148		hypothetical protein FLJ11286	26	3.4
	448731	A1522273	Hs.42640	ESTs	26	3.2
	424250	AF073310		Insulin receptor substrate 2	2.6	2.5
	433468	AA832055		ESTs, Weakly similar to ALU1_HUMAN ALU S	2.6	3.3
80	419925	AA159850	Hs.93765	lipoma HMGIC fusion partner	26	4.6
	441364	AW450466		ESTS	2.6	2.6
	425922	AL157466			2.5 2.5	2.7 2.5
	434974	AA778711	Hs.4310	eukaryotic translation initiation factor	4.0	2.3

				managat contrib	2.5	25.4
	408392 432426			KIAA1641 protein ESTs	2.5	10.0
	435623	AI417073	Hs.107265	ESTs .	2.5	2.1 2.6
_	452683	A1089575		progesterone membrane binding protein Homo sapiens cDNA: FLJ21616 fis, clone C	2.5 2.5	3.7
5	410582 441328	AW867197 AI982794		ESTs	2.5	9.2
	453983	H94997	Hs.16450	ESTs	2.5	26.1 2.3
	438826	R26709		hypothetical protein from EUROIMAGE 1669	2.5 2.5	20.3
10	427899 427820	AA829286 BE222494	Hs.181062 Hs.180919	serum amyloid A1 inhibitor of DNA binding 2, dominant neg	2.5	3.5
10	458933	AI638429		RAN binding protein 1	25	3.5 2.3
	444871	U46386		sorting nexin 3	2.5 2.5	29
	411329 424074	AL360265 A1902456	Hs.69554 Hs.210761	hypothetical protein FLJ20552 ESTs	2.5	4.0
15	43898B	H30039	Hs.107674	ESTs	2.5	2.7
	412836	AA121384	Hs.191446	ESTs	2.5 2.5	5.7 3.0
	430189	A1298841 M93425	Hs.135133 Hs.62	ESTs, Weakly similar to ORF YNL310c (S.c protein tyrosine phosphatase, non-recept	2.5	13.4
	432841 416926	H03109	Hs.108920	HT018 protein	2.5	2.8
20	451429	AA525993	Hs.173699	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.5 2.5	3.9 4.2
	416388	Al417358	Hs.73677	ESTs protein inhibitor of activated STAT prot	2.5	7.5
	421561 436480	Z45399 AJ271643	Hs.105779 Hs.87469	putative acid-sensing ion channel	2.5	2.6
	416273	AW575691	Hs.79123	KIAA0084 protein	2.5 2.5	2.6 2.6
25	427149	H94688	Hs.173737	ras-related C3 botulinum toxin substrate transcription factor 4	2.5 2.5	2.2
	453041 446899	A1680737	Hs.289068 Hs.16426	podocalyzin-like	2.5	4.7
	447301	AW958124		HP1-BP74	2.5	3.2 2.4
•	447769	AW873704		ESTS	2.5 2.5	2.5
30	447754	AW073310 BE073913	Hs.163533 Hs.173515	Homo sapiens cDNA FLJ14142 fis, clone MA uncharacterized hypothalamus protein HT0	2.5	23.6
	427087 440903	A1468079	Hs.126623	ESTs	2.5	2.3
	432353	NM_01655	B Hs.274411	SCAN domain-containing 1	2.5 2.5	4.1 2.5
25	408196	AL034548	Hs.43627	SRY (sex determining region Y)-box 22 ESTs	2.5	3.9
35	411373 452402	BE326276 Al138530	Hs.8861 Hs.22216	peroxisome proliferative activated recep	2.5	24
	429998	AJ458063	Hs.57841	ESTs	2.5 2.5	2.6 3.7
	421772	Z24958	Hs.108139	zinc finger protein 212 Homo sapiens cDNA: FLJ21962 fis, clone H	2.5 2.5	2.1
40	442573 444677	H93366 AL110212	Hs.7567 Hs.9242	purine-rich eternent binding protein B	2,5	3.4
70	441887	AW967865		ESTs	2.5	3.3 4.8
	451031	Al360187	Hs.4254	ESTs	2.5 2.5	2.4
	432450 41 5 860	Al990739 D56051	Hs.77868 Hs.78888	ORF diazepam binding inhibitor (GABA recepto	2.5	4.8
45	439630	AA313607		Homo sapiens cDNA: FLJ22145 fis, clone H	2.4	23
	428607	AB002353	Hs.186840		2.4 2.4	4.0 2.5
	415402	AA164687 AL030996		ESTs hypothetical protein LOC57187	2.4	2.2
	446888 439208	AK000299		dynactin p62 subunit	2.4	2.4
50	452900	AA626794	Hs.250655	prothymosin, alpha (gene sequence 28)	2.4 2.4	3.4 3.6
	408657	AA782601			24	2.5
	439143 439867	AJ359214 AA84751		FSTs	2.4	9.3
	408138	AA53574) Hs.301967	Homo sapiens mRNA; cDNA DKFZp434M196 (fr	2.4 2.4	5.6 4.2
55	428386	R17298 D86962	Hs.295923 Hs.81875	seven in absentia (Drosophila) homolog 1 growth factor receptor-bound protein 10	2.4	2.2
	417289 405268	000002	115.01010	•	2.4	3.1
	439734	AC00501		cAMP response element-binding protein CR	2.4 2.4	3.6 2.4
60	445378	AV65356 D82418	4 Hs.226946 Hs.29626	6 ESTs ESTs, Weakly similar to unknown [D.melan	2.4	22.0
Ü	454085 427354	T57896	Hs.19109	5 ESTs	2.4	3.6
	452906	BE20703			2.4 2.4	2.2 3.6
	450065	AL05010 AA81093			2.4	2.7
65	451091 414839	X63692	Hs.77462	DNA (cytosine-5-)-methyltransferase 1	2.4	2.6
7.0	420303	AA25828	2 Hs.27843	6 KIAA1474 protein	2.4 2.4	2.0 2.6
	437058	AA74364			24	4.4
	417446 421454	AL11867 A166038		8 chorionic somatomammotropin hormone 1 (p	2.4	3.5
70	434943	Al92981	9 Hs.320	xeroderma pigmentosum, complementation g	24	6.4 3.0
	446342	BE2986			2.4 2.4	2.1
	452847 422506	AK0008 R20909			2.4	2.2
	405204			THE TAX DISTRICT COMMENT	2.4	4.3 11.7
75	419441	AW023			2.4 2.4	21
	442293 451484				2.4	2.0
	431464			KIAA1151 protein	24	2.1 2.8
90	442724	AA3555	25 Hs.1596	04 cysteinyl-IRNA synthetase	2.4 2.4	2.8 6.6
80	405517 413822		Hs.2720	44 ESTs, Weakly similar to ALU1_HUMAN ALU S	2.4	3.8
	413622			0 Homo sapiens cDNA FLJ12488 fis, clone NT	24	2.3 8.1
	408636		925 Hs.4668	O CGI-12 protein	2.4	0,1

	409142	AL136877	Hs.50758	chromosome-associated polypeptide C	24	24
	422043	AL133649		Homo sapiens mRNA; cDNA DKFZp434A139 (fr	24	21
	424687			matrix metalloproteinase 9 (gelatinase 8	24	26
5	442560			ESTs	24	4.9
3	418126 413313			ESTs glycyl-tRNA synthetase	24 - 24	11.7 2.1
	415167			ESTs	24	4.4
	440040			ESTs	24	3.4
	443595		Hs.9613	PPAR(gamma) angiopoietin related protein	2.4	10.7
10	438977	AA482026		ESTs	24	2.8
	452068	AA772149	Hs.16979	ESTs	24	5.4
	428500	AI815395		delta-6 fatty acid desaturase	24 24	22
	408503	AW119059	Hs.63163 Hs.284217	ESTs, Weakly similar to UDP-GalNAc:polyp	24 24	2.7 4.8
15	433401 412676	AF039698 NM_000165		serologically defined colon cancer enlig gap junction protein, alpha 1, 43kD (con	24	2.2
13	453753	BE252983	Hs.35088	ubiquitin specific protesse 1	24	2.8
	424050	AA211218	Hs.138381	famesyltransferase, CAAX box, alpha	24	3.9
	440225	BE295782	Hs.159	tumor necrosis factor receptor superfami	2.4	76.7
	430512	AF182294	Hs.241578	U6 snRNA-associated Sm-like protein LSm8	2.4	12.3
20	415156	X84908	Hs.78060	phosphorylase kinase, beta	2.4	10.4
	435975	AL118990	Hs.41997	alpha-1-B glycoprotein	2.4	7.7
	429831	AA564489	Hs.137526	ESTs	24	4.1
	407373	AA031576	Hs.143812	Home sapiens cDNA FLJ12956 fis, clone NT	24 24	3.3 3.8
25	422221 451351	AA306649 AW058261	Hs.168213	gb:EST177656 Jurket T-cells VI Homo sapl ESTs, Weakly similar to ALU1_HUMAN ALU S	2.4	3.3
23	410082	AA081594	Hs.158311	Musashi (Drosophila) homolog 1	24	2.5
	430304	AL122071	Hs.238927	Homo sapiens mRNA; cDNA DKFZp434H1235 (f	2.4	6.5
	418863	AL135743	Hs.25566	ESTs	2.4	5.2
	448414	BE391820	Hs.21145	Homo sapiens cDNA: FLJ22489 fis, clone H	2.4	3.7
30	428351	AK001701	Hs.183779	Homo seplens cDNA FLJ10590 fis, clone NT	2.4	6.2
	425750	AL050276	Hs.159456	zinc finger protein 288	2.4	5.1
	426295	AW367283	Hs.75839	zinc finger protein 6 (CMPX1)	· 24 24	113.6
	408772	W88532	Hs.254562	ESTs	2.4	12.3 4.0
35	426307	F24978	Hs.294084	ESTs	2.4	2.5
55	405203 453537	AA036755	Hs.283681	ESTs	24	3.6
	431427	AK000401	Hs.252748	Homo sapiens cDNA FLJ20394 fis, clone KA	2.4	6.2
	458021	Al885190	Hs.156089	ESTs, Weakly similar to KIAA1339 protein	2.4	4.3
	453928	BE222198	Hs.143851	ESTs	2.4	2.6
40	446853	AV660630	Hs.87627	disrupter of silencing 10	2.3	9.7
	441626	AA281167	Hs.111911	ESTs	2.3	23.0
	446138	AW504182	Hs.13999	KIAA0700 protein	2.3	2.2
	452568	AA805634	Hs.3337	transmembrane 4 superfamily member 1	2.3 2.3	22.2 8.0
45	417565	AW852858	Hs.22862	ESTs Homo sapiens cDNA: FLJ22286 fis, clone H	2.3	5.1
43	420088 421456	AC006486 AW579842	Hs.298033 Hs.104557	hypothetical protein FLJ10697	23	25
	412093	BE242691	Hs.14947	ESTs	2.3	31.4
	428172	U09367	Hs.182828	zinc finger protein 136 (clone pHZ-20)	2.3	4.9
	450447	AF212223	Hs.25010	hypothetical protein P15-2	2.3	23
50	436001	AW903849	Hs.173840	HUEL (C4orf1)-interacting protein	2.3	4.1
	414786	Al246482	Hs.249989	ESTs	2.3	2.1
	459284	AF155660	Hs.34401	mitochondrial solute carrier	2.3 2.3	2.9 2.6
	452701		Hs.30332	glutamine-fructose-6-phosphate transamin acyl-Coenzyme A dehydrogenese family, me	23	3.9
55	446320 446669	AF126245 AW972832	Hs.14791 Hs.29468	ESTs	2.3	3.8
23	434616	D79338	Hs.239720	CCR4-NOT transcription complex, subunit	2.3	3.6
	452135	Al492175	Hs.301805	ESTs	2.3	2.3
	408696	AW958157	Hs.16542	ESTs .	2.3	2.8
	436176	AL121422	Hs.184013	ESTs, Highly similar to unnamed protein	23	3.2
60	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi	23	17.0
	414197	W44877	Hs.55501	ESTs	2.3 2.3	11.8 4.2
	445270	AI762154	Hs.54982	Homo sapiens cDNA FLJ14014 fls, clone HE vascular endothelial growth factor	2.3	5.1
	412247 426494	AF022375 AL119528	Hs.73793 Hs.170098	KIAA0372 gene product	2.3	4.4
65	405687	P4,113320	113.110050	turanorz gano procesa	2.3	2.2
•	417410	AF063020	Hs.82110	PC4 and SFRS1 interacting protein 1	2.3	2.0
	450747	AI064821	Hs.48306	ESTs, Highly similar to EWS_HUMAN RNA-BI	23	3.8
	433680	Al805366	Hs.199945		2.3	6.7
70	420025	AF184939	Hs.94392	LDL induced EC protein	2.3	24
70	413407	AJ356293	Hs,75339	inositol polyphosphate phosphatase-like	23 23	3.1
	452908	AB001451	Hs.30965	neuronal She adaptor homolog	2.3	3.0 2.0
	424414 435791	AI361002 AA243086	Hs.94814 Hs.25204	Homo sapiens cDNA FLJ12168 fis, clone MA chondrollin 4-O-sulfotransferase 2	23	24
	457635	AV660976	Hs.3569	hypothetical protein	23	6.9
75	427985	A1770170	Hs.65583	ESTs	2.3	23
	445498	AV654019	Hs.180402		2.3	23
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	23	4.1
	450368	AU077158	Hs.24930	tubulin-specific chaperone a	23	3.5
90	444614	R44284	Hs.2730	heterogeneous nuclear ribonucleoprotein	23	2.6
80	448607	AL042506	Hs.21599	Homo sapiens cDNA FLJ10107 fis, clone HE	2.3 2.3	2.8 2.2
	447975 429767	BE378418 AW793022	Hs.127240 Hs.218329		23	11.5
	408877	AA479033			23	23

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	448481	W15284	Hs.74832	ESTs		23	3.3
	452833		Hs.30736	KIAAD124 protein		2.3	2.8
	421057		Hs.42679	ESTs		23	11.0
5	408885 427615		Hs.48712 Hs.179817	hypothetical protein FLJ20736 CGI-82 protein		23 23	4.6 2.3
J	448861	AL049951	Hs.22370	Homo sapiens mRNA; cDNA DKFZp564O0122 (f		2.3	6.3
	430154	AW58305B	Hs.234726	serine (or cysteine) proteinase inhibito		2.3	34.6
	428494	AA233439	Hs.184634	hypothetical protein FLJ20005		2.3 2.3	10.2 3.2
10	422987 408216	AW407887 AA741038	Hs.301772 Hs.6670	serine/threonine kinase 11 (Peutz-Jegher ESTs		23	3.3
	407862	BE548267	Hs.50724	Homo sapiens cDNA FLJ10934 fis, clone OV		2.3	5.7
	432215	AU076609	Hs.2934	ribonucleotide reductase M1 polypeptide		23	2.1
	410086 444853	A1268405 AW576245	Hs.13467 Hs.149740	Homo sapiens BAC clone RP11-121A8 from 7 Homo sapiens mRNA for FLJ00028 protein,		23 23	2.2 4.5
15	413284	AU077055	Hs.289107	baculoviral IAP repeat-containing 2		2.3	4.8
	445547	D86181	Hs.273	galactosylceramidase (Krabbe disease)		2.3	2.5
	420258	AA477514	Hs.96247	translin-associated factor X		2.3 2.3	3.5 2.7
	437223 437353	C15105 AA749195	Hs.107884 Hs.143746	ESTs ESTs		2.3	2.6
20	426224	BE085860	Hs.168075	karyopherin (importin) beta 2		2.3	36.1
	402575	Z23024	Hs.138860	Rho GTPase activating protein 1		2.3	3.1
	430712	AW044647 NM_003966	Hs.196284	ESTs sema domain, seven thrombospondin repeat		2.3 2.3	2.4 2.4
	452038 425180	U00115	Hs.155024	B-cell CLL/lymphoma 6 (zinc finger prote		2.3	4.3
25	441648	H05734	Hs.30559	ESTs		2.3	2.1
	424130	AL050136	Hs.140945	Homo sapiens mRNA; cDNA DKFZp586L141 (fr		2.3	2.9
	414682 423814	AL021154 AF105020	Hs.76884 Hs.132989	inhibitor of DNA binding 3, dominant neg putative protein O-mannosyltransferase		2.3 2.3	12.2 3.7
	423614	A1638184	Hs.106334	Homo saplens clone 23836 mRNA sequence		2.3	2.3
30	427882	AA640987	Hs.193767	ESTs		23	10.2
	442159	AW163390	Hs.8123	chromobox homolog 3 (Drosophila HP1 gamm		2.3 2.3	4.4 2.4
	412541 447217	BE009398 BE465754	Hs.74002 Hs.17778	nuclear receptor coactivator 1 neuropilin 2		2.3	3.0
	452336	AA960961	Hs.29147	hypothetical protein FLJ11015		2.3	4.1
35	423913		Hs.301055	hepatocellular carcinoma-associated anti		2.3	3.4
	411737	AW160339	Hs.71791	hypothetical protein		2.2 2.2	2.0 2.4
	412276 456974	BE262621 M12529	Hs.73798 Hs.169401	macrophage migration inhibitory factor (apolipoprotein E		22	2.4
	416033	NM_012201		Golgi apparatus protein 1		2.2	10.4
40	406739	Al566709	Hs.182426	ribosomal protein S2		2.2	115.3
	448646	AU077149	Hs.21704	transcription factor 12 (HTF4, helix-loo		22 22	4.2 3.6
	437371 451413	AK000868 AA448974	Hs.5570 Hs.26367	hypothetical protein FLJ10006 PC3-96 protein		2.2	6.2
	408665	T88845	Hs.112200	ESTs, Weakly similar to ALU7_HUMAN ALU S		2.2	3.2
45	437548	Al701596	Hs.121592	ESTs		2.2	3.0
	452053	A1750575	Hs.173933	nuclear factor I/A		2.2 2.2	3.3 3.4
	428303 441376	AW974476 H94227	Hs.183601 Hs.6592	regulator of G-protein signalling 16 ESTs, Weakly similar to salivary proline		2.2	2.5
	413399	BE091833	110.0002	gb:IL2-BT0731-260400-076-F04 BT0731 Homo		2.2	2.1
50	448913	AA194422	Hs.22564	myosin VI		2.2	2.4
	439053	BE244588 A1634046	Hs.6456 Hs.157313	chaperonin containing TCP1, subunit 2 (b ESTs		2.2 2.2	3.1 3.5
	428065 425846	AA102174	Hs.159629	myosin IXB		2.2	7.1
	426404	AA377607	Hs.273138	EŚTs		2.2	3.3
55	423464		0 Hs.128856	CSR1 protein		2.2 2.2	2.1 9.1
	436135 450476	D85390 AL045285	Hs.5057 Hs.246849	carboxypeptidase D ESTs, Moderately similar to ALU6_HUMAN A		22	2.5
	420798	W93774	Hs.99936	keratin 10 (epidermolytic hyperkeratosis		2.2	2.8
60	433530	BE349534	Hs.281789			2.2	2.1
60	436297	A1084582	Hs.5105	hypothetical protein FLJ 10569 Homo sapiens chromosome 19, cosmid R3218		2.2 2.2	2.4 2.3
	433058 435924	H86865 AW029203	Hs.280666 Hs.191952	ESTs		2.2	3.2
	417125	AW181998	Hs.81248	CUG triplet repeat, RNA-binding protein		2.2	2.3
65	449338	H73444	Hs.394	adrenomedullin		2.2 2.2	18.3 3.1
UJ	446065 410668	AA085191 BE379794	Hs.6949 Hs.65403	ESTs, Weakly similar to T2D3_HUMAN TRANS hypothetical protein		2.2	2.5
	424992	AW290893		Homo sapiens cDNA: FLJ21561 fis, clone C		2.2	10.8
	437801	AA613866		Homo sapiens mRNA; cDNA DKFZp564L222 (fr	•	2.2	2.5
70	412491	W31589	Hs.73957	RABSA, member RAS oncogene family homolog of mouse quaking QKI (KH domain		2.2 2.2	2.4 3.4
70	446392 450503	AF142419 R35917	Hs.15020 Hs.25042	Homo sapiens mRNA full length insert cDN		22	2.8
	432476	T94344		gb:ye31h10.s1 Stratagene lung (937210) H		2.2	2.6
	424251	AA677466				2.2	5.0
75	456619	AV647917				2.2 2.2	2.6 2.1
13	433411 424714	A1658666 A1114630	Hs.49994 Hs.208334			22	2.7
	416326	AF186780	Hs.79219	RalGDS-like gene; KIAA0959 protein		2.2	2.2
	407696	A1697340	Hs.76549			2.2	6.5
80	445939 414765	BE018658 X07854	Hs.14100: Hs.77269			2.2 2.2	4.4 6.2
50	414765 407136	T64896	Hs.28742		•	2.2	2.8
	453665	AA626250	Hs.18116	5 eulcaryotic translation elongation factor		2.2	2.3
	433608	AW34000	5 Hs.16448	5 ESTs		2.2	2.1
				. 1	27		

	447040	05040700				
	447648	BE619752	Hs.66053	ESTs. Wealty similar to S22126 finger pr	2.2	4.1
	433139	AB029826	Hs.47649	3-methylcrotonyl-CoA carboxytase biotin-	2.2	11.7
	413433		Hs.289068	transcription factor 4	2.2	2.2
5	421535	AB002359	Hs.105478	phosphoribosylformylglycinamidine syntha	2.2	2.2
)	428591	BE313029	Hs.185807	Homo sapiens clone 24758 mRNA sequence	2.2	4.8
	417248	AA329449	Hs.247302	twisted gastrulation	2.2	2.5
	403966				2.2	5.2
	437112	AA744692	Hs.166539	ESTs	2.2	3.0
10	414799	Al752416	Hs.77326	insulin-like growth factor binding prote	2.2	4.9
10	431049	AA846576	Hs.103267	hypothetical protein FLJ22548 similar to	2.2	4.4
	422100	A1096988	Hs.111554	ADP-ribosylation factor-like 7	2.2	2.5
	426543	AV650198	Hs.170311	heterogeneous nuclear ribonucleoprotein	2.2	2.4
	423720	AL044191	Hs.23388	Homo sapiens cDNA: FLJ21310 ffs, clone C	2.2	4.2
1.5	443804	AL135352	Hs.255883	ESTs	2.2	2.2
15	435080	Al831760	Hs.155111	ESTs	2.2	2.5
	452808	AF244135	Hs.30670	hepatocellular carcinoma-associated anti	2.2	7.1
	433934	AW273261	Hs.216292	ESTs	2.2	21
	432004	BE018302	Hs.2894	placental growth factor, vascular endoth	2.2	4.4
20	452518	AA280722	Hs.24758	ESTs .	2.2	3.0
20	409600	AJ011679	Hs.55099	Homo sapiens mRNA; cDNA DKFZp586D2123 (f	2.2	23
	448965	AF092134	Hs.22679	CGI-24 protein	2.2	4.0
	444954	AW247076	Hs.12163	eukaryotic translation initiation factor	2.2	5.3
	458894	AW292171	Hs.23978	scaffold attachment factor B	2.2	2.5
^-	402269				2.2	2.2
25	423798	AF047033	Hs.301617	Homo saplens mRNA full length insert cDN	2.2	4.0
	413836	W92003	Hs.70614	ESTs	2.2	3.6
	432231	AA339977	Hs.274127	CLST 11240 protein	21	2.1
	412204	Al125507	Hs.130829	ESTs	2.1	3.0
	438807	AA848011	Hs.124570	ESTs, Wealdy similar to reverse transcri	2.1	2.2
30	404170			· •	2.1	41.6
	434858	AW979012	Hs.134462	ESTs	21	2.2
	426982	AA149707	Hs.173091	ubiquitin-like 3	2.1	2.1
	421939	BE169531	Hs.109727	TAK1-binding protein 2; KIAA0733 protein	2.1	26.5
	442432	BE093589	Hs.38178	Homo sapiens cDNA: FLJ23468 fis, clone H	2.1	3.7
35	424950	AA602917	Hs.156974	ESTs	2.1	19.9
-	418123	AA669830	Hs.83530	hypothetical protein	2.1	4.6
	440467	AK001519	Hs.7194	CGI-74 protein	2.1	5.3
	437092	AA744292	Hs.181244	major histocompatibility complex, class	2.1	3.0
	421579	NM_002975		stem cell growth factor, lymphocyte secr	21	3.3
40	428953	AA306610	Hs.194676	DKFZP434C013 protein	2.1	5.0
	457313	AF047002	Hs.241520	transcriptional coactivator	2.1	3.5
	420570	Al453665	Hs.290870	ESTs, Weakly similar to S23650 retroviru	2.1	2.1
	446918	AL135125	Hs.13913	KIAA1577 protein	2.1	2.3
	427567	N24236	Hs.179662	nucleosome assembly protein 1-like 1	2.1	2.8
45	446363	AL117440	Hs.301967	Homo sapiens mRNA; cDNA DKFZp434M196 (fr	2.1	4.0
	428482	AJ290352	Hs.184592	KIAA0344 gene product	2.1	2.8
	456559	AJ336273	Hs.102548	glucocorticoid receptor DNA binding fact	2.1	23
	442819	BE622721	Hs.301766	ESTs, Weakly similar to hypothetical pro	2.1	27.1
	428808	AA436007	Hs.188780	ESTs	2.1	5.0
50	414893	AA215295	Hs.77578	ubiquilin specific protease 9, X chromos	2.1	15.9
-	447023	AA356764	Hs.17109	Integral membrane protein 2A	2.1	3.0
	402250	AV655272	Hs.20252	novel Ras family protein	2.1	4.2
	429952	AF080158	Hs.226573	inhibitor of keppa light polypeptide gen	2.1	7.9
	420006	H14429	Hs.94300	serologically defined colon cancer antig	2.1	5.6
55	407316	AA031663	Hs.28802	centaurin-alpha 2 protein	2.1	4.4
JJ	417139	M69043	Hs.81328	nuclear factor of kappa light polypeptid	2.1	103.2
	414774	X02419	Hs.77274	plasminogen activator, urokinase	2.1	29.9
	430488	D19589	Hs.4220	ESTs, Moderately similar to tetracycline	2.1	25.5
	428680	U69199	Hs.90259	ESTs, Weakly similar to alpha 1 [H.sapie	21	2.5
60	448501	AA332316	Hs.4273	hypothetical protein FLJ13159	2.1	2.0
•	422552	N39729	Hs.118243	deoxyribonuclease II, lysosomal	21	2.9
	419476	AW953030	Hs.59425	Homo sapiens cDNA: FLJ23323 fis, clone H	2.1	3.1
	408681	AW953853	Hs.292833	ESTs	2.1	3.9
	417353	AA375752	Hs.76362	general transcription factor IIA, 2 (12k	21	4.1
65	422070	AF149785	Hs.111126	pituitary tumor-transforming 1 interacti	21	4.9
05	442711	AF151073	Hs.8645	hypothetical protein		
	450139	AK001838	Hs.296323	Homo sapiens cDNA FLJ10976 fis, clone PL	2.1 2.1	2.2
		BE066058				7.4
	452897		Hs.269233	ESTS	21	4.2
70	409147 433028	A1889208 A1199144	Hs.17283	hypothetical protein FLJ10890	21	4.5
70			Hs.283737	AD-017 protein	2.1	2.6
	407831	BE613377	Hs.15580	Homo sapiens cDNA: FLJ22276 fis, clone H	2.1	8.5
	417871	AA521368	Hs.24252	ESTS	21	2.9
	428754	A1521102	Hs.301374	ESTs, Moderately similar to ALU5_HUMAN A	2.1	5.3
75	430127	AA219498	Hs.233952	proteasome (prosome, macropain) subunit,	2.1	4.3
13	442622	NM_000435		Notch (Drosophila) homolog 3	2.1	8.5
	414242	AA749230	Hs.22666	ESTs	2.1	2.8
	433323	AA805132	Hs.30701	ESTs	2.1	5.0
	439022	AA356599	Hs.173904	ESTs	21	6.4
80	443357	AW016773		apolipoprotein C-II	21	2.0
οU	449103	T24968	Hs.23038	HSPC071 protein	2.1	2.7
	427512	AB018322	Hs.179507	KIAA0779 protein	2.1	20
	426728		Hs.171957	triple functional domain (PTPRF interact	21	2.9
	440112	AA099014	Hs.231029	ESTs	2.1	23

					0.4	
	446920		Hs.31257	Homo sapiens cDNA FLJ13634 fis, clone PL gene with multiple splice variants near	21 21	4.8 2.9
	428459 432842		Hs.184411 Hs.279525	hypothetical protein PRO2605	21	23
	438829		Hs.204214	ESTs	2.1	2.7
5	411442		Hs.101810	Homo sapiens cDNA FLJ14232 fis, clone NT	2.1	2.2
	409423		Hs.43071	ESTs, Weakly similar to AF151900 1 CGI-1	2.1	2.2
	456804		Hs.139851	caveolin 2	21	15.2
	434536		Hs.3903	Cdc42 effector protein 4; binder of Rho	21 21	2.8 25.0
10	447126 442328		Hs.62954 Hs.265237	ferritin, heavy polypeptide 1 ESTs	2.1	2.1
10	444488		Hs.184796	ESTs, Weakly similar to PET2_HUMAN OLIGO	2.1	2.9
	438874	H02780	10.101100	gb:yj41a11.r1 Soares placenta Nb2HP Horno	2.1	10.6
	412805		Hs.296287	ESTs	2.1	4.6
	446334	U52427	Hs.14839	polymerase (RNA) II (DNA directed) polyp	2.1	2.3
15	427201		Hs.173933	nuclear factor I/A	2.1	5.1
	436997	AA741151	Hs.137323	ESTs	2.1 2.1	3.0 2.3
	426369	AF134157 F06838	Hs.169487 Hs.14763	Kreisler (mouse) maf-related leucine zip ESTs	. 21	2.4
	453613 413276	Z24725	Hs.75260	mitogen inducible 2	21	5.5
20	422050	AA302741	Hs.25786	ESTs	2.1	4.0
	424797	AA622394	Hs.153177	ribosomal protein S28	2.1	2.1
	437365	AW965771	Hs.91065	hypothetical protein DKFZp761B2423	2.1	3.0
	412482	A1499930	Hs.181043	KIAA0788 protein	2.1	2.7
25	418662	AI801098	Hs.151500	ESTs	2.1 2.1	2.1 2.1
25	404030	41475005	11- 400040	ESTs	21	3.8
	437802 441130	Al475995 Al160734	Hs.122910 Hs.283429	SMC (mouse) homolog, X chromosome	21	3.5
	416084	L16991	Hs.79006	deoxythymidylate kinase (thymidylate kin	2.1	7.4
	409944	BE297925	Hs.57687	four and a half LIM domains 3	2.1	6.3
30	425421	L11669	Hs.157145	tetracycline transporter-like protein	2.1	7.1
	428399	NM_006276		splicing factor, arginine/serine-rich 7	2.1	2.7
	421313	NM_014923		KIAA0970 protein	2.1	2.6 4,7
	445229	BE276013	Hs.172364	Homo sapiens mRNA for FLJ00086 protein,	2.1 2.1	14.7
35	401001	NM_004341	Un 15/050	carbamoyl-phosphate synthetase 2, aspart	21	7.2
22	425159 438855	AW946276	Hs.6441	tissue inhibitor of metalloproteinase 2	2.1	4.9
	433369	Z49254	Hs.3254	mitochondrial ribosomal protein L23	2.1	25.0
	433228	F28212	Hs.284247	KIAA1491 protein	2.1	5.1
	445392	AA057478	Hs.23272	ESTs	2.0	2.3
40	433891	AA613792		gb:no97h03.s1 NCI_CGAP_Pr2 Homo sapiens	. 20	2.5
	432572	AI660840	Hs.191202	ESTs, Weakly similar to ALUE_HUMAN !!!!	2.0 2.0	2.9 12.1
	448474	AI792014	Hs.13809	ESTs protein phosphatase 2, regulatory subuni	20	2.9
	427045 444916	H86504 AB028956	Hs.173328 Hs.12144	KIAA1033 protein	20	4.2
45	439177	AW820275	Hs.76611	ESTs	2.0	3.3
15	423533		Hs.129751	interleukin 17 receptor	2.0	5.0
	430057	AW450303	Hs.2534	bone morphogenetic protein receptor, typ	2.0	2.3
	424429	U63830	Hs.146847	TRAF family member-associated NFKB activ	2.0	12.7
50	428385	AF112213	Hs.184062		2.0	4.6 16.4
50	458946	AA009716	Hs.42311	ESTs	2.0 2.0	4.9
	444816 426829	Z48633 Al761241	Hs.283742 Hs.301719		20	2.4
	433619	AW965275			2.0	4.4
	421985	AK001779	Hs.110445		2.0	3.8
55	439895	AB037773	Hs.6762	hypothetical protein FLJ10595	2.0	2.2
	449188	AW072939	Hs.23200	myotubularin related protein 1	2.0	2.2
	404820	41.000404	U- 450557	have what alsha 2 (DAC ashed 1 import	2.0 2.0	2.7 2.5
	425811 422163	AL039104 AF027208	Hs.159557 Hs.297332		20	3.7
60	431172	AI125639	Hs.250666		2.0	10.2
00	415200	AL040328	Hs.301912		2.0	2.1
	458176	Al961519	Hs.140309		2.0	5.0
	407895	R44203	Hs.265540		2.0	4.6
65	449816	AI701457	Hs.38694	ESTs	2.0 2.0	2.0 5.7
65	422976	AU076657	Hs.1600 Hs.152230	sec61 homolog) ESTs	2.0	11.7
	430220 435446	BE378277 AA682305			2.0	4.2
	431031	AA830335			2.0	14.1
	425233	Z17861	Hs.155218		20	5.6
70	426458	DB3032	Hs.169984		2.0	5.9
	421965	AA301100		gb:EST14128 Testis tumor Homo sapiens cD	20	2.1
	427128	AW301984			2.0 2.0	6.3 2.1
	449722 450816	BE280074 BE271927			20	24
75	453507	AF083217			2.0	13.1
	422801	AF125672			2.0	3.5
	418178	AA043951	Hs.83715	Sjogren syndrome antigen B (autoantigen	20	3.9
	417819	A1253112	Hs.13354		2.0	4.0
οΛ	414787	AL049332			2.0 2.0	4.0 7.0
80	447032 431742	AK000310) Hs.17138 52 Hs.26828		20	2.5
	448431	BE613061			2.0	6.5
	456444	AA884517			2.0	2.5
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```
419178
                        NM_006284 Hs.89657
                                                   TATA box binding protein (TBP)-associate
                                                                                                                                     6.0
2.2
2.1
2.1
2.6
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                        AI074585
                                      Hs.58440
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                                      Hs.87627
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                                      Hs.76252
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                                                    Homo saptens mRNA for HKR1, partial cds
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                                      Hs.129037
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                                                                                                                                     6.5
12.4
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                                                                                                                        2.0
2.0
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AI339732
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Hs.13144
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3.1
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AF086387 W72711 W77884
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           433891
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                       1883_13
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                                        AW968207 AA468415 AU185163 AW450843 Al568752 AW137191
           TABLE 4C:
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Ref:
                                Unique number corresponding to an Eos probeset
55
                                Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
                                Indicates DNA strand from which exons were predicted.
           Strand:
           Nt_position:
                                Indicates nucleotide positions of predicted exons.
60
           Pkey
400859
                         Ref
                                       Strand
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                                                     169926-170121
                                       Plus
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                         9909420
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                                                    108716-111112
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            402605
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                         8081591
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            404048
                         3688074
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            405268
                         4156151
                                       Minus
            405204
                         7230116
                                       Phrs
                         9454624
                                                     114757-114877
            405517
                                       Plus
            405203
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1168-1324,5492-5611,23445-23851
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                         8568881
            403966
                                       Phis
                         3128156
            402269
                                       Minus
            404170
                         9930793
                                                     168836-169248
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	40.4000	7074000	Ot	440262 454740	
	404030 401001			149362-151749 113631-113762	
	404820	4678240	Plus	20475-21085	
5					
_		ABOU'T 43 GE	NES UPREGU	LATED IN GLIOBLASTOMA THAT ENCODE PRED	DICTED MEMBRANE PROTEINS
	Pkey: ExAccn:			identifier number number, Genbank accession number	
	UnigenelD:	Uniger	ne number		
10	Unigene Ti		ne gene title	to hade alter	
	R1: R2:		of brain tumor (of brain tumor (to body attas to normal brain	
					R1 R2
15	Pkey 415817	ExAcon U88967	UnigeneID Hs.78867	Unigene title protein tyrosine phosphatase, receptor-t	72.0 11.3
13	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	54.2 7.1
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	22.0 7.6 21.2 3.0
	415910 412986	U20350 X81120	Hs.78913 Hs.75110	chemokine (C-X3-C) receptor 1 cannabinoid receptor 1 (brain)	18.6 18.6
20	417355	D13168	Hs.82002	endothelin receptor type B	16.4 16.4
	419721	NM_001650	Hs.288650	aquaporin 4	16.2 4.4 13.9 13.9
	452355 410227	N54926 AB009284	Hs.29202 Hs.61152	G protein-coupled receptor 34 exostoses (multiple)-like 2 ·	11.9 2.9
	419723	AL120193	Hs.92614	Homo sapiens growth differentiation fact	7.4 3.5
25	414825	X06370	Hs.77432	epidermal growth factor receptor (avian	6.9 6.4 4.8 7.2
	443898 422033	AW804296 AW245805	Hs.9950 Hs.110903	Sec61 gamma claudin 5 (transmembrane protein deleted	4.3 6.1
	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity la, re	4.2 34.8
20	431556	AF016028	Hs.260039	sarcospan (Kras oncogene-associated gene	4.0 3.8 · 3.7 4.2
30	435869 440516	AF255910 S42303	Hs.54650 Hs.161	vascular endothelial junction-associated cadherin 2, type 1, N-cadherin (neuronal	3.5 5.1
	428141	D50402	Hs.182611	solute carrier family 11 (proton-coupled	3.5 2.4
	428484	AF104032	Hs.184601	solute carrier family 7 (calionic amino Glutarnate receptor subunit	3.4 2.8 · 3.3 2.4
35	431053 445070	S40369 NM_000677	Hs.249141 Hs.258	adenosine A3 receptor	3.2 7.6
55	430890	X54232	Hs.2699	glypican 1	3.2 4.3
	423422	AC005175	Hs.128425	NY-REN-24 antigen solute carrier family 16 (monocarboxylic	3.2 4.0 3.1 2.6
	413367 447471	NM_006517 AF039843	Hs.75317 Hs.18676	sprouty (Drosophila) homolog 2	3.0 4.1
40	427150	BE616183	Hs.173737	ras-related C3 botulinum toxin substrate	3.0 4.1
	422676	D28481	Hs.1570 Hs.238272	histamine receptor H1 inositol 1,4,5-triphosphate receptor, ty	3.0 2.1 3.0 6.3
	430293 453496	AI416988 AA442103	Hs.33084	solute carrier family 2 (facilitated glu	2.8 7.4
4.5	428281	AA194554	Hs.183434	ATPase, H+ transporting, lysosomal (vacu	2.7 3.2 2.4 4.4
45	417446	AL118671	Hs.82163 Hs.74471	monoamine oxidase B gap junction protein, alpha 1, 43kD (con	2.4 4.4 2.4 2.2
	412676 440225	NM_000165 BE295782	Hs.159	tumor necrosis factor receptor superfami	2.4 76.7
	450447	AF212223	Hs.25010	hypothetical protein P15-2	2.3 2.3 2.3 4.1
50	410310 452036	J02931 NM_003966	Hs.62192 Hs.27621	coagulation factor til (thromboplastin, sema domain, seven thrombospondin repeat	23 24
50	447217	BE465754	Hs.17778	neuropilin 2	2.3 3.0
	447023	AA356764	Hs.17109	integral membrane protein 2A	2.1 3.0 2.1 4.9
	422070 456804	AF149785 AI421645	Hs.111126 Hs.139851	pituitary tumor-transforming 1 interacti caveolin 2	2.1 15.2
55	430057	AW450303	Hs.2534	bane morphogenetic protein receptor, typ	20 23
	422163	AF027208	Hs.297332		20 3.7 20 24
	414482	S57498	Hs.76252	endothelin receptor type A	20 P
	<u></u>				
60				NREGULATED IN GLIOBLASTOMA set identifier number	
	Pkey: ExAccn:	Exe	emplar Accessi	on number, Genbank accession number	
	Unigena	ID: Uni	gene number		
65	Unigene R1:	Title: Uni	gene gene title io of normal br	ein to body atlas	
05	R2:	Rat	io of normal br	ain to brain tumor .	
	_			Trut-	R1 R2
	Pkey 439340	Ex Accn AB032436	UnigenelD Hs.6535	Title brain-specific Na-dependent Inorganic ph	4.47 77.82
70	424846		Hs.1832	neuropeptide Y	4.49 55.32
	428874		Hs.194366		7.06 45.64 9.45 44.59
	416836 401412		Hs.80247	chalecystokinin exon	3.20 32.56
	451835	T63643	Hs.20971	ESTs, Weakly similar to ALU7_HUMAN ALU S	3.21 28.93
75	412768	AW996044			3.16 28.12 3.27 27.04
	415448 411305		Hs.952 Hs.69547	solute carrier family 10 (sodium/bile ac myelin basic protein	13.80 25.92
	438054	AA776626	Hs.62183	ESTs	3.59 25.06
80	410837		Un 15Jet	gb:ILO-HT0205-231199-145-a07 HT0205 Homo 9 synaptotagmin 1	o 3.05 24.43 6.92 23.67
60	425121 455763		Hs.154679 Hs.12818	0 B-cell translocation gene 4	3.29 23.32
	429656	X05608	Hs.21158	4 neurofilament, light polypeptide (68kD)	8.03 22.56 4.12 21.82
	451892	Al821302	Hs.15783	4 ESTs	4,12 21.02

	424922	BE386547	Hs.217112	ECTe Worlds startles to country to a se		
	411666	AF106564	Hs.71346	ESTs, Weakly similar to Similarity to Ye	4.41	21.28
	432247	AA531287	Hs.105805	neurofilament 3 (150kD medium) ESTs	5.27	21.20
_	436812	AW298067	13.10000	gb:UI-H-BW0-eip-g-09-0-UI.s1 NCI_CGAP_Su	3.25	21.14
5	422234	AF119818	Hs.113287	discs, large (Drosophila) homolog-associ	3.02	21.12
_	435708	Al362949	Hs.75169	ESTs	3.38	20.50
	423135	N67655	Hs.26411	ESTs	8.79	20.45
	440600	Al807691	Hs.126351	ESTs	6.82	20.28
	405230	cNp1_7656		exon	3.56	20.09
10	456915	N55540	Hs.78026	ESTs, Wealdy similar to similar to ankyr	3.31	19.95
	425130	AA448208	Hs.99163	ESTs	3.14	19.40
	416812	H91010	Hs.44940	ESTs	3.53	19.20
	454171	AW854832		gb:QV2-CT0261-201099-011-f05 CT0261 Homo	3.54	19.08
	457463	AW877031	Hs.272321	Homo saplens cDNA FLJ12571 fis, done NT	3.78	19.04
15	454589	AW809699		gb:MR4-ST0124-241199-026-e12 ST0124 Homo	3.13 4.10	18.91
	418104	T05726	Hs.177130	ESTs	3.17	18.60
	416357	T82050	Hs.268907	EST8	3.17	18.41
	414583	S78296	Hs.76888	internexin neuronal intermediate filamen	5.55	18.13 18.13
00	447694	AI420083	Hs.170303	ESTs	3.56	17,79
20	427627	R87582	Hs.179915	guanine nucleotide binding protein (G pr	4.63	17.65
	428010	AA806554	Hs.185375	ESTs	3.03	17.40
	417159	R01761		gb:ye81f10.s1 Soares fetal liver spleen	3.23	17.38
	436788	AA766908 ·	Hs.259047	ESTs	3.16	17.21
25	459349	AW749381		gb:QV3-BT0381-170100-060-c02 BT0381 Homo	3.26	17.10
25	450214	BE439763	Hs.227571	regulator of G-protein signalling 4	3.86	17.04
	438068	Al927209	Hs.283089	HMT1 (hnRNP methyltransferase, S. cerevi	3.54	16.48
	437268	AI754847	Hs.227571	regulator of G-protein signalling 4	5.63	16.32
	435315	AA700240	Hs.165402	ESTs	4.06	16.12
20	424240	AB023185	Hs.143535	calcium/calmodulin-dependent protein kin	4.69	15.92
30	412446	AI768015	Hs.92127	ESTs	5.44	15.75
	449714	AB033015	Hs.23941	KIAA1189 protein	4.59	15.43
	435832	AA425688	Hs.41641	Bruno (Drosophila) -like 4, RNA binding	4.63	14.97
	437397	AA349847	Hs.4221	hypothetical protein DKFZp761H039	5.93	14.81
35	435502	L13266	Hs.105	glutamate receptor, tonotropic, N-methyl	3.29	14.61
33	414187	BE312141		gb:601145962F1 NIH_MGC_19 Homo saplens c	3.37	14.46
	417868	AI078534	Hs.122592	ESTs	7.57	14.22
	428536	Al143139	Hs.2288	visinin-like 1	5.16	13.98
	402125	c18p3_155	11. 7005	exon	3.11	13.94
40	440503	NM_006539	Hs.7235	calcium channel, voltage-dependent, gamm	3.49	13.92
40	419090 437665	T85201	Hs.188468	ESTs	3.25	13.79
	457113	AA765417 Al734016	Hs.292053	ESTs	3.07	13.79
	424933	AW999974	Hs.270508 Hs.5181	ESTs	3.50	13.69
	443489	A1073512	Hs.133916	proliferation-associated 2G4, 38kD	3.59	13.48
45	404289	c6p3_5821	ns.133910	ESTs exon	3.24	13.20
	406534	ph2_4616		exon	3.99	13.12
	423280	AA324037			3.89	13.10
	455421	AW937661	Hs.288324	gb:EST26901 Cerebellum II Homo septens c Homo septens cDNA FLJ13283 fis, clone OV	3.38	13.03
	433725	AF063559	Hs.283919	Homo sapiens clone HQ0117 PRO0117 mRNA,	3.04	12.93
50	416660	R98905	Hs.35992	ESTs	3.71	12.85
	407593	AW044083	Hs.237008	ESTs	3.92	12.74
	451734	NM_006176	Hs.26944	neurogranin (protein kinase C substrate,	3.85	12.67
	410366	Al267589	Hs.25214	hypothetical protein	7.41	12.59
	405348	cNp3_13716		exon	7.89 3.45	12.50
55	442338	Al761976	Hs.156080	ESTs	3.69	12.42 12.35
	424458	M29273	Hs.1780	myelin associated glycoprotein	4.72	12.33
	431400	AA504607		gb:aa63a02.s1 NCI_CGAP_GC81 Homo sapiens	3.42	12.29
	417754	R13027	Hs.268703	ESTs	3.35	12.18
C 0	440184	AB002297	Hs.7022	dedicator of cyto-kinesis 3	6.15	12.11
60	431339	AA506294	Hs.257266	ESTs	3.50	11.97
	452265	BE501516	Hs.114772	ESTs	3.82	11.96
	419297	AA446040	Hs.98640	Homo sapiens cDNA: FLJ21069 fis, clone C	3.16	11.86
	424991	AA775471	Hs.241467	ESTs	3.03	11.64
65	431988	AC002302	Hs.77202	protein kinase C, beta 1	3.78	11.62
05	450987	AA017202	Hs.32794	ESTs	3.28	11.61
	440607	AA894559	Hs.192097	ESTs	3.11	11.60
	454566	AW807605		gb:MR4-ST0098-120100-001-b06 ST0098 Homo	3.26	11.54
	442000	H38671	Hs.8071	KIAA0735 gene product; synaptic vesicle	3.44	11.51
70	437948	AA772920		gb:ae73c09.s1 Stratagene schizo brain S1	3.16	11.46
70	401081	c11p3_921		exon	3.18	11.35
	438919	AW979114		gb:EST391224 MAGE resequences, MAGP Horno	4.16	11.35
	454578 422279	AW809178	Un 444004	gb:MR4-ST0118-261099-012-c07 ST0118 Homo	3.02	11.27
	453101	H69644	Hs.114231	C-type lectin-like receptor-2	3.35	11.13
75	455836	AW952776 BE145795	Hs.94943	ESTS	3.21	11.07
, ,	413324	V00571	Ue 75904	gb:MR0-HT0208-101299-103-a12 HT0208 Homo	3.61	10.83
	412266	N59006	Hs.75294 Hs.26133	corticotropin releasing hormone	3.72	10.71
	436887	AW953157	Hs.193235	ESTs .	3.80	10.60
	454968	AW849046	110.100200	gb:iL3-CT0214-150300-085-H06 CT0214 Homo	7.24	10.56
80	418162	T11958		gb:A802R Heart Homo saplens cDNA ctone A	3.05	10.53
	425537	AB007913	Hs.158291	KIAA0444 protein	3.07	10.50
	436230	Al248723	Hs.17711	ESTs	3.07 3.09	10.46
	431169	AW971240		gb:EST383329 MAGE resequences, MAGL Homo	3.02	10.45
				2 (MIN)	3.02	10.43

	447359	NM_012093		adenylate kinase 5	5.91	10.40
	457187	AA443927		EST	3.30 3.02	10.39 10.35
	407539	X91103		gb:H.sapiens mRNA for Hr44 protein.	3.02	10.35
5	452855	R17746		ESTs	3.03	10.20
)	440352	Al692322		ESTs -	3.11	10.17
	456116 458172	Z28528 BE007237	113.172004	gb:PM0-BN0139-050500-003-g09 BN0139 Homo	3.32	10.14
	445881	Al263029		ESTs	3.04	10.11
	454059	NM_003154	Hs.37048	statherin	3.27	9.97
10	402624	c1p1_2660		exon	3.05	9.94
	441539	AA937200	Hs.192939	ESTs	3.27 3.03	9.82 9.78
	412172	N76794		gb:yv45g07.r1 Soares fetal liver spleen gb:zv01d05.r1 NCI_CGAP_GCB1 Homo sapiens	4.09	9.73
	427942	AA417856 BE041837	Hs.120316	ESTs	3.25	9.73
15	436867 454688	AW814472	18.120010	gb:MR3-ST0203-010200-109-b06 ST0203 Homo	3.41	9.73
15	446122	Al362790	Hs.181801	ESTs	3.40	9.71
	420480	AL137361	Hs.98173	hypothetical protein	3.03	9.56
	433447	U29195	Hs.3281	neuronal pentraxin II	3.72	9.54
00	407178	AA195651	Hs.104106	ESTs	3.89 3.06	9.47 9.45
20	415614	F12926	Hs.165998	DKFZP564M2423 protein	3.99	9.39
	450518	BE245175	Hs.270893	ESTs qb:RC3-BT0319-120200-014-a06 BT0319 Homo	3.45	9.32
	455675 456459	BE065984 AA253074	Hs.146261	ESTs	4.08	9.30
	423420	AJ571364	Hs.128382	Homo sapiens mRNA; cDNA DKFZp761I1224 (f	5.18	9.23
25	455644	BE064521		gb:RC4-BT0311-250200-014-d02 BT0311 Homo	3.02	9.20
	419800	AA282392	Hs.191525	ESTs	3.28	9.16
	430964	Y10929	Hs.248167	zinc finger protein 186 (Kruppel type)	3.04 3.02	9.00 9.00
	409716	AL117454	Hs.56027	Homo saplens mRNA; cDNA DKFZp586J1717 (f	3.33	8.99
30	412962	AW839578	Hs.18160 Hs.195929	Homo sapiens cDNA FLJ11550 fis, clone HE ESTs, Weakly similar to pre-serum amyloi	3.50	8.96
30	445040 451496	AW444934 AW503407	ns. 190929	gb:UI-HF-BNO-akw-d-11-0-UI.r1 NIH_MGC_50	3.17	8.94
	424617	AA344151		gb:EST50059 Gall bladder I Homo sapiens	3.25	8.91
	441914	AA971496	Hs.128465	ESTs	3.42	8.88
~-	405320	cNp3_12168		exon	3.30	8.84
35	449179	AI633785	Hs.196561	ESTs	3.43 3.13	8.84 8.78
	400335	Y13187	Hs.248066	Homo sapiens dmd gene, intron 11 gb:lL3-CT0213-280100-056-A04 CT0213 Homo	4.16	8.74
	454962	AW847645 AW081681	Hs.269064	ESTs	3.09	8.73
	407803 455260	AW878317	113.203007	gb:MR3-OT0007-260300-206-e09 OT0007 Homo	3.78	8.70
40	431096	AA324358	Hs.249227	Homo sapiens DNA, cosmid clones TN62 and	4.01	8.67
	424481	R19453	Hs.1787	proteolipid protein (Pelizaeus-Merzbache	8.12	8.63
	407616	AW054849	Hs.246831	ESTs, Weakly similar to CIKG_HUMAN VOLTA	3.08	8.53 8.51
	434589	AF147363	11-000004	gb:Homo sapiens full length insert cDNA	3.26 5.78	8.48
45	439239	AI031540 AW810708	Hs.235331	ESTs gb:MR2-ST0129-051099-007-g07 ST0129 Homo	3.34	8.47
73	410926 430004	U27768	Hs.227571	regulator of G-protein signalling 4	4.26	8.45
	409623	AW449185		gb:UI-H-BI3-akg-e-05-0-UI.s1 NCI_CGAP_Su	3.32	8.43
	420156	AW449258	Hs.6187	ESTs	3.40	8.38
50	411555	AF113537	Hs.70669	HMP19 protein	5.85 3.17	8.34 8.34
50	408509	AA497035	Hs.110502	ESTs ESTs	3.02	8.33
	442368 457870	Al698577 AA732217	Hs.202481 Hs.294054		3.04	8.32
	437254	AA831258	110.201001	gb:oc73f04.s1 NCI_CGAP_GCB1 Homo sapiens	3.35	8.24
	415508	R39236		gb:yc91d03.s1 Soares infant brain 1NIB H	3.07	8.22
55	409483	U49379	Hs.54506	diacylglycerol kinase, epsilon (64kD)	3.31	8.20
	435229	AA676556	Hs.269515		3.21 3.22	8.19 8.17
	458120	W21398	Hs.54523	ESTs, Wealdy similar to cytochrome P-450 ESTs	3.78	8.16
	444613 41.7050	H29627 N39540	Hs.79092 Hs.108029		4.06	8.14
60	425607	U09860	Hs.158333	nortease, serine, 7 (enterokinase)	3.68	8.06
•••	413263	BE075131		gb:PM1-BT0585-110200-003-g03 BT0585 Homo	3.40	8.04
	424549	AI873205	Hs.183114		3.27	8.03
	452689	F33868	Hs.284176		3.03 3.28	8.01 8.00
65	405476	cNp3_1994	0	exon	3.58	7.99
03	403932 407095	c5p1_533 AF011757	Hs.105937	exon 7 RAGE binding protein	3.32	7.96
	415967	H11124	115.10030	gb:ym14h07.s1 Soares infant brain 1NIB H	3.10	7.96
	417555			gb:yr67c10.r1 Soares fetal liver spleen	3.05	7.95
	448985		Hs.22777	carbonic anhydrase XI	5.30	7.79
70	428689				3.87	7.74
	424140		Hs.14130		4.68 3.08	7.74 7.74
	441099				3.10	7.73
	448589 406112			exon	3.22	7.70
75	458439			9 ESTs, Weakly similar to strong similarit	3.22	7.69
	429859			2 protein tyrosine phosphatase, receptor t	3.15	7.68
	412090	AW955826		ESTs, Weakly similar to ALU6_HUMAN ALU S	3.01	7.67
	413547			gb:RC1-HT0229-080100-015-f09 HT0229 Homo	3.01 3.04	7.66 7.63
80	447772 411123		Hs.16139	9 ESTs gb:CM1-ST0283-071299-061-d08 ST0283 Homo	3.72	7.61
80	411132 425490				3.15	7.60
	454568			gb:MR0-HT0079-051099-002-d01 HT0079 Homo	3.16	7.59
	439099			KIAA1379 protein	3.40	7.57

	415669	NM_005025	Hs.78589	serine (or cysteine) proteinese inhibito	5.71	7.57
	428175	Al810774	Hs.98376	ESTs	3.04	7.55
	413162	BE068115	1.0.0001	gb:CM1-BT0368-061299-060-g07 BT0368 Homo	3.43	7.54
_	451361	AA053854	Hs.235390	Homo sapiens mRNA; cDNA DXFZp761B101 (fr	3.11	7.53
5	442527	AF150289	Hs.205436	ESTs	3.31	7.53
	450407	NM_000810	Hs.24969	gamma-aminobutyric acid (GABA) A recepto	5.24 3.13	7.53 7.47
	456966 441799	AI589569 AW292276	Hs.190082 Hs.127872	ESTs ESTs	3.38	7.41
	424185	AA279752	Hs.142570	Homo sapiens clone 24629 mRNA sequence	3.16	7.40
10	429783	AA811987	Hs.125779	ESTs	3.13	7.38
	429268	AA205386	Hs.198481	RAR-related orphan receptor B	3.48	7.38
	400708	c11p1_1292		exxon	3.33	7.35
	402598	BE314624	Hs.3128	polymerase (RNA) II (DNA directed) polyp	3.04	7.33
15	455377	AW905347		gb:QV2-NN1073-220400-159-66 NN1073 Homo	3.03	7.33
15	435070	Al821270	Hs.116930	ESTB	3.03 3.03	7.33 7.25
	405427 455149	cNp3_17682 AW861879		exon ab:CMO-CT0341-260100-160-h12 CT0341 Homo	3.56	7.24
	402816	c1p3_2531		exon	3.13	7.21
	422890	Z43784	Hs.78713	solute carrier family 25 (mitochondrial	3.40	7.15
20	422297	AW961290	Hs.155615	ESTs	3.44	7.10
	412686	AW984068		gb:RC0-HN0006-160300-011-e06 HN0006 Homo	3.91	7.09
	436383	BE065178		gb:RC1-BT0314-020200-012-h01 BT0314 Homo	3.09	7.09
	412290	BE069037	11- 40004	gb:QV3-BT0379-161299-040-e12 BT0379 Homo	3.04 4.22	7.08 7.07
25	415486	H12214	Hs.13284 Hs.175931	ESTs ESTs	3.05	7.06
23	407728 448548	AW071502 R13209	Hs.21413	solute carrier family 12, (potassium-chi	5.93	7.05
	417275	X63578	Hs.81849	parvalbumin	4.08	7.04
	418425	AJ871247	Hs.6262	ESTs	4.10	7.04
	440558	AA889574	Hs.177511	ESTs	3.28	7.04
30	411427	AW846080		gb:MR3-CT0176-081099-002-b09 CT0176 Homo	3.11	7.03
	422272	AI452421	Hs.77965	Clk-associating RS-cyclophilin	3.39	7.03
	410816	AW806175		gb:MR1-UM0108-130400-003-a06 UM0108 Homo	3.30 9.93	7.02 7.01
	418375	NM_003081	Hs.84389	synaptosomal-associated protein, 25kD ESTs	3.10	7.01
35	421627 447258	Al138551 BE047911	Hs.97318	gb:tz44a05.y1 NCI_CGAP_Bm52 Homo sapien	3.09	6.99
33	455547	AW994078		ab:RC3-BN0036-090200-011-h02 BN0036 Homo	3.35	6.98
	432209	AW971278		gb:EST383367 MAGE resequences, MAGL Homo	3.49	6.92
	404541	c8p1_6409		exon	4.62	6.89
40	451539	AA059467	Hs.218933	ESTs	3.01	6.88
40	429954	AI918130	Hs.21374	ESTs	3.82	6.87
	411138	AW819500	11. 004003	gb:RCS-ST0293-180100-012-C07 ST0293 Homo	3.08 3.33	6.87 6.85
	447464	AW444957	Hs.201897	ESTs, Weakly similar to ALU4_HUMAN ALU S gb:QV4-ST0212-091199-023-c09 ST0212 Homo	3.35 3.16	6.84
	454713 415734	AW815111 NM_014747	Hs.78748	KIAA0237 gene product	5.00	6.84
45	429667	AA456275	Hs.44841	ESTs .	3.09	6.80
7.5	403008	c21p3_2374	125,44041	exon	3.04	6.78
	446079	T56522	Hs.154030	EST ₈	3.11	6.75
	441869	NM_003947	Hs.8004	huntingtin-associated protein interactin	4.49	6.75
50	437804	AA828257	Hs.124324	ESTs	3.42	6.73
50	436454	AA757615	Hs.291509	ESTs	3.01 3.12	6.72 6.70
	416334	H53139	Hs.36271	ESTs gb:CM2-HT0502-140200-088-d08 HT0502 Homo	3.05	6.68
	455965 445085	BE167014 Al569295	Hs.179285	ESTs	3.19	6.68
	445611	AW418497	Hs.145583	ESTs	3.61	6.68
55	437762	T78028	Hs.154679	synaptotagmin 1	7.21	6.68
	416268	H49111		gb:yo21c07.r1 Soares adult brain N2b5HB5	3.02	6.67
	449766	AI668690	Hs.54773	ESTs	3.25	6.64
	443100	A)033188		gb:ow94e08.s1 Soares_fetal_liver_spleen_	3.07 3.12	6.64 6.60
60	408070 451602	AW148852 AW008846	Hs.60857	gbxf05d05.x1 NCI_CGAP_Bm35 Homo saplen ESTs	3.05	6.59
O	441447	AA934077	Hs.126980		4.06	6.59
	445078	AI869975	Hs.4775	junclophilin 3	4,25	6.59
	434501	AF143878	Hs.194152		3.25	6.58
	415960	R49020	Hs.24974	ESTs .	3.34	6.58
65	403395	c3p1_11541		exon	3.59	6.57
	403061	c2p1_10450		exon	3.06 3.28	6.56 6.56
	419232	AI382037	Hs.87421 Hs.165636	ESTs hypothetical protein DKFZp761C07121	6.50	6.56
	425984 403717	AW836277 c4p1_3133	rts.103030	exon	3.52	6.53
70	452178	AW043576	Hs.171929		3.38	6.53
	455758	R15709	Hs_284231		4.42	6.52
	433858	N69243	Hs.192974	Homo sapiens cDNA FLJ12735 fis, clone NT	3.58	6.52
	425440	AA357518		gb:EST66256 LNCAP cells I Homo sapiens c	3.15	6.49 6.47
75	419412	AW161058	Hs.90297	synuclein, beta	5.60 3.47	6.47 6.47
75	423678	AW963357	Hs.7847	ESTs ESTs	3.47 3.10	6.46
	416625 451854	R97839 T92536	Hs.35758 Hs.194096		3.28	6.46
	406732		Hs.2064	vimentin	3.71	6.44
	434619		Hs.32810	ESTs	3.05	6.44
80	413797	BE167274	Hs.5996	ESTs	3.23	6.44
	438612		Hs.29212	B ESTs	3.39	6.42 6.42
	412317		Un 450400	gb:RC1-BN0014-210100-012-f05 BN0014 Homo	3.46 3.03	6.42 6.41
	422159	N76767	Hs.15340	S ESTs	3.03	0.41

				51 1.1 (0001FT)	3.46	6.35
	429290 427334	AF203032	Hs.198760 Hs.119486	neurofilament, heavy polypeptide (200kD) ESTs, Weakly simitar to transmembrane re	3.93	6.35
	427334 453839	R44789 AL138417	TIS. 115400	gb:DKFZp434B1729_r1 434 (synonym: htes3)	3.06	6.34
_	429096	AB011106		KIAA0534 protein	3.12	6.33
5	444609	AW571659		ESTs	3.30 3.11	6.33 6.33
	419515	S81944		gamma-aminobutyric acid (GABA) A recepto ESTs	3.14	6.30
	418900 437979	BE207357 AA774318		ESTs	3.25	6.29
	410359	R38624		ESTs	4.74	6.28
10	415990	R76929	Hs.29633	ESTs	3.39 3.00	6.28 6.28
	419392	W28573	U= 444024	gb:51f10 Human retina cDNA randomly prim ATPase, aminophospholipid transporter (A	3.06	6.26
	424312 444762	AB013452 AI733700	Hs.144931 Hs.143883	ESTs	3.09	6.25
	447785	AL041765	Hs.161423	ESTs	3.05	6.22
15	418199	AA884555	Hs.86603	ESTs	3.55 3.73	6.22 6.21
	440582	AA993337	Hs.129082	ESTs	3.69	6.21
	457766 426814	AL119470 AF036943	Hs.145631 Hs.172619	ESTs KIAA1106 protein	4.71	6.21
	412018	BE148152	10.112010	gb:RC4-HT0231-041199-012-b04 HT0231 Homo	3.36	6.21
20	414699	AI815523	Hs.76930	synuclein, alpha (non A4 component of am	3.68 3.54	6.19 6.18
	420127	AA360399	Hs.44811	ESTs	3.08	6.18
	418833 441265	AW974899 AA927180	Hs.292776 Hs.153261	ESTs ESTs	3.21	6.17
	413408	R51793	Hs.21745	ESTs	3.56	6.15
25	434512	AW139932	Hs.188941	ESTs	3.56	6.15
	422253	W81526	Hs.118329	ESTs	5.04 3.24	6.10 6.10
	439950	AW937417	Hs.293561	ESTs	3.54	6.10
	417210	N99228 BE272198	Hs.49162 Hs.283869	ESTs Human DNA sequence from clone RP5-1013A2	3.35	6.10
30	414306 411265	AW834695	115.205005	gb:RC0-LT0001-261199-031-D05 LT0001 Homo	3.07	6.10
50	412734	AW993498		gb:RC2-BN0033-170300-019-b08 BN0033 Homo	3.36	6.09
	425172	AA447729	Hs.12714	ESTs	5.40	6.06 6.02
	451759	W23161	Hs.32886	ESTs	3.21 3.50	6.02
35	432154	AI701523	Hs.112577	ESTs exon	3.92	5.96
33	401313 446951	c13p1_435 Al350575	Hs.156730	ESTs	3.20	5.95
	440917	AA909651	Hs.160025	ESTs	3.06	5.94
	405961	ph0_14521		exon	3.12	5.91
40	428737	AA984728	Hs.192760	kinesin family member 5A	3.05 3.62	5.90 5.89
40	417292	N69197	Hs.191361 Hs.21754	ESTs Homo sapiens mRNA full length insert cDN	3.52	5.88
	448681 452524	AL109781 AW136499	Hs.29796	Homo sapiens mRNA; cDNA DKFZp434D1319 (f	3.07	5.88
	426575	M74826	Hs.170808	glutamate decarboxylase 2 (pancreatic is	4.08	5.87
	423641	AL137256	Hs.130489	Homo sapiens mRNA; cDNA DKFZp761K0912 (f	3.28	5.87
45	420755	AI699437	Hs.165268	ESTs	3.17 3.28	5.86 5.86
	448116	AW352276	Hs.170700	ESTs gb:PM3-HN0011-200300-001-f01 HN0011 Homo	3.00	5.83
	412694 437612	AW984373 AA827715	Hs.105153	Homo sapiens cDNA FLJ14230 fis, clone NT	3.09	5.82
	411522	AW850286	12.100.00	gb:IL3-CT0219-161199-031-H11 CT0219 Homo	3.26	5.81
50	456910	BE185921	Hs.98073	ESTs	3.20	5.80 5.80
	439915	Al521791	Hs.252358	ESTs	3.55 3.23	5.80
	404403	c8p1_1094	,	exou exou	3.51	5.78
	405332 411167	cNp3_1301 AW820204	,	gb:QV2-ST0296-190100-029-c11 ST0296 Homo	3.04	5.78
55	416139	H21109	Hs.172853	ESTs	3.63	5.77
	434222	AF119886	Hs.283941		3.65	5.77 5.75
	415247	F02431	Hs.6581	ESTs	3.08 3.42	5.75 5.75
	446037	AI076806	Hs.282965 Hs.271200		3.80	5.72
60	450478 446588		Hs.282954	ESTe	3.29	5.72
O.	413118	05005000	7.2.2	ab:RC3-BT0319-100100-012-c11 BT0319 Homo	3.03	5.72
	416946	NM_01232		mitogen-activated protein kinase 8 inter	3.91 3.06	5.72 5.72
	454751			gb:RC3-ST0281-240400-015-c10 ST0281 Homo ESTs, Highly similar to unnamed protein	3.54	5.71
65	457194 438601		Hs.35406 Hs.16322		3.26	5.71
05	439032		Hs.27441		3.10	5.67
	408940		Hs.662	cerebellin 1 precursor	3.32	5.67
	437700	AA766060			3.23 3.85	5.66 5.65
70	416061		Hs.26119	ESTs gb:RC1-HT0598-020300-011-h11 HT0598 Homo	3.04	5.64
70	452861 430330				3.51	5.63
	435312		Hs.4865	voltage-gated sodium channel beta-3 subu	5.67	5.62
	400710			exon	3.04	5.61
	45713) NM_00565	51 Hs.18367		3.31 3.93	5.60 5.60
75	43451			Homo sapiens clone IMAGE:121736 mRNA seq alutamate receptor, metabotropic 3	3.93 3.67	5.58
	43427 44085		Hs.3786 0 Hs.24671		3.30	5.58
	45708				3.37	5.57
80	43188		Hs.10551	0 ESTs	3.67	5.56
	40075	8 AA158742	2 Hs.22508	Homo sapiens cDNA FLJ14280 fis, clone PL	3.43 3.36	5.55 5.52
	45537			gb:CM3-NN1040-200400-156-d03 NN1040 Homo	3.10	5.50
	44075 45186		1 Hs.2454(Hs.3318)		3.38	5.50
	40100	A 149191				

	453100	AW806871	Hs.224786	ESTs	3.30	5.49		
	433940	H05129	Hs.7459	cyclic AMP-regulated phosphoprotein, 21	3.24	5.49		
	454935	AW846075		gb:MR3-CT0176-081099-002-b02 CT0176 Homo	3.26	5.48		
5	435447	AI872932	Hs.142442	HP1-BP74	3.89	5.47		
,	402953 456233	c20p3_3451 AA2033339		exon	3.28	5.47		
	407718	AW070784	Hs.243243	gb:zx56a01.r1 Soares_fetal_liver_spteen_ EST	3.02 3.30	5.47 5.45		
	417429	Al950629	Hs.286237	Homo sapiens cDNA FLJ11841 fis, clone HE	3.31	5.45 5.38		
4.0	446408	Al797169	Hs.208486	ESTs	3.07	5.37		
10	441792	AW873635	Hs.143962	ESTs	3.19	5.35		
	450661	AW952160	Hs.32916	ESTs	3.70	5.35		
	433932	AW954599	Hs.169330	neuronal protein	6.78	5.33		
	427002 428741	AA524093 AA461386	Hs.23158	ESTs	4.00	5.32		
15	446383	T05816	Hs.92511	gb:zx70h06.r1 Soares_lotal_fetus_Nb2HF8_ EST	3.10	5.32		
	442988	AI026130	Hs.131683	EST8	3.39 3.07	5.30 5.29 .		
	426713	Al655299	Hs.130055	ESTs	3.33	5.29		
	421294	AA713486	Hs.180291	ESTs	3.44	5.28		
20	406452	ph2_21981		exou	3.20	5.28		
20	423508	AW604297	Hs.129711	hepatitis A virus cellular receptor 1	3.26	5.27		
	442114	BE217975	Hs.157021	ESTs	3.32	5.26		
	432508 425604	AI808915	Hs.190201	ESTs	3.46	5.26		
	417925	U94320 R26789	Hs.158330 Hs.23995	neuropeptide Y receptor Y5 ESTs	3.26	5.23		
25	444448	H66317	Hs.143660	ESTS	3.08 3.81	5.23 5.22		
	413024	AF036268	Hs.75149	SH3-domain GRB2-like 2	3.71	5.22		
	437911	AA848010	Hs.124250	ESTs .	3.11	5.18		
	435406	F26698	Hs.4884	calcium/calmodulin-dependent protein kin	4.95	5.17		
20	407131	R98679		gb:yr31c03.s1 Soares fetal liver spleen	3.30	5.16 .		
30	435776	Al537162	Hs.263988	ESTs	3.14	5.13		
	455532 457352	AW984828		gb:RC1-HN0015-120400-021-h11 HN0015 Homo	3.14	5.13		
	437332 428670	AA489099 AA431682	Hs.134832	gb:aa56h09.s1 NCI_CGAP_GCB1 Homo sapiens ESTs	3.48	5.12		
	445962	Al268410	Hs.201386	ESTs	3.17 3.14	5.12 5.12		
35	418153	R13696	Hs.112830	ESTs	3.16	5.10		
	440565	AW103823	Hs.131586	ESTs	3.08	5.10		
	431446	AW294929	Hs.255369	Homo sapiens cDNA FLJ10265 fis, done HE	3.42	5.09		
	456036	BE536554	Hs.75839	zinc finger protein 6 (CMPX1)	3.21	5.09		
40	420883	AI735488	Hs.111436	ESTs	3.17	5.08		
40	455528	AW984757	Un 24.42C	gb:RC1-HN0015-040400-011-g10 HN0015 Homo	3.35	5.08		
	408442 446093	R59608 Al346849	Hs.21435 Hs.145896	ESTs ESTs	3.10	5.07		
	403489	c3p1_2255	F15. 143030	exon	3.30 3.43	5.06 5.05		
	405278	cNp3_1070		exon	3.05	5.03		
45	412804	H18857	Hs.22547	EST8	3.63	5.03		
	458407	W90022	Hs.186809	ESTs, Highly similar to LECT2 precursor	3.52	5.03		
	407367	AA130773		gb:zo13d01.r1 Stratagene colon (937204)	3.51	5.02		
	439108	AW163034	Hs.6467	synaptogyrin 3	5.63	5.01		
50	445335 435404	Al220339	Hs.166775	ESTs	3.21	5.01		
50	400404	Al240661	Hs.124995	ESTs	3.99	5.00		
	TABLE 6B:							
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55	Accession:	Genb	ank accession	numbers				
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	Pkey 410837	CAT Number	Accession	NAMES ASD DECOMPTS DECOMPTS AND SESSO AND SESSO AND SESSO AND SESSO ASSESSMENT ASSESSMENT AND SESSO ASSESSMENT ASSE				
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		-		W809662 AW810151				
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                                          AW984388 AW984392 AW984379 AW984351 AW984381 AW984377 AW984366 AW984348 AW984391 AW984373 AW984372 AW984353 AW984362 BE143505 BF374194 BF374190 AW850286
                                           AW993498 AW993484 AW993490 BF512974
              412734
                          1245451 1
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              412694
                          1243393_1
              411522
                           1089092_1
                                           AW820323 AW820314 AW820321
                          1071740_1
1490760_1
              411167
                                           BE066079 BE065939 BE065956
                                           AW819132 AW819122 AW819018 AW819135 AW819126 AW819024 AW819012 AW819141 BE177663 AW994738 AI923735 BF948431 BF948329
              413118
                           1070838_1
              454751
  50
                           319757_1
              452861
                                           AW904029 AW904030 AW904039 AW904031 AW904032 AW904046
              455374
                           1161013_1
                                           AW846075 AW846103 BF333976 AW846077 AW846122 AW846129 AW846095 AW846076 BF333979 BF333978 AW846092
              454935
456233
                           1083098 1
                           2635744_1
                                           AA203339 AA906160 AA929005
                                           AA451386 AA433841 AA433845
AW984828 AW984787 AW984806 AW984817 AW984826 AW984822 AW984773 AW984786 AW984803 AW984796
              428741
                           1384399_1
  55
                           1243692_1
              455532
                                           AW968968 AA489099 N72933 AA489184
                           1233795 1
              457352
                                           AW984734 AW984757 AW984797 AW984745
                           1243660_1
              455528
               407367
                           4907 1
                                            AF085963 H72550 H72951 AA130773
  60
              TABLE 6C:
                                    Unique number corresponding to an Eos probeset Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA
              Pkey:
Ref;
                                    sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495
                                    Indicates DNA strand from which exons were predicted.
               Strand:
   65
                                    Indicates nucleotide positions of predicted exons.
               Nt_position:
                                                           Nt_position
               Pkey
401412
405230
                                            Strand
                           7940103
                                                           43347-45776
                                            Minus
                            7249032
                                            Minus
                                                           97493-97682
   70
                                                           172732-172868
                402125
                            4033680
                                            Plus
                                                           15049-15286,30267-30457
40463-40586,41191-41336,41856-41986,4300
                            2769644
7711477
                                            Plus
                404289
                                            Plus
                406534
                                                           43310-43462
                405348
                            2914717
                                             Minus
                                                           105163-105305
31308-31439
                401081
                            3478647
                                            Plus
   75
                402624
                            7885063
                                             Minus
                                                           118511-118926,119175-119331
                405320
                            3478667
                                             Minus
                            2121229
                                                           69890-70883
                                             Plus
                405476
                             7454203
                                             Minus
                                                           8142-8753
                403932
                                                           61863-62028
                            9133145
7249204
                                             Plus
                406112
                                                            118115-119445
    80
                400708
                                             Plus
                             7243901
                                             Minus
                405427
                                                            25104-25291
                            6723302
                                             Minus
                402816
                                                            103456-103664
                404541
                            8318559
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                            Minus
                                      144947-145075
        403061
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                            Plus
        403717
                7259747
                            Minus
                                      79166-79758
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        401313
                9212516
                                      190842-191090
                            Minus
        405961
                8190197
                            Plus
                                      45132-45254
        404403
                 7272157
                            Minus
                                      72053-72238
                            Minus
        405332
                3169141
                                      70483-71207
        400710
                7249204
                            Pkis
                                      156753-157120
10
                9408724
        402953
                            Minus
                                      122603-122743
        406452
                9588380
                            Minus
                                      76322-76427
        403489
                                      38897-39212
                 7331314
                            Minus
        405278
                 6139075
                            Minus
                                      3863-3965,4823-4891,5439-5529,6043-6170
15
        TABLE 7A: EXTENDED GLIOBLASTOMA SEQUENCES: This table includes sequence information for 21 DNA and protein sequences
        Gene name: Protein tyrosine phosphatase, receptor-type, Z polypeptide 1
        Unigene number: Hs.78867
20
        Probeset Accession #: M93426
        Nucleic Acid Accession #: NM_002851
Coding sequence: 148-7092
                                21
                                                           41
                                                                        51
                    11
25
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                                                                                         60
                                                                                       120
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        CAGCTCCTCT GTGTTTGCCG CCTGGATTGG GCTAATGGAT ACTACAGACA ACAGAGAAAA
                                                                                        240
        CITGTTGAAG AGATTGGCTG GTCCTATACA GGAGCACTGA ATCAAAAAAA TTGGGGAAAG
                                                                                        300
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        AAATATCCAA CATGTAATAG CCCAAAACAA TCTCCTATCA ATATTGATGA AGATCTTACA
                                                                                        360
        CAAGTAAATG TGAATCTTAA GAAACTTAAA TTTCAGGGTT GGGATAAAAC ATCATTGGAA
        AACACATTCA TTCATAACAC TGGGAAAACA GTGGAAATTA ATCTCACTAA TGACTACCGT
                                                                                        480
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                                                                                        540
                                                                                        600
35
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                                                                                        720
        GATTTCAAAG CGATTATTGA TGGAGTCGAA AGTGTTAGTC GTTTTGGGAA GCAGGCTGCT
                                                                                        780
        TTAGATCCAT TCATACTGTT GAACCTTCTG CCAAACTCAA CTGACAAGTA TTACATTTAC
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         ACAGTTAGCA TCTCTGAAAG CCAGTTGGCT GTTTTTTGTG AAGTTCTTAC AATGCAACAA
                                                                                        960
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TTCTCTAGAC AGGTGTTTTC CTCATACACT GGAAAGGAAG AGATTCATGA AGCAGTTTGT
                                                                                       1020
                                                                                       1080
         AGTTCAGAAC CAGAAAATGT TCAGGCTGAC CCAGAGAATT ATACCAGCCT TCTTGTTACA
         TGGGAAAGAC CTCGAGTCGT TTATGATACC ATGATTGAGA AGTTTGCAGT TTTGTACCAG
                                                                                       1200
45
         CAGTTGGATG GAGAGGACCA AACCAAGCAT GAATTTTTGA CAGATGGCTA TCAAGACTTG
                                                                                       1260
         GGTGCTATTC TCAATAATTT GCTACCCAAT ATGAGTTATG TTCTTCAGAT AGTAGCCATA
                                                                                       1320
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         AATCCTGAAC TTGATCTTTT CCCTGAATTA ATTGGAACTG AAGAAATAAT CAAGGAGGAG
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AACCAAATCA GGAAAAAGGA ACCCCAGATT TCTACCACAA CACACTACAA TCGCATAGGG
                                                                                       1500
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                                                                                       1560
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         GCAACTTCTG CTATCCCATT CATCTCTGAG AACATATCCC AAGGGTATAT ATTTTCCTCC
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GTATACAATG GTGAGACACC TCTTCAACCT TCCTACAGTA GTGAAGTCTT TCCTCTAGTC
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         TOGGECTIGE ATGCTACGEC TGTATTICCE AGTGTCGATG TGTCATTTGA ATCCATCCTG
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TTTCGCCATC TGCATACAGT TTCTCAAATC CTTCCACAAG TTACTTCAGC TACCGAGAGT
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                                                                                       2700
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                                                                                       2940
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         GATTCTGTGG GTGTAACTTA TCAGGGTTCC TTATTTAGCG GCCCTAGCCA TATACCAATA
         CCTAAGTCTT CGTTAATAAC CCCAACTGCA TCATTACTGC AGCCTACTCA TGCCCTCTCT GGTGATGGGG AATGGTCTGG AGCCTCTTCT GATAGTGAAT TTCTTTTACC TGACACAGAT
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                                                                                       3180
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         TCTGTGTTTG GTGATGATAA TAAGGCGCTT TCTAAAAGTG AAATAATATA TGGAAATGAG
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         ACTGAACTGC AAATTCCTTC TTTCAATGAG ATGGTTTACC CTTCTGAAAG CACAGTCATG
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94608-94785,95096-95233

403008

6070396

Ptus

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        3900
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                                                                                            4260
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         TIGCTGTTTC CTTCTAAGGC AACTTCTGAG CTGAGTCATA GTGCCAAATC TGATGCCGGT
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         CAAAAGCACA ATGATGGAAA AGAGGAAAAT GACATTCAGA CTGGTAGTGC TCTGCTTCCT
         CTCAGCCCTG AATCTAAAGC ATGGGCAGTT CTGACAAGTG ATGAAGAAAG TGGATCAGGG
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                                                                                            4860
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GTGGTTCTTG TGGGTATTCT CATCTACTGG AGGAAATGCT TCCAGACTGC ACACTTTTAC
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                                                                                            5160
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          GCAAGTAGTG GGTTTACTGA AGAATTTGAG ACACTGAAAG AGTTTTACCA GGAAGTGCAG
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          AGCTGTACTG TTGACTTAGG TATTACAGCA GACAGCTCCA ACCACCCAGA CAACAAGCAC
                                                                                            5400
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          AAGAATCGAT ACATAAATAT CGTTGCCTAT GATCATAGCA GGGTTAAGCT AGCACAGCTT
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         AGACCAAAAG CTTATATTGC TGCCCAAGGC CCACTGAAAT CCACAGCTGA AGATTTCTGG AGAATGATAT GGGAACATAA TGTGGAAGTT ATTGTCATGA TAACAAACCT CGTGGAGAAA
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          GGAAGGAGAA AATGTGATCA GTACTGGCCT GCCGATGGGA GTGAGGAGTA CGGGAACTTT
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          CTGGTCACTC AGAAGAGTGT GCAAGTGCTT GCCTATTATA CTGTGAGGAA TTTTACTCTA AGAAACACAA AAATAAAAAA GGGCTCCCAG AAAGGAAGAC CCAGTGGACG TGTGGTCACA
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          AATTATTTGG TACAAACTGA GGAGCAATAT GTCTTCATTC ATGATACACT GGTTGAGGCC
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                                                                                             6240
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          TCAAATATAC AGCAGAGTGA CTATTCTGCA GCCCTAAAGC AATGCAACAG GGAAAAGAAT
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GAAGGCACAG ACTACATCAA TGCCTCCTAT ATCATGGGCT ATTACCAGAG CAATGAATTC
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                                                                                             6420
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                                                                                             6600
                                                                                             6660
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          GAAGCTACAC AGGATGATTA TGTACTTGAA GTGAGGCACT TTCAGTGTCC TAAATGGCCA
AATCCAGATA GCCCCATTAG TAAAACTTTT GAACTTATAA GTGTTATAAA AGAAGAAGCT
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TCTTTAGTTT AACACAGAAA GGGGTGGGGG GACTCACATC TGAGCATTGT TTTCCTCTTC
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  60
                                                                                              7200
                                                                                              7260
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                                                                                              7500
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           ATACCTTCAT TTTGAAAGAA GTTTTTATGA GAATAACACC TTACCAAACA TTGTTCAAAT
                                                                                              7860
           GGTTTTTATC CAAGGAATTG CAAAAATAAA TATAAATATT GCCATTAAAA AAAAAAAAA 7920
           А АААААААА АААААААА
  75
           <u>Protein sequence 1</u>

Gene name: Protein tyrosine phosphatase, receptor-type, 2 polypeptide 1
            Unigene number: Hs.78867
            Protein Accession #: NP_002842
            Signal sequence: 1-20
Pfam domain: carb anhydrase [38-300]
   80
            Transmembrane domains: 1639-1661
Cellular Localization: plasma membrane
1 11 21 31
                                                                                 51
                                       1
                                                                              139
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MRILKRFLAC IQLLCVCRLD WANGYYROOR KLVEEIGWSY TGALNQKNWG KKYPTCNSPK
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PKASKITFHW GKCNMSSDGS EHSLEGQKFP LEMQIYCFDA DRFSSFEEAV KGKGKLRALS
                                                                                                     120
          ILFEVGTEEN LDFKAIIDGV ESVSRFGKQA ALDPFILLNL LPNSTDKYYI YNGSLTSPPC
                                                                                                    240
          TDTVDWIVPK DTVSISESQL AVFCEVLTMQ QSGYVMLMDY LQNNFREQQY KFSRQVFSSY
                                                                                                    300
          TGKEEIHEAV CSSEPENVQA DPENYTSLLV TWERPRVVYD TMIEKPAVLY QQLDGEDQTK
          HEFLTDGYQD LGAILNNLLP NMSYVLQIVA ICTNGLYGKY SDQLIVDMPT DNPELDLFPE
         LIGTEETIKE EEEGKDIEEG ALVNPGRDSA TNOIRKKEPO ISTTTHYNRI GTKYNEAKTN
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         RSPTRGSEFS GKGDVFNTSL NSTSQPVTKL ATEXDISLTS QTVTKLPPHT VEGTSASLND
                                                                                                    540
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         GSKTVLRSPH MNLSGTAESL NTVSITEYEB ESLLTSFKLD TGAEDSGGSS PATGAIPPIS
ENISGGYIPS SENPETITYD VLIPESARNA SEDSTSSGSE ESLKDPSMEG NVWPPSSTDI
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                                                                                                    720
          TEVTPHAFTP SSRQQDLVST VNVVYSQTTQ PVYNGETPLQ PSYSSEVFPL VTPLLLDNQI
                                                                                                    780
         LNTTPAASSS DSALHATPVF PSVDVSPESI LSSYDGAPLL PPSSASFSSE LFRHLHTVSQ
                                                                                                    840
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         ILPQVTSATE SDKVPLHASL PVAGGDLLLE PSLAQYSDVL STTHAASETL EFRICALVSQ
KTLMFSQVEP PSSDAMMHAR SSGPEPSYAL SDNEGSQHIF TVSYSSAIPV HDSVGVTYQG
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LNASLQETSV SISSTKGMFP GSLAHTTTKV FDHEISQVPE NNFSVQPTHT VSQASGDTSL
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         KPVLSANSEP ASSDPASSEM LSPSTQLLFY ETSASFSTEV LLQPSFQASD VDTLLKTVLP
                                                                                                   1200
         AVPSDPILVE TPKVDKISST MLHLIVSNSA SSENMLHSTS VPVPDVSPTS HMHSASLQGL
                                                                                                   1260
         TISYASEKYE PVLLKSESSH QVVPSLYSND ELFQTANLEI NQAHPPKGRH VFATPVLSID
         EPLNTLINKL IHSDEILTST KSSVTGKVFA GIPTVASDTF VSTDHSVPIG NGHVAITAVS
                                                                                                   1380
         PHRDGSVTST KLLPPSKATS ELSHSAKSDA GLVGGGEDGD TDDDGDDDDD RDSDGLSIHK
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         PGKSPSANGL SCHENDICKEE NDICTGSALL PLSPESKANA VLTSDEESGS GQGTSDSLNE
NETSTDPSPA DTNEKDADGI LAAGDSEITP GPPQSPTSSV TSENSEVFHV SEARASNSSH
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         ESRIGLAEGL ESEKKAVIPL VIVSALTFIC LVVLVGILIY WRKCFQTAHF YLEDSTSPRV
                                                                                                   1680
         ISTPPTPIPP ISDDVGAIPI KHYPKHVADL HASSGPTEEP ETLKEFYQEV QSCTVDLGIT
ADSSNHPDNK HKNRYINIVA YDHSRVKLAQ LAEKDGKLTD YINANYVDGY NRPKAYIAAQ
30
                                                                                                   1800
         GPLKSTAEDF WRMIWEHNVE VIVMITNLVE KGRRKCDQYW PADGSEEYGN FLVTOKSVOV
                                                                                                   1860
         LAYYTVRNFT LRNTKIKKGS QKGRPSGRVV TQYHYTQWPD MGVPEYSLPV LTFVRKAAYA
                                                                                                   1920
         KRHAVGPVVV HCSAGVGRTG TYIVLDSMLQ QIQHEGTVNI FGFLKHIRSQ RNYLVQTEEQ
                                                                                                   1980
         YVFIHDTLVE AILSKETEVL DSHIHAYVNA LLIEGPACKT KLEKCPQLLS QSNIQQSDYS
AALKQCNREK NRTSSIIPVE RSRVGISSLS GEGTDYINAS YIMGYYQSNE FIITQHPLLH
35
                                                                                                   2100
         TIKDFWRMIW DHNAQLVVMI PDGQNMAEDE FVYWPNKDEP INCESFKVTL MAEEHKCLSN
                                                                                                   2160
         EEKLIIQDFI LEATQDDYVL EVRHFQCPKW PNPDSPISKT FELISVIKEE AANRDGPMIV
         HDEHGGVTAG TFCALTTLMH QLEKENSVDV YQVAKMINLM RPGVFADIEQ YQFLYKVILS 2280
         LVSTROBENP STSLDSNGAA LPDGNIAESL ESLV
40
         DNA SEQUENCE 2
         Gene name: tyrosylprotein sulfotransferase 1
         Unigene number: Hs.110903
         Probeset Accession #: D61594
45
         Nucleic Acid Accession #: NM_003596
         Coding sequence: 82-1194
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                                      21
                                                      31
                                                                                   51
         GTAGACTGTC CATGGCCTGA ACATTTTCCG AAAATCATTT TGAGCAAAAT ATCTGTTTAA TAACAAGATA ACCACATCAA GATGGTTGGA AAGCTGAGC AGAACTTACT ATTGGCATGT CTGGTGATTA GTTCTGTGAC TGTGTTTTAC CTGGGCCAGC ATGCCATGGA ATGCCATCAC
50 -
                                                                                                    180
         CGGATAGAGG AACGTAGCCA GCCAGTCAAA TTGGAGAGCA CAAGGACCAC TGTGAGAACT
GGCCTGGACC TCAAAGCCAA CAAAACCTTT GCCTATCACA AAGATATGCC TTTAATATTT
ATTGGRGGTG TGCCTCGGAG TGGAACCACA CTCATGAGGG CCATGCTGGA CGCACATCCT
                                                                                                     240
                                                                                                    360
55
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                                                                                                     420
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CCTTATTTAT GTAATAAAGA TCCTTTTGCC CTGAAATCTT TAACTTACCT TTCTAGGTTA
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TGCATGTTGG TTCACTATGA ACAACTTGTC TTACATCCTG AACGGTTGGT GAGAACACTC
                                                                                                    840
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65
                                                                                                   1020
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                                                                                                   1080
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TTCCAACTAC CTGACTTTCT TAAAGAAAAA CCACAGACTG AGCAAGTGGA GTAGCAGAAC
CAGGAGCCTC TTCCATACAT GAGGAAAGAT TGCTGCCTTT TCAGCAGAAG GGAAATTCCT
                                                                                                   1140
                                                                                                   1260
70
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                                                                                                   1380
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                                                                                                   1560
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                                                                                                   1620
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         TTTTTCAAAA TAAAAGCTTT CAATGTGA
80
         Protein sequence 2
         Gene name: tyrosylprotein sulfotransferase 1
         Unigene number: Hs.110903
         Protein Accession #: NP_003587
Signal sequence: 1-21
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Transmembrane domains: none found
           Cellular Localization: plasma membrane
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           MVGKLKONLL LACLVISSVT VFYLGOHAME CHHRIEERSQ PVKLESTRTT VRTGLDLKAN
KTPAYHKOMP LIFIGGVPRS GTTLMRAMLD AHPDIRCGEE TRVIPRILAL KOMWSRSSKE
 5
                                                                                                                           120
           KIRLDEAGVT DEVLDSAMQA FILEIIVKHG EPAPYLCNKD PFALKSLTYL SRLPPNAKFL
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           LMVRDGRASV HSMISRKVTI AGFDLNSYRD CLTKWNRAIE TMYNQCMEVG YKKCMLVHYE
QLVLHPERWM RTLLKFLQIP WNHSVLHHEE MIGKAGGVSL SKVERSTDQV IKPVNVGALS
                                                                                                                           240
           KWVGKIPPDV LQDMAVIAPM LAKLGYDPYA NPPNYGKPDP KIIENTRRVY KGEFQLPDFL
                                                                                                                           360
10
            KEKPOTEOVE
           DNA sequence 3
Gene name: interleukin 13 receptor, alpha 2
            Unigene number: Hs.25954
Probeset Accession #: R52795
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            Nucleic Acid Accession #: NM_000640
            Coding sequence: 94-1236
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                                                21
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AGAGGCAATA TCAAGGTTTT AAATCTCGGA GAAATGGCTT TCGTTTGCTT GGCTATCGGA
ATAAAGGTTA ACCCTCCTCA GGATTTTGAG ATAGTGGATC CCGGATACTT AGGTTATCTC
TATTTGCAAT GGCAACCCCC ACTGTCTCTG GATCATTTTA AGGAATGCAC AGTGGAATAT
GAACTAAAAT ACCGAAACAT TGGTAGTGAA ACATGGAAGA CCACTATTAC TAAGGAATCA
CATTACAAAG ATCGGTTTGA TCTTAACAAG GCCATTGAAG CGAAGATAC CACCCTTTTA
                                                                                                                            120
                                                                                                                             240
                                                                                                                             300
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             CATTACAAAG ATGGGTTTGA TCTTAACAAG GGCATTGAAG CGAAGATACA CACGCTTTTA
CCATGGCAAT GCACAAATGG ATCAGAAGTT CAAAGTTCCT GGGCAGAAAC TACTTATTGG
                                                                                                                             480
             ATATCACCAC AAGGAATTCC AGAAACTAAA GTTCAGGATA TGGATTGCGT ATATTACAAT
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             AACTTGTTTT ACTGGTATGA GGGCTTGGAT CATGCATTAC AGTGTGTTGA TTACATCAAG
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                                                                                                                             660
                                                                                                                             720
             TTCTATATTT GTGTTAATGG ATCATCAGAG AACAAGCCTA TCAGATCCAG TTATTTCACT
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TTTGATTATG AAATTGAGAT CAGAGAAGAT GATACTACCT TGGTGACTGC TACAGTTGAA
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                                                                                                                             960
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                                                                                                                            1140
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                                                                                                                            1200
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              45
              Protein sequence 3
              Gene name: interleukin 13 receptor, alpha 2 Unigene number: Hs.25954
Probeset Accession #: R52795
   50
               Protein Accession # NP_000631
               Signal sequence: 1-23
               FN3 domain: 155-322
               Transmembrane domains: 340-362
               Cellular Localization: plasma membrane
1 11 21 31
                                                                                                          51
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               MAFVCLAIGC LYTPLISTTP GCTSSSDTEI KVNPPQDFEI VDPGYLGYLY LQWQPPLSLD
HPKECTVEYE LKYRNIGSET WKTIITKNLH YKDGFDLNKG IEAKIHTLLP WQCINGSEVQ
SSWAETTYWI SPQGIPETKV QDMDCVYYNW QYLLCSWKPG IGVLLDTNYN LFYWYEGLDH
                                                                                                                               120
               ALQCVDYIKA DGQNIGCRPP YLEASDYKDF YICVNGSSEN KPIRSSYFTF QLQNIVKPLP
PVYLTFTRES SCEIKLKWSI PLGPIPARCF DYEIEIREDD TTLVTATVEN ETYTLKTTNE
                                                                                                                               240
   60
                                                                                                                                300
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               LLLRKPNTYP KMIPEFFCDT
    65
                DNA sequence 4
                Gene name: chemokine (C-X3-C) receptor 1
                Unique number: Hs.78913
                Probeset Accession #: U20350
                Nucleic Acid Accession #: NM_001337
                Coding sequence: 46-1113
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                                                                                                           51
                                                                       31
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                                                                                                                                 180
     75
                C'IEGTIGGAA ATTIGTIGGT AGTGTTTGCC CTCACCAACA GCAAGAGCC CAAGAGTGTC
ACCGACATT ACCTCCTGAA CCTGGCCTTG TCTGATCTGC TGTTTGTAGC CACTTTGCCC
TTCTGGACTC ACTATTTGAT AAATGAAAAG GGCCTCCACA ATGCCATGTG CAAATTCACT
                                                                                                                                 240
                                                                                                                                 300
                                                                                                                                 360
                ACCECCTTCT TCTTCATCGG CTTTTTTGGA AGCATATTCT TCATCACCGT CATCAGCATT
GATAGGTACC TGGCCATCGG CGTCTGGGCA GCAGCCATTT TGGTGGAGC ACCCCAGTTC
GGCGTCACCA TCAGCCTAGG CGTCTGGGCA GCAGCCATTT TGGTGGAGC ACCCCAGTTC
                                                                                                                                 420
                                                                                                                                  480
     80
                                                                                                                                  540
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ATCTGGCCCG TGCTCCGCAA TGTGGAAACA AATTITCTTG GCTTCCTACT CCCCCTGCTC
                                                                                                                                  600
                                                                                                                                  660
                 ATTATGAGTT ATTGCTACTT CAGAATCATC CAGACGCTGT TTTCCTGCAA GAACCACAAG
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15
         Protein sequence 4
         Gene name: chemokine (C-X3-C) receptor 1
         Unigene number: Hs.78913
         Protein Accession #: NP_001328
         Signal sequence: 1-44
Pfam domain: 7tm_1 [48-293]
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         Cellular Localization: plasma membrane
                                    21
                      11
         MDQPPESVTE NFEYDDLABA CYIGDIVVFG TVFLSIPYSV IFAIGLVGNL LVVFALTNSK
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25
         KPKSVTDIYL LNLALSDLLF VATLPFWTHY LINEKGLHNA MCKPTTAFFF IGFFGSIFFI
                                                                                                120
         TVISIDRYLA IVLAANSMIN RTVQHGVTIS LGVWAAAILV AAPQEMPTKQ KENECLGDYP
EVLQEIWPVL RNVETNFLGF LLPLLIMSYC YPRIIQTLFS CKNHKKAKAI KLILLVVIVF
FLFWTPYNVM IPLETLKLYD FPPSCDMRKD LRLALSVTET VAFSHCCLNP LIYAFAGEKF
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         RRYLYHLYGK CLAVLCGRSV HVDFSSSESQ RSRHGSVLSS NFTYHTSDGD ALLLL
30
         DNA seguence 5
         Gene name: cannabinoid receptor 1 (brain)
         Unigene number: Hs.75110
         Probeset Accession #: 412986
Nucleic Acid Accession #: NM_001840
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                                                                                                240
                                                                                                300
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                                                                                                 780
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                                                                                                 960
55
                                                                                               1020
                                                                                               1080
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                                                                                               1200
                                                                                               1260
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                                                                                               1380
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                                                                                               1680
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                                                                                               1860
70
                                                                                               1920
          GAGATATTIT GTAAAATGTA TTATGTCCTG TGAGATGTGT ATCAGTGTTT ATGTGCTATT
                                                                                               1980
          AATATTTGTT TAGTTCAGCC AAACTGAAAG GTAGACTTTT ATGAGAACAA TGGACAAGCA
          GTGGATACGT GTCAATGTGT GCACTTTTTT TCTATATTAT TGCCCATGAT ATAACTTTAG 2100
         AAATAAACCT TAATATTTCT TCCCAAAAAA AAAAA
75
          Protein sequence 5
         Gene name: cannabinoid receptor 1 (brain) Unigene number: Hs.75110
          Protein Accession #: NP_001831
80
          Signal sequence: none found Pfam domain: 7tm 1 [133-397]
          Transmembrane domains: 121-143, 156-178, 195-217, 237-259, 276-298, 344-366, 378-400 Cellular Localization: plasma membrane
                       11
                                     21
                                                                  41
                                                                                51
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	MITAGORPOL VPADQVNITE FIRESUSSER ENHANCED KITALOGSVIF VYSFIDFHVF	180
5	INVESTIGATION TACKET TACKET TACKET ATTRIBUTE PLAYKRIVER PRAVVAPCEM	240
	WITATVIAVE PERGENCERE OSVESSITVE EPPOARMDIR LAKTLYLILV VLIICWGPLL	300 360
	AIMPOURCE MAKITETURA ECSMICLINS TVNPIIYALE SKOLEHAFES MEPSCEGIAQ	420
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	Gene name: endothelin receptor type B	
	Unigene number: Hs.82002 Probeset Accession #: D13168	
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	Coding sequence: 238-1566 1 11 21 31 41 51	
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	ABGATCARCA CABROCAGE CAGCOCCAC COGACCCTT CTGGACAGG TAGCAGCATG CAGCCCCTC CAAGTCTGTG CGGACGCGC CTGGTTGCGC TGGTTCTTGC CTGCGGCCTG	240 300
	THE THE CONTROL OF THE PROPERTY OF THE PROPERT	360
25	ACCORDAGE TRANSPORTED ACCORDAGE ACCORDAGE CCAAGGGTTC CAACGCCAGT	420 480
	CTGGGGGGT CGTTGGCACC TGGGGAGGTG CCTAAAGGAG ACAGGACGGC AGGATCTCCG CCACGCACCA TCTCCCCTCC CCCGTGCCAA GGACCCATCG AGATCAAGGA GACTTTCAAA	540
	THE CAMERA OF COORTICITIC COCCUTTICTS TITISTICS GRATCATUS GARCICUACA	600
20	TACATCARCA CONTINUES GARCAROTGC ATGCGRAACG GTCCCARTAT CITGATCGCC CTTCTGAGAA TTATCTACAA GARCAROTGC ATGCGRAACG GTCCCATCAA TGTCTACAAG AGCTTGGCTC TGGGAGACCT GCTGCACATC GTCATTGACA TCCCTATCAA TGTCTACAAG	660 720
30	ACCIONAL ACCIONAL ACCIONAL ATTROCARCT GAGATGTGTA AGCTGGTGCC TITUATACAG	780
	CHECHGEOR AGGARATCAC TETECTGAGT CTATGTECTC TGAGTATTGA CAGATATCGA AAAGCCTCCG TGGGAATCAC TGTGCTGAGT CTATGTGCTC TGAGTATTGA CAGATATCGA GCTGTTGCTT CTTGGAGTAG AATTAAAGGA ATTGGGGTTC CAAAATGGAC AGCAGTAGAA	840 900
	ASSESSMENT OF CONTROL	960
35	AMARINA COR TOCK CTACAR ACGARCTTAT CTGCGAATCT GCTTGCTTCA TCCCGTTCAG	1020 1080
	AAGACAGCTT TCATGCAGTT TTACAAGACA GGTTTTTTTATACAC TAATGACCTG TGAAATGTTG	1140
	ACARAR OFFICENTICA CATTOCTTA AATGATCACC TAAAGCAGAG ACGGGAGIG	1200
40	AGGARGATIC TGAAGCTCAC TCTTTATAAT CAGAATGATC CCAATAGATG TGAACCTTTTG	1260 1320
40	ACCOMPANY TO THE TOTAL CONTROL OF A TOTAL TOTAL ATTENDED TO THE TOTAL TO	1380
	ARCON ARMO COCCURATOR COTCACCADA AGATTCAAAA ACTGCTTTAA GTCATGCTTA	1440 1500
	AGCCARTOR CICAGOCATT TGAAGAAAAA CAGTCCTTGG AGGAAAAGCA GTCGTGCTTA AAGTTCAAAG CTAATGATCA CGGATATGAC AACTTCCGTT CCAGTAATAA ATACAGCTCA	1560
45	TATIOGACO ACTATEC ACTETATTEC ATTETETA TATIOGACO AAGICATIAA	1620
	AACAAAATGA AACATTTGCC AAAACAAAAC AAAAAACTAT GTATTTGCAC AGCACACTAT	1680 1740
	THE COCCERT CARROLANT CACTOGGAAT TAAGAAAGCC TCGTCGTGAA AGCACTTAAT	1800
50	TTITTACAGT TAGCACTICA ACATAGCTCT TAACAACTC CAGGATATTC ACACAACACT TAGGCTTAAA AATGAGCTCA CTCAGAATTT CTATTCTTC TAAAAAGAGA TTTATTTTTA	1860 1920
50	AMERANGE ACTORDATAT AAAGGAAGAA TAAGTCACTG TAAAACAGAA CITITAAATG	1980
	ANGORDANE PACECRATET AND TETTAL ANTICTTAA AACAACTIT CAATTAATAT	2040 2100
	TATCACACTA TTATCAGATT GTAATTAGAT GCAAATGAGA GAGCAGTTTA GTTGTTGCAT TTTTCGGACA CTGGAAACAT TTAAATGATC AGGAGGGAGT AACAGAAAGA GCAAGGCTGT	2160
55	TOTAL AND CAPTACACTT TOACTAGAAG CCCAAACCTC AGCATTCTGC AATATGTAAC	2220
	CARCATGTCA CARACAAGCA GCATGTAACA GACTGGCACA TGTGCCAGCT GAATTTAAAA TATAATACTT TTAAAAAGAA AATTATTACA TCCTTTACAT TCAGTTAAGA TCAAACCTCA	2280 2340
	CARROLDAR MACARTETT GRADGECTAT CCCARAGGE TITTITGAAT CIGICATICA	2400
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00	THE PROPERTY AND AND CARGOCAGE CETGEGETEA TAGETTIACH ATGUAGAGAG	2580
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	COLUMN CONTRACTOR AND	3000
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	AND THE PROPERTY OF TAXABLE OF GGCCACATE TTGGAAATAA GCTAGTAATG	3240
	TIGITITCIG TCAATATIGA ATGIGATIGAT ACAGTAAACC AAAACCCAAC AATGIGGCA GAAAGAAAGA GCAATAATAA TTAATTCACA CACCATATIG ATTCTATITA TAAATCACCC	3360
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	CATTITAGAC TCTCAATTIT AAATTAATTI TGAATCACTA ATATITICAC AGITTATTACA	3540
	TOTAL TARGET CONTROL OF A TOTAL CONTROL OF A TOTAL CONTROL OF THE TOTAL	3600
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	TARGETTA AND TARGETT ANTATAGEA CAGACAAAAT TATTGTTAAC ATGGATGTA	3840
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	GIGGRIANS PROPERTY TO THE PROPERTY OF THE PROP	

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Cellular Localization: plasma membrane
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                                                                                   1920
                                                                                   1980
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                                                                                     4380
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                                                                                      4500
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          ACTICCATTC CATTGITTTG AAACTCAGTA TGCGGCCCCT GTCTTGCTGT CATGAAATCA GCAAGAGAGG ATGACACATC AAATAATAAC TCGGATTCCA GCCCACATTG GATTCATCAG CATTTGGACC AATAGCCCAC AGCTGAGAAT GTGGAATACC TAAGGATAAC ACCGCTTTTG
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                                                                                      4740
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           Protein sequence 10
           Gene name: epidermal growth factor receptor (avian erythroblastic leukemia Unigene number: Rs.77432
           Protein Accession #: NP_005219
           Signal sequence: 1-27
           Pfam domain: Recep_L_domain [57-190, 372-492]
   70
           Transmembrane domains: 646-668
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                                                31
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           VLGNLEITYV QRNYDLSFLK TIQEVAGYVL IALNTVERIP LENLQIIRGN MYYENSYALA
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           VLSNYDANKT GLKELPMRNI QEILHGAVRF SNNPALCKVE SIQMRDIVSS DFLSNMSMDF
QNHLGSCOKC DPSCPNGSCW GAGEENCQKL TKIICAQQCS GRCRGKSPSD CCHNQCAAGC
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                                                                                        300
           VTDHGSCVRA CGADSYEMEE DGVRKCKKCE GPCRKVCNGI GIGEFKDSLS INATNIKHFK
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           NCTSISGDLH ILPVAFRGDS FTHTPPLDPQ ELDILKTVKE ITGFLLIQAW PENRTDLHAF
                                                                                         420
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            ENLBIIRGRT KQHGQFSLAV VSLNITSLGL RSLKEISDGD VIISGNKNLC YANTINWKKL
                                                                                         480
            FGTSGQKTKI ISNRGENSCK ATGQVCHALC SPEGCWGPEP RDCVSCRNVS RGRECVDKCK
            LLEGEPREPV ENSECTOCHP ECLPQAMNIT CTGRGPDNCI QCAHYIDGPH CVKTCPAGVM
            GENNTLYWKY ADAGHYCHLC HPNCTYGCTG PGLEGCPTNG PKIPSIATGM VGALLLLLVV
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        CLTSTVQLIT QLMPFGCLLD YVREHKDNIG SQYLLNWCVQ IAKGROVYLED RRLVHRDLAA
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        RNVLVKTPQH VKITDFGLAK LLGAEEKEYH AEGGKVPIKW MALESILHRI YTHQSDVWSY
                                                                                        900
        GVTVWELMTF GSKPYDGIPA SEISSILEKG ERLPQPPICT IDVYMIMVKC WMIDADSRPK
                                                                                        960
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                                                                                       1140
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        APOSSEFIGA
        DNA sequence 11
        Gene name: claudin 5 (transmembrane protein deleted in velocardiofacial syndrome)
        Unique number: Hs.110903
15
        Probeset Accession #: AW245805
        Nucleic Acid Accession #: NM_003277
        Coding sequence: 121-777
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                                                                                         240
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                                                                                        1200
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         Protein sequence 11
         Gene name: claudin 5 (transmembrane protein deleted in velocardiofacial syndrome)
Unigene number: Hs.110903
         Protein Accession #: NP_003268
Signal sequence: none found
Pfam domain: PMP22 Claudin [4-181]
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         Transmembrane domains: 5-27, 74-96, 123-145, 164-186
         Cellular Localization: plasma membrane
1 11 21 31
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         HMQCKVYDSV LALSTEVQAA RALTVSAVLL AFVALFVTLA GAQCTTCVAP GPAKARVALT
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         LCCGAWVCTG RPDLSFPVKY SAPRRPTATG DYDKKNYV
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         Gene name: vascular endothelial junction-associated molecule
          Unigene number: Hs.54650
          Probeset Accession #: AA410345
         Nucleic Acid Accession #: AF255910
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         Coding sequence: 241-1137
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                                                                                           240
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         Protein sequence 12
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         Gene name: vascular endothelial junction-associated molecule
        Unigene number: Hs.54650
Protein Accession #: AAF81223
         Signal sequence: 1-22
         Igc2 domain: 41-116, 146-221
Transmembrane domains: 239-261
Cellular Localization: plasma membrane
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         Gene name: solute carrier family 11 (proton-coupled divalent metal ion Unigene number: Hs.182611
         Probeset Accession #: D50402
         Nucleic Acid Accession #: NM_000578
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         Coding sequence: 1-1653
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GATCTTCAGC TNGGNCCNGT GGCGGGATTC AAACTTCTCT GGGTGCTGCT CTGGGCCACC
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                                                                                               480
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          Gene name: solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1
          Unigene number: Hs.182611
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          Protein Accession #: NP_000569
          Signal sequence: none found
          Pfam domain: Nramp [78-463]
          Transmembrane domains: 58-80, 88-110, 159-181, 195-217, 284-306, 349-379, 394-416, 432-454, 468-490, 501-523
                                       plasma membrane
          Cellular Localization:
 70
                                      21
                                                   31
                        11
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LRDLSGLNDL LNVLQSLLLP VAVLPILTFT SMPTLMQEFA NGLLNKVVTS SIMVLVCTIN
                                                                                                360
                                                                                                420
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           DNA sequence 14
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Gene name: solute carrier family 7 (cationic amino acid transporter, y+

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Unigene number: Hs.184601
       Probeset Accession #: AF104032
       Nucleic Acid Accession #: NM_003486
       Coding sequence: 53-1576
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       Unigene number: Hs.184601
        Protein Accession #: NP_003477
        Pfam domain: aa permeases [46-481]
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       Transmembrane domains: 52-74, 82-104, 120-142, 145-167, 169-191, 200-222, 237-259, 275-297, 323-345, 371-393,
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       Cellular Localization: plasma membrane
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          Signal sequence: 1-27
Pfam domain: ANF receptor [343-400];PBPe domain [416-785, 799-838]
          Transmembrane domains: 297-319, 544-566, 624-646, 803-825
Cellular Localization: plasma membrane
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Unique number: Hs.258
        Protein Accession #: NP_000668
        Signal sequence: none found
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        Pfam domain: 7tm 1 [29-282]
        Transmembrane domains: 12-34, 50-72, 86-108, 120-150, 179-201, 229-251
Cellular Localization: plasma membrane
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        Unigene number: Hs.2699
Probeset Accession #: X54232
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        Nucleic Acid Accession #: NM_002081
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                   Signal sequence: none found
                   Pfam domain: Glypican protein [2-490]
                    Transmembrane domains: none found
  30
                    Cellular Localization: plasma membrane
                                                                 21
                    MELRARGWWL LCAAAALVAC ARGDPASKSR SCGEVRQIYG AKGFSLSDVP QAEISGEHLR
ICPQGYTCCT SEMEENLANR SHAELETALR DSSRVLQAML ATQLRSFDDH FQHLLNDSER
                                                                                                                                                                                     120
   35
                    TLQATPPGAF GELYTQNARA FROLYSELRL YYRGANLHLE ETLAEFWARL LERLFKQLHP
                                                                                                                                                                                     180
                    QLLLPDDYLD CLGKQAEALR PFGEAPRELR LRATRAFVAA RSFVQGLGVA SDVVRKVAQV
PLGPECGRAV MKLVYCAHCL GVPGARPCPD YCRNVLKGCL ANQADLDAEW RNLLDSMVLI
                                                                                                                                                                                      240
                    TDKFWGTSGV ESVIGSVHTW LAEAINALQD NRDILTAKVI QGCGNPKVNP QGPGPEEKRR
RGKLAPRERP PSGTLEKLVS BAKAQLEDVQ DFWISLPGTL CSEKMALSTA SDDRCWNGMA
                                                                                                                                                                                      360
                                                                                                                                                                                       420
    40
                     RGRYLPEVMG DGLANQINNF EVEVDITKPD MTIRQQIMQL KIMTNRLRSA YNGNDVDFQD
                      ASDDGSGSGS
                      DNA sequence 18
                      Gene name: NY-REN-24 antigen
     45
                      Unigene number: Hs.128425
                      Nucleic Acid Accession #: AF155102
                      Coding sequence: 27-908
                                                                                                     31
                                               11
                      GCGAGGGCGA GGGCGAGGCG GTGCTCATGG AGGAGGACCT GATCCAGCAG AGCCTGGACG
      50
                      120
                                                                                                                                                                                         180
                                                                                                                                                                                         240
                       GCATGGGCCA GGACGAGGCG CACGCAAGC CGCGCTTCTT CAACCGCGTG CACACGGGCT
                                                                                                                                                                                         300
      55
                       TCGAGTGGAA CAAGTACAAC CAGACGCACT ACGACTTTGA CAACCCACCG CCCAAGATCG
                                                                                                                                                                                         420
                       480
       60
                                                                                                                                                                                          660
                        GGGTGCCACA GCCCAGGTCG GAGTGGCCCA GCCGGCAGGC TTGTTCTTCA GCATCCGACG
GGAACATCTC CAACAGAAGC AAAACGGAAA GTGCCTCCCG GACCCCCAGA GGGCCACCCA
                                                                                                                                                                                           B40
                        ACCTCACCAG TCACCAGCCC CAGACCACCC ACAGCCCCTC CCAGACACCC CGCCTCATCT
GGAAATAGTT CCGTTTGTTT CTCTAAAAAG ACTTGTAGGT GGGAAAAAAA ATCTTTTGTT
                                                                                                                                                                                          900
       65
                         CTCATGGAAT TGGCCTATTG GCAAGATCGC ATGTTTTTT AATAAACGTT GTATTTTAGA
                                                                                                                                                                                        1020
                         AAAATA
         70
                         Protein sequence 18
                         Gene name: NY-REN-24 antigen
Unigene number: Hs.128425
                          Protein Accession #: AAD42868
                          Signal sequence: none found
Transmembrane domains: none found
         75
                           Cellular Localization: plasma membrane
                                                                         21
                                                                                                         31
                                                                                                                                   41
                           GEGEAVLME EDLIQOSLDD YDAGRYSPRL LTAHELPLDA HVLEPDEDLQ RLQLSRQQLQ
                                                                                                                                                                                             60
                          GEGEAVIME EDLIQQSILID YHAGRISHKI ILAGEBUFUN HAKYAPRIK RFYNRVETGF
TGDASESAE DIFFRRAKE MGQDEAQFSV EMPLITCAYI MADKYAPRIK RFYNRVETGF
TGDASESAE DIFFRRAKE MGQDEAQFSV EMPLITCAYI MADKYAPRIK RFYNRVETGF
MKYNQTHY DFDNPPKIV QGYKFNIFYP DLIDKRSTPE YFLEACADIK DFAILRFTRG
KRGHRFQDR QPRVGILAPP RLPHPVCQRH LPAVLSIQAL PLSAVITALGN GRPGGPRATI
LRGHRFQDR QPRVGILAPP RLPHPVCQRH LPAVLSIQAL PLSAVITALGN GRPGGPRATI
          80
                                                                                                                                                                                          180
                                                                                                                                                                                           240
                            POPRSEMPS ROACSSASDG NISNRSKTES ASRTPRGPPN LTSHOPOTTH SPSQTPRLIM
```

```
DNA sequence 19
       Gene name: tumor necrosis factor receptor superfamily, member 1A
       Unigene number: Hs.159
       Probeset Accession 8: BR295782
 5
       Nucleic Acid Accession #: NM_001065
       Coding sequence: 256-1623
                               21
                   11
                                                                   51
        CGGCCCAGTG ATCTTGAACC CCAAAGGCCA GAACTGGAGC CTCAGTCCAG AGAATTCTGA
                                                                                  60
10
       GAAAATTAAA GCAGAGAGGA GGGGAGAGAT CACTGGGACC AGGCCGTGAT CTCTATGCCC
       GAGTETCAAC CETCAACTGT CACCECAAGG CACTTGGGAC GTECTGGACA GACCGAGTEC
CGGGAAGCCC CAGCACTGCC GETGCCACAC TGCCCTGAGC CCAAATGGGG GAGTGAGAGG
                                                                                 240
        CCATAGCTOT CTGGCATGGG CCTCTCCACC GTGCCTGACC TGCTGCTGCC GCTGGTGCTC
                                                                                 300
       CTGGAGCTGT TGGTGGGAAT ATACCCCTCA GGGGTTATTG GACTGGTCCC TCACCTAGGG
                                                                                 360
15
       GACAGGGAGA AGAGAGATAG TGTGTGTCCC CAAGGAAAAT ATATCCACCC TCAAAATAAT
       TOGATTIGCT GTACCAAGTG CCACAAAGGA ACCTACTTGT ACAATGACTG TOCAGGCCCG
                                                                                 480
       GGGCAGGATA CGGACTGCAG GGAGTGTGAG AGCGGCTCCT TCACCGCTTC AGAAAACCAC
                                                                                 540
       CTCAGACACT GCCTCAGCTG CTCCAAATGC CGAAAGGAAA TGGGTCAGGT GGAGATCTCT
       TCTTGCACAG TGGACCGGGA CACCGTGTGT GGCTGCAGGA AGAACCAGTA CCGGCATTAT
TGGAGTGAAA ACCTTTTCCA GTGCTTCAAT TGCAGCCTCT GCCTCAATGG GACCGTGCAC
                                                                                 660
20
                                                                                 720
        CTCTCCTGCC AGGAGAAACA GAACACCGTG TGCACCTGCC ATGCAGGTTT CTTTCTAAGA
                                                                                 780
       GAAAACGAGT GTGTCTCCTG TAGTAACTGT AAGAAAAGCC TGGAGTGCAC GAAGTTGTGC
       CTACCCCAGA TTGAGAATGT TAAGGGCACT GAGGACTCAG GCACCACAGT GCTGTTGCCC
                                                                                 900
        CTGGTCATTT TCTTTGGTCT TTGCCTTTTA TCCCTCCTCT TCATTGGTTT AATGTATCGC
                                                                                 960
25
       TACCAACEGT GGAAGTCCAA GCTCTACTCC ATTGTTTGTG GGAAATCGAC ACCTGAAAAA
                                                                                1020
       GAGGGGGAGC TTGAAGGAAC TACTACTAAG CCCCTGGCCC CAAACCCAAG CTTCAGTCCC
                                                                                1080
       ACTOCAGGOT TOACCOCCAC COTGGGCTTC AGTCCCGTGC CCAGTTCCAC CTTCACCTCC
                                                                               1140
        AGCTCCACCT ATACCCCCGG TGACTGTCCC AACTTTGCGG CTCCCCGCAG AGAGGTGGCA
                                                                                1200
       CCACCCTATC AGGGGGCTGA CCCCATCCTT GCGACAGCCC TOGCCTCCGA CCCCATCCCC
                                                                                1260
30
       AACCCCCTTC AGAAGTGGGA GGACAGCGCC CACAAGCCAC AGAGCCTAGA CACTGATGAC
CCCGCGACGC TGTACGCCGT GGTGGAGAAC GTGCCCCCGT TGCGCTGGAA GGAATTCGTG
                                                                               1320
                                                                               1380
        CGGCGCCTAG GGCTGAGCGA CCACGAGATC GATCGGCTGG AGCTGCAGAA CGGGCGCTGC
                                                                                1440
        CTGCGCGAGG CGCAATACAG CATGCTGGCG ACCTGGAGGC GGCGCACGCC GCGGCGCGAG
                                                                                1500
       GCCACGCTGG AGCTGCTGGG ACGCGTGCTC CGCGACATGG ACCTGCTGGG CTGCCTGGAG
                                                                                1560
35
       GACATCGAGG AGGCGCTTTG CGGCCCCGCC GCCCTCCCGC CCGCGCCCAG TCTTCTCAGA
                                                                                1620
       TGAGGCTGCG CCCCTGCGGG CAGCTCTAAG GACCGTCCTG CGAGATCGCC TTCCAACCCC
                                                                                1680
        ACTITITICI GGAAAGGAGG GGTCCTGCAG GGGCAAGCAG GAGCTAGCAG CCGCCTACTI
       GGTGCTAACC CCTCGATGTA CATAGCTTTT CTCAGCTGCC TGCGCGCCGC CGACAGTCAG
                                                                                1800
        CGCTGTGCGC GCGGAGAGAG GTGCGCCGTG GGCTCAAGAG CCTGAGTGGG TGGTTTGCGA
                                                                                1860
40
        GGATGAGGGA CGCTATGCCT CATGCCCGTT TTGGGTGTCC TCACCAGCAA GGCTGCTCGG
                                                                                1920
        GGGCCCTGG TTCGTCCCTG AGCCTTTTTC ACAGTGCATA AGCAGTTTTT TTTGTTTTTG
                                                                                1980
        TTTTGTTTTG TTTTGTTTTT AAATCAATCA TGTTACACTA ATAGAAACTT GGCACTCCTG
                                                                               2040
        TGCCCTCTGC CTGGACAAGC ACATAGCAAG CTGAACTGTC CTAAGGCAGG GGCGAGCACG
                                                                                2100
        GAACAATGGG GCCTTCAGCT GGAGCTGTGG ACTTTTGTAC ATACACTAAA ATTCTGAAGT
45
        Protein sequence 19
       Gene name: tumor necrosis factor receptor superfamily, member lA Unigene number: Hs.159
50
        Protein Accession #: NP_001056
        Signal sequence: 1-29
        TNPR domain: 44-81, 84-125, 127-166, 168-195
        Transmembrane domains: 211-234
        Cellular Localization: plasma membrane
55
                         21
                  11
                                         31
        MGLSTVPDLL LPLVLLELLV GIYPSGVIGL VPHLGDREKR DSVCPOGKYI HPONNSICCT
        KCHKGTYLYN DCPGPGQDTD CRECESGSFT ASENHLRHCL SCSKCRKEMG QVEISSCTVD
                                                                                 120
        RDTVCGCRKN QYRHYWSENL FQCFNCSLCL NGTVHLSCQE KQNTVCTCHA GFFLRENECV
                                                                                 180
60
        SCSNCKKSLE CTKLCLPQIE NVKGTEDSGT TVLLPLVIPP GLCLLSLLFI GLMYRYQRWK
SKLYSIVCGK STPEKEGELE GTTTKPLAPN PSPSPTPGFT PTLGFSPVPS STFTSSSTYT
                                                                                 300
        PGDCPNFAAP RREVAPPYQG ADPILATALA SDPIPNPLQK WEDSAHKPQS LDTDDPATLY
                                                                                 360
        AVVENVPPLR WKEFVRRLGL SDHEIDRLEL QNGRCLREAQ YSMLATWRRR TPRREATLEL
        LGRVLRDMDL LGCLEDIEEA LCGPAALPPA PSLLR
65
        DNA sequence 20
        Gene name: prominin (mouse)-like 1
        Unigene number: Hs.112360
        Probeset Accession #: R40057
70
        Nucleic Acid Accession #: NM_006017
        Coding sequence: 38-2635
                   11
                               21
                                            31
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75
        GTTGCTGCTG GGGCTGTGCG GGAACTCCTT TTCAGGAGGG CAGCCTTCAT CCACAGATGC
        TCCTAGGCT TGGAATTATG AATTGCCTGC AACAAATTAT GAGACCCAAG ACTCCCATAA
                                                                                  180
        AGCTGGACCC ATTGGCATTC TCTTTGAACT AGTGCATATC TTTCTCTATG TGGTACAGCC
                                                                                  240
        GCGTGATTTC CCAGAAGATA CTTTGAGAAA ATTCTTACAG AAGGCATATG AATCCAAAAT
                                                                                  300
        TGATTATGAC AAGCCAGAAA CTGTAATCTT AGGTCTAAAG ATTGTCTACT ATGAAGCAGG
GATTATTCTA TGCTGTGTCC TGGGGCTGCT GTTTATTATT CTGATGCCTC TGGTGGGGTA
                                                                                  360
80
                                                                                  420
        TTTCTTTTGT ATGTGTCGTT GCTGTAACAA ATGTGGTGGA GAAATGCACC AGCGACAGAA
                                                                                  480
        GGAAAATGGG CCCTTCCTGA GGAAATGCTT TGCAATCTCC CTGTTGGTGA TTTGTATAAT
        AATAAGCATT GGCATCTTCT ATGOTTTTGT GGCAAATCAC CAGGTAAGAA CCCGGATCAA
                                                                                  600
        AAGGAGTOGG AAACTGGCAG ATAGCAATTT CAAGGACTTG OGAACTCTCT TGAATGAAAC
                                                                                  660
```

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TCCAGAGCAA ATCAAATATA TATTGGCCCA GTACAACACT ACCAAGGACA AGGCGTTCAC
          AGATCTGAAC AGTATCAATT CAGTGCTAGG AGGCGGAATT CTTGACCGAC TGAGACCCAA
                                                                                                          780
                                                                                                          840
          CATCATCCCT GTTCTTGATG AGATTAAGTC CATGGCAACA GCGATCAAGG AGACCAAAGA
         GGCGTTGGAG AACATGAACA GCACCTTGAA GAGCTTGCAC CAACAAAGTA CACAGCTTAG
                                                                                                          900
          CAGCAGTCTG ACCAGCGTGA AAACTAGCCT GCGGTCATCT CTCAATGACC CTCTGTGCTT
                                                                                                          960
 5
          GGTGCATCCA TCAAGTGAAA CCTGCAACAG CATCAGATTG TCTCTAAGCC AGCTGAATAG
                                                                                                        1020
          CAACCCTGAA CTGAGGCAGC TTCCACCCGT GGATGCAGAA CTTGACAACG TTAATAACGT
                                                                                                        1080
         TCTTAGGACA GATTTGGATG GCCTGGTCCA ACAGGGCTAT CAATCCCTTA ATGATATACC TGACAGAGTA CAACGCCAAA CCACGACTGT CGTAGCAGGT ATCAAAAGGG TCTTGAATTC
                                                                                                        1140
                                                                                                        1200
          CATTGGTTCA GATATCGACA ATGTAACTCA GCGTCTTCCT ATTCAGGATA TACTCTCAGC
                                                                                                         1260
10
          ATTCTCTGTT TATGTTANTA ACACTGAAGG TTACATCCAC AGAAATTTAC CTACATTGGA AGAGTATGAT TCATACTGGT GGCTGGGTGG CCTGGTCATC TGCTCTCTGC TGACCCTCAT
                                                                                                         1320
                                                                                                         1380
          CGTGATTTTT TACTACCTGG GCTTACTGTG TGGCGTGTGC GGCTATGACA GGCATGCCAC
                                                                                                         1440
          CONGACTATT TACTACLING GETTACTOR TOGGSTOTOG GGCTATGAC GCCATCACC CGAGGCTGT TCTCCAACAC CGAGGCTGT TCTCCATCG TTGGAGTTGG ATTAAGTTC CFCTTTTGCT GGATATTGAT GATCATTGTG GTTCTTACCT TTGTCTTTGG TGCAAATGTG GAAAACTGA TCTGTGAACC TTACACGAGC AAGGAATTAT TCCGGGTTTT GGATACACCC TACTTACTAA ATGAAGACTG GGATACTAT CTCTCTGGGA AGCTATTTAA
                                                                                                         1500
                                                                                                         1560
15
                                                                                                         1620
                                                                                                         1680
          TAAATCAAAA ATGAAGCTCA CTTTTGAACA AGTTTACAGT GACTGCAAAA AAAATAGAGG
          CACTTACGGC ACTCTTCACC TGCAGAACAG CTTCAATATC AGTGAACATC TCAACATTAA
TGAGCATACT GGAAGCATAA GCAGTGAATT GGAAAGTCTG AAGGTAAATC TTAATATCTT
                                                                                                         1800
20
                                                                                                         1860
          TCTGTTGGGT GCAGCAGGAA GAAAAAACCT TCAGGATTTT GCTGCTTGTG GAATAGACAG
                                                                                                         1920
          AATGAATTAT GACAGCTACT TGGCTCAGAC TGGTAAATCC CCCGCAGGAG TGAATCTTTT ATCATTTGCA TATGATCTAG AAGCAAAAGC AAACAGTTTG CCCCCAGGAA ATTTGAGGAA
                                                                                                          1980
                                                                                                         2040
           CTCCCTGAAA AGAGATGCAC AAACTATTAA AACAATTCAC CAGCAACGAG TCCTTCCTAT
                                                                                                          2100
          AGAACAATCA CTGAGCACTC TATACCAAAG CGTCAAGATA CTTCAACGCA CAGGGAATGG
ATTGTTGCAG AGAGTAACTA GGATTCTAGC TTCTCTGGAT TTTGCTCAGA ACTTCATCAC
 25
                                                                                                          2220
           ANALITACITA CANTINATA GASTICITAGE TITCIGARI TITCIGARA ACITATICAC
ARACATACT TCCTCTGTTA TTATTGAGGA ARCTARGAGG TATGGAGGAC CANTANTAGG
ATATTTTGA CATTATCTGC AGTGGATCGA GTTCTCTATC AGTGAGAAG TGGCATCGTG
CAAACCTGTG GCCACCGCTC TAGATACTGC TGTTGATGTC TTTCTGTGTA GCTACATTAT
                                                                                                          2280
                                                                                                          2400
           CGACCCCTTG AATTTGTTTT GGTTTGGCAT AGGAAAAGCT ACTGTATTTT TACTTCCGGC
                                                                                                          2460
 30
           TCTAATTTTT GCGTTAAAC TGGCTAAGTA CTATCGTCGA ATGGATTCGG AGGACGTGTA CGATGATGTT GAAACTATAC CCATGAAAAA TATGGAAAAT GGTAATAATG GTTATCATAA
                                                                                                          2520
                                                                                                          2580
           AGATCATGTA TATGGTATTC ACAATCCTGT TATGACAAGC CCATCACAAC ATTGATAGCT GATGTTGAAA CTGCTTGAGC ATCAGGATAC TCAAAGTGGA AAGGATCACA GATTTTTGGT
                                                                                                          2640
                                                                                                          2700
           AGTTTCTGGG TCTACAAGGA CTTTCCAAAT CCAGGAGCAA CGCCAGTGGC AACGTAGTGA
 35
           CTCAGGCGGG CACCAAGGCA ACGGCACCAT TGGTCTCTGG GTAGTGCTT AAGAATGAAC
ACAATCACGT TATAGTCCAT GGTCCATCAC TATTCAAGGA TGACTCCCTC CCTTCCTGTC
TATTTTTGTT TTTTACTTTT TTACACTGAG TTTCTATTTA GACACTACAA CATATGGGGT
                                                                                                          2820
                                                                                                          2880
                                                                                                          2940
            GITTGTTCCC ATTGGATGCA TTTCTATCAA AACTCTATCA AATGTGATGG CTAGATTCTA
            ACATATTGCC ATGTGTGGAG TGTGCTGAAC ACACACCAGT TTACAGGAAA GATGCATTTT
                                                                                                           3060
  40
           ACCITATION ANGESTSTAT ATACCTTTIG TTACCACAGA GITTITIANA CANATGAGTA TTATAGGACT TTCTTCTANA TGAGCTANAT ANGTCACCAT TGACTTCTTG GTGCTGTTGA
                                                                                                          3120
                                                                                                          3180
            AAATAATCCA TTTTCACTAA AAGTGTGTGA AACCTACAGC ATATTCTTCA CGCAGAGATT
            TTCATCTATT ATACTTTATC AAAGATTGGC CATGTTCCAC TTGGAAATGG CATGCAAAAG 3300 CCATCATAGA GAAACCTGCG TAACTCCATC TGACAAATTC AAAAGAGAGA GAGAGATCTT 3360
  45
            GAGAGAGAA TECTETTOT TCAAAAGTG AGTGTTTTA ACAGATGCA ATTACGGTGT
ACAGTTTAAC AGAGTTTCT GTTGCATTAG GATAACATT AATTGGAGTG CAGCTAACAT
GAGTATCATC AGACTAGTAT CAAGTGTTCT AAAATGAAT ATTGGAGAG CCTGTCACAA
                                                                                                           3420
                                                                                                           3480
                                                                                                           3540
            TTCTTAGATC TGGTGTCCAG CATGGATGAA ACCTTTGAGT TTGGTCCCTA AATTTGCATG
                                                                                                           3600
            AAAGCACAAG GTAAATATTC ATTTGCTTCA GGAGTTTCAT GTTGGATCTG TCATTATCAA 3660
AAGTGATCAG CAATGAAGAA CTGGTCGGAC AAAATTTAAC GTTGATGTAA TGGAATTCCA 3720
  50
             GATGTAGGCA TTCCCCCCAG GTCTTTTCAT GTGCAGATTG CAGTTCTGAT TCATTTGAAT 3780
             AAAAAGGAAC TTGGC
   55
             Protein sequence 20
             Gene name: prominin (mouse)-like 1
Unigene number: Hs.112360
             Protein Accession #: NP_006008
             Signal sequence: 1-21
Transmembrane domains: 105-127, 157-179, 438-460, 482-504, 784-806
   60
             Cellular Localization: plasma membrane
                                           21
                                                           31
             MALVIGSILL IGICGNSFSG GOPSSTDAPK AWNYELPATN YETODSHKAG PIGILFELVH
             IFLYVVQPRD FPEDTLRKFL QKAYESKIDY DKPETVILGL KIVYYEAGII LCCVLGLLFI
                                                                                                              120
   65
             ILMPLVGYFF CMCRCCNKCG GEMHQRQKEN GPFLRKCFAI SLLVICIIIS IGIFYGFVAN
                                                                                                              180
             HQVETRIKRS RKLADSNFKD LRTLLNETPE QIKYILAQYN TTKDKAFTDL NSINSVLGGG
                                                                                                              240
             ILDRIRPNII PVLDEIKSMA TAIKETKEAL ENMISTLKSL HQQSTQLSSS LTSVKTSLRS
SLADPLCLVH PSSETCNSIR LSLSQLNSNP ELRQLPPVDA ELDNVNNVLR TDLDGLVQQG
YQSLNDIPDR VQRQTTTVVA GIRRVLNSIG SDIDNVTQRL PIQDILSAFS VYVNNTESYI
                                                                                                              300
                                                                                                              360
   70
                                                                                                              420
              HRNLPTLEEY DSYWWLGGLV ICSLLTLIVI PYYLGLLCGV CGYDRHATPT TRGCVSNTGG
                                                                                                              480
              VPLMVGVGLS PLPCWILMII VVLTFVFGAN VEKLICEPYT SKELFRVLDT PYLLNEDWEY
                                                                                                              540
              YLSGKLFNKS KMKLTFEQVY SDCKKNRGTY GTLHLQNSFN ISEHLNINEH TGSISSELES
                                                                                                               600
                                                                                                               660
              LKVNLNIFIL GAAGRKNLQD FAACGIDRMN YDSYLAQTGK SPAGVNLLSF AYDLEAKANS
              LPPGNLRNSL KRDAQTIKTI HQQRVLPIEQ SLSTLYQSVK ILQRTGNGLL ERVTRILASL
                                                                                                               720
    75
              DFAQNFITNN TSSVIIEETK KYGRTIIGYF EHYLQWIEPS ISEKVASCKP VATALDTAVD
                                                                                                               780
              VFLCSYIIDP LNLFWFGIGK ATVFLLPALI PAVKLAKYYR RMDSEDVYDD VETIPMKNME
              NGNNGYHKDH VYGIHNFVMT SPSQH
    80
              DNA sequence 21
              Gene name: G protein-coupled receptor 39
              Unique number: Hs.85339
              Nucleic Acid Accession #: NM_001508
              Coding sequence: 1-1362
```

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11
                                              21
          ATGCCTTCAC CCAGCCTCCC GGGCAGTGAC TGCTCCCAAA TCATTGATCA CAGTCATGTC
CCCGAGTTTG AGGTGGCCAC CTGGATCAAA ATCACCCTTA TTCTGGTGTA CCTGATCATC
                                                                                                                       120
 5
           TTCGTGATGG GCCTTCTGGG GAACAGCGCC ACCATTCGGG TCACCCAGGT GCTGCAGAAG
           AAAGGATACT TGCAGAAGGA GGTGACAGAC CACATGGTGA GTTTGGCTTG CTCGGACATC
                                                                                                                       240
           TIGGIGITCC ICATOGGCAT GCCCATGGAG TICTACAGCA TCATCIGGAA TCCCCTGACC
                                                                                                                       300
          AGGICCAGCT ACACCCTGTC CTGCAAGCTG CACACTTTCC TCTTCGAGGC CTGCAGCTAC
GCTACGCTGC TGCACGTGCT GACACTCAGC TTTGAGGGCT ACATCGCCAT CTGTCACCCC
                                                                                                                       360
10
           TYCAGGTACA AGGCTGTGTC GGGACCTTGC CAGGTGAAGC TGCTGATTGG CTTCGTCTGG
                                                                                                                        480
          GTCACCTCCG CCCTGGTGGC ACTGCCCTTG CTGTTTGCCA TGGGTACTGA GTACCCCCTG
GTGAACGTGC CCAGCCACCG GGGTCTCACT TGCAACCGCT CCAGCACCCG CCACCACGAG
                                                                                                                       540
                                                                                                                        600
           CAGCCCGAGA CCTCCAATAT GTCCATCTGT ACCAACCTCT CCAGCCGCTG GACCGTGTTC
           CAGTCCAGCA TCTTCGGCGC CTTCGTGGTC TACCTCGTGG TCCTGCTCTC CGTAGCCTTC
                                                                                                                        720
15
           ATGTGCTGGA ACATGATGCA GGTGCTCATG AAAAGCCAGA AGGGCTCGCT GGCCGGGGGC
                                                                                                                        780
           ACGCGGCCTC CGCAGCTGAG GAAGTCCGAG AGCGAAGAGA GCAGGACCGC CAGGAGGCAG
                                                                                                                        B40
           ACCATCATCT TCCTGAGGCT GATTGTTGTG ACATTGGCCG TATGCTGGAT GCCCAACCAG
           ATTOGGAGGA TCATGGCTGC GGCCAAACCC AAGCACGACT GGACGAGGTC CTACTTCOGG
                                                                                                                        960
           GOGTACATGA TOCTOCTOCC CTTCTCGGAG ACGTTTTTCT ACCTCAGCTC GGTCATCAAC
                                                                                                                      1020
           CCGCTCCTGT ACACGCTGTC CTCGCAGCAG TTTCGGCGGG TGTTCGTGCA GGTGCTGTGC
20
                                                                                                                      1080
           TGCCGCCTGT CGCTGCAGCA CGCCAACCAC GAGAAGCGCC TGCGCGTACA TGCGCACTCC
           ACCACOGACA GOGCCGCTT TGTGCAGGGC COGTTGCTCT TGGGGTCCCG GCGCCAGTCC 1200
TCTGCAAGGA GAACTGAGAA GATTTTCTTA AGCACTTTTC AGAGCGAGGC CGAGCCCCAG 1260
TCTAAGTCCC AGTCATTGAG TCTGGAGTCA CTAGAGCCCA ACTCAGGCGC GAAACCAGCC 1320
25
           AATTCTGCTG CAGAGAATGG TTTTCAGGAG CATGAAGTTT GA
           Protein sequence 21
Gene name: G protein-coupled receptor 39
           Unigene number: Hs.85339
30
           Protein Accession #: NM_001508, NP_001409
Signal sequence: none found
Pfam domains: 7tm_1 [72-172, 224-344]
           Transmembrane domains: 32-54, 68-90, 111-133, 151-173, 221-243, 280-301, 320-342
Cellular Localization: plasma membrane
1 11 21 31 41 51
35
           MASPSLPGSD CSQIIDHSHV PEFEVATWIK ITLILVYLII FVMGLLGNSA TIRVTQVLQK
                                                                                                                          60
           KGYLQKEVTD EMVSLACSDI LVPLIGMPME PYSIIWNPLT TSSYTLSCKL HTFLFEACSY
ATLLHVLTLS PERYIAICHP FRYKAVSGPC QVKLLIGFVW VTSALVALPL LPAMGTEYPL
                                                                                                                        120
                                                                                                                         180
40
            VNVPSHRGLT CNRSSTRHHE QPETSNMSIC TNLSSRWTVF QSSIFGAFVV YLVVLLSVAF
                                                                                                                         240
           MCWNMOQVLM KSQKGSLAGG TRPPQLRKSE SEESRTARRQ TIIPLRLIVV TLAVCWMFNQ
IRRIMAAAKP KHDWTRSYFR AYMILLPFSE TFFYLSSVIN PLLYTVSSQQ FRRVFVQVLC
CRLSLQHANH EKRLRVHAHS TTDSARFVQR PLLFASRRQS SARRTEKIFL STFQSEAEPQ
                                                                                                                         300
                                                                                                                         360
            SKSQSLSLES LEPNSGAKPA NSAAENGFQE HEV
45
            TABLE 8A: ABOUT 1260 GENES UP-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT TISSUES
            Table BA lists about 1260 genes up-regulated in glioblastoma compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip
           array such that the ratio of "average" glioblastoma to "everage" normal adult tissues was greater than or equal to 2.5. The "average" glioblastoma level was set to the 75th percentile amongst various glioblastoma turnors. The "average" normal adult tissue level was set to the 85th percentile amongst various non-matignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the non-matignant tissues was subtracted from both the numerator and the denominator
 50
            before the ratio was evaluated.
            Pkey:
                                 Unique Eos probeset identifier number
                                 Exemplar Accession number, Genbank accession number
 55
            UnigenelD:
                                 Unigene number
            Unigene Title:
                                 Unigene gene title
                                 Ratio of 75th percentile tumor to 85th percentile normal body tissue
                                       UnigeneID Unigene Title
Hs.2868 peripheral myelin protein 2
            Pkey
431917
                        ExAcon
 60
                        D16181
                                                     protein kinase C binding protein 2
             427343
                        AI880044
                                        Hs.176977
                                                                                                                          74.2
             455601
                        A1368680
                                        Hs.816
                                                      SRY (sex determining region Y)-box 2
                        AI699994
                                                      peripheral myelin protein 2
                                                                                                                          71.6
            428321
                                        Hs. 2868
                                                                                                                           70.7
                        AW016610
                                       Hs.129911
                                                      ESTs
            412719
 65
                                       Hs.315369
                                                      Homo sapiens cDNA: FLJ23075 fis, clone L
                        AW237014
             449494
                                                     protein tyrosine phosphatase, receptor-t
solute carrier family 1 (glial high affi
delta (Drosophila)-like 3
Homo sapiens mRNA; cDNA DKFZp761C1712 (f
NK-2 (Drosophila) homolog B
             415817
                        U88967
                                        Hs.78867
                                                                                                                           64.3
             413472
                        BE242870
                                        Hs.75379
                                                                                                                           60.1
                                                                                                                           52.3
             456759
                        RF259150
                                       Hs.127792
                        AL133731
                                        Hs.4774
                                                                                                                           46.7
             435147
 70
             425842
                        AI587490
                                        Hs.159623
                                                                                                                           40.1
                        AA984472
                                        Hs.74554
                                                      KIAA0080 protein
                                                                                                                           39.0
             412733
                        NM_003081
                                                      synaptosomal-associated protein, 25kD SRY (sex determining region Y)-box 11
             418375
                                       Hs.84389
Hs.32964
                                                                                                                           38.7
                                                                                                                           37.2
             453392
                        1123752
                                                      Homo sepiens mRNA; cDNA DKFZp761J1324 (f
             423849
                         AL157425
                                        Hs.133315
 75
             413333
                         M74028
                                        Hs.75297
                                                      fibroblast growth factor 1 (acidic)
                                                                                                                           32.8
                                                      catenin (cadherin-associated protein), d
             416829
                         AB013805
                                        Hs.80220
                                                                                                                           31.8
                                                      Homo sapiens cDNA FLJ20099 fis, clone CO
                                        Hs.272227
                                                                                                                           31.8
             431941
                         AK000106
                                        Hs.47448
                         BE465204
                                                      ESTs
             436878
                                                      myelin-associated oligodendrocyte basic
                         D28114
                                         Hs.169309
                                                                                                                           30.9
             426325
 80
                                                      achaete-scute complex (Orosophila) homol
             425057
                         AA826434
                                        Hs.1619
                                                                                                                           30.4
                                                                                                                           30.2
                                                      protocadherin 9
             445711
                         AF169692
                                        Hs.12450
                         F05538
                                        Hs.12825
                                                      ESTS
             439415
                                                      hypothetical protein FLJ12015
                         N46664
                                        Hs.169395
             430838
```

	429466	M85835	Hs.12827	ESTs	25.9
	447004	AW296968	Hs.157539	ESTs	25.3
	424581	M62062	Hs.150917	catenin (cadherin-associated protein), a	24.8 24.8
5	452744 441285	AI267652 NM_002374	Hs.30504 Hs.167	Homo sapiens mRNA; cDNA DKFZp434E082 (fr microtubule-associated protein 2	24.3
•	453642	Al370936	Hs.34074	dipeplidylpeplidase VI	24.3
	424140	Z48051	Hs.141308	myelin oligodendrocyte glycoprotein	24.2 24.2
	450133 408562	AW969769 Al436323	Hs.105201 Hs.31141	ESTs Homo sapiens mRNA for KIAA1568 protein,	24.2 23.3
10	448672	Al955511	Hs.225106	ESTs	22.7
	435708	Al362949	Hs.75169	ESTs	22.0
	407034	U84540	Hs.117183	gb:Human dystrobrevin isoform DTN-3 (DTN ESTs	21.9 21.7
	407168 431019	R45175 NM_005249	Hs.2714	forkhead box G1B	21.5
15	409049	Al423132	Hs.146343	ESTs	21.4
	433896	AW294729	Hs.274461	ESTs	21.1 21.0
	445041 418738	T64183 AW388633	Hs.282982 Hs.6682	solute carrier solute carrier family 7, (cationic amino	20.4
	444378	R41339	Hs.12569	ESTs	20.0
20	411305	BE241596	Hs.69547	myelin basic protein	19.9 19.8
	437414 441016	AW894071 AW138653	Hs.48448 Hs.25845	hypothetical protein DKFZpS47C176 ESTs	19.6
	440435	AL042201	Hs.21273	transcription factor NYO-sp10	18.5
05	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transl	18.4
25	452461	N78223 U46745	Hs.108106 Hs.54435	transcription factor dystrobrevin, alpha	18.1 18.1
	409395 417183	R52089	Hs.172717	ESTs	18.0
	409638	AW450420	Hs.21335	ESTs	18.0
30	428392	H10233	Hs.2265	secretory granule, neuroendocrine protei	18.0 17.0
30	449611 446692	Al970394 Z44514	Hs.197075 Hs.156829	ESTs Homo sapiens mRNA for KIAA1763 protein,	16.9
	425088	AA663372	Hs.169395	hypothetical protein FLJ12015	16.9
	444471	AB020684	Hs.11217	KIAA0877 protein	16.8
35	421659 431725	NM_014459 X65724	Hs.106511 Hs.2839	protocadherin 17 Narrie disease (pseudoglioma)	16.7 16.6
23	429276	AF056085	Hs.198612	G protein-coupled receptor 51	16.6
	416892	L24498	Hs.80409	growth arrest and DNA-damage-inducible,	16.5
	441440	A1807981	Hs.30495 Hs.9012	ESTs ESTs, Weakly similar to S26650 DNA-bindi	15.7 15.7
40	449433 421264	Al672096 AL039123	Hs.103042	microtubute-associated protein 18	15.5
	415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	15.3
	413597	AW302885 Al221919	Hs.117183 Hs.173438	ESTs hypothetical protein FLJ10582	15.1 14.9
	424945 447414	D82343	Hs.18551	neuroblastoma (nerve tissue) protein	14.9
45	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	14.8
	416857	AA188775	Hs.292453	ESTs	14.7 14.6
	419721 411078	NM_001650 Al222020	Hs.288650 Hs.182364	aquaporin 4 CocoaCrisp	14.4
	453924	R49295	Hs.24886	ESTs	14.4
50	409389	AB007979	Hs.301281	Homo sapiens mRNA, chromosome 1 specific	14.3 14.1
	430130 41090 9	AL137311 AW898161	Hs.234074 Hs.53112	Homo sapiens mRNA; cDNA DKFZp761G02121 (ESTs, Moderately similar to ALU8_HUMAN A	14.0
	412266	N59006	Hs.26133	ESTs	14.0
55	412986	X81120	Hs.75110	cannabinoid receptor 1 (brain)	14.0 14.0
33	424790 439239	AL119344 AJ031540	Hs.13326 Hs.235331	ESTs, Weakly similar to 2004399A chromos ESTs	14.0
	441497	R51064	Hs.23172	ESTs	14.0
	445495	BE622641	Hs.38489	ESTs, Weakly similar to I38022 hypotheti	14.0 13.7
60	414245 429900	BE148072 AA460421	Hs.75850 Hs.30875	WAS protein family, member 1 ESTs	13.6
00	448595	AB014544	Hs.21572	KIAA0644 gene product	13.6
	449605	AW138581	Hs.198416	ESTs	13.6 13.6
	452526 420547	W38537 AF155140	Hs.280740 Hs.98738	hypothetical protein MGC3040 gonedotropin-regulated testicular RNA he	13.3
65	441350	AB020690	Hs.7782	paraneoplastic antigen MA2	13.3
	420077	AW512260	Hs.87767	ESTs	13.2
	424120 456965	T80579 AW131888	Hs.290270 Hs.172792		13.2 13.2
	423361	AW170055	Hs.47628	ESTs	13.1
70	428409	AW117207	Hs.98523	ESTs	12.9
	417160 451621	N76497 A1879148	Hs.1787 Hs.26770	proteolipid protein 1 (Pelizaeus-Merzbac fatty acid blnding protein 7, brain	12.6 12.5
	411379	Al816344	Hs.12554	ESTs, Weakly similar to NPL4_HUMAN NUCLE	12.5
75	436954	AA740151	Hs.13042	5 ESTs	12.4
75	430691	C14187 Al985544	Hs.103531		12.4 12.4
	433551 422544		Hs.12450 Hs.11814		12.2
	427540	R12014	Hs.20976	ESTs .	12.1
80	435524		Hs.24889	formin 2 ESTs	12.1 12.1
OV	415849 428845		Hs.6806 Hs.15361		11.9
	442671	AI005668	Hs.13477	9 EST	11.9
	444396	T65213	Hs.4257	ESTs	11.8

	452752	AW044058	Us 22570	MAARRO mateix	44.0
	425523	AB007948	Hs.33578 Hs.158244	KIAA0820 protein KIAA0479 protein	11.8
	416072	AL110370	Hs.79000	growth associated protein 43	11.8 11.7
_	440184	AB002297	Hs.7022	dedicator of cyto-kinesis 3	11.7
5	428976	AL037824	Hs.194695	ras homolog gene family, member i	11.6
	444783	AK001468	Hs.62180	anillin (Orosophila Scraps homolog), act	11.6
	448299	AA497044	Hs.20887	hypothetical protein FLJ10392	11.6
	414214	049958	Hs.75819	glycoprotein M6A	11.5
10	428982	NM_005097	Hs.194704	feucine-rich, glioma inactivated 1	11.5
10	405238				11.4
	420362	U79734	Hs.97206	huntingtin interacting protein 1	11.4
	422980	N46569	Hs.76722	CCAAT/enhancer binding protein (C/EBP),	11.4
	424918 434277	R13982 X77748	Hs.169309	myelin-associated oligodendrocyte basic	11.4
15	451952	AL120173	Hs.3786 Hs.301663	glutamate receptor, metabotropic 3 ESTs	11.4
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfot	11.3 11.3
	424278	AK000723	Hs.144517	hypothetical protein FLJ20716	11.3
	429418	AI381028	Hs.118769	ESTs	11.3
	429918	AW873986	Hs.119383	ESTs	11.3
20	443912	R37257	Hs.184780	ESTs	11.3
	448743	AB032962	Hs.21896	KIAA1136 protein	11.3
	420092	AA814043	Hs.88045	ESTs	11.2
	408081	AW451597	Hs.167409	ESTs	11.2
25	411642	NM_014932	Hs.71132	neuroligin 1	10.9
25	415170	R44386	Hs.164578	ESTs	10.9
	426320	W47595	Hs.169300	transforming growth factor, beta 2	10.8
	450568 425799	AL050078 T08133	Hs.25159 Hs.182906	Homo sapiens cDNA FLJ10784 fis, clone NT	10.8
	423853	AB011537	Hs.133466	Homo sepiens mRNA for KIAA1872 protein, slit (Drosophila) homolog 1	10.8 10.7
30	400293	N51002	Hs.306480	Homo sapiens mRNA; cDNA DKFZp761E2112 (I	10.7
50	447773	AI423930	Hs.36790	ESTs, Weakly similar to putative p150 [H	10.7
	448321	NM_005883	Hs.20912	adenomatous polyposis coli (ika	10.5
	448533	AL119710	Hs.21365	nucleosome assembly protein 1-like 3	10.5
	440684	A1253123	Hs.127356	ESTs, Highly similar to S21424 nestin [H	10.3
35	444017	U04840	Hs.214	neuro-oncological ventral antigen 1	10.3
	438380	T06430	Hs.6194	chondroitin sulfate proteoglycan BEHAB/b	10.3
	440471	AA886146	Hs.307944	ESTs	10.2
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	10.1
40	439978	BE139460	Hs.124673	Homo sapiens cDNA FLJ11477 fis, clone HE	10.1
40	448902	Z45998	Hs.22543	Homo sapiens mRNA; cDNA DKFZp76111912 (f	10.1
	424932 431721	R14070 AB032996	Hs.315369 Hs.268044	Homo sapiens cDNA: FLJ23075 fis, clone L KIAA1170 protein	9.9 9.9
	419088	AI538323	Hs.52620	Integrin, beta 8	9.8
	420602	AF060877	Hs.99236	regulator of G-protein signalling 20	9.8
45	436511	AA721252	Hs.291502	ESTs	9.8
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	9.7
	449539	W80363	Hs.58446	ESTs	9.7
	412959	D87458	Hs.75090	KIAA0282 protein	9.6
50	412811	H06382	Hs.21400	ESTs	9.6
50	449300	AI656959	Hs.222165	ESTs	9.6
	426344	H41821	Hs.322469	transcriptional activator of the c-fos p	9.5
	419271	N34901 M93119	Hs.238532	ESTs	9.5
	419078 451516	AI800515	Hs.89584 Hs.12024	Insulinoma-associated 1 ESTs	9.4 9.4
55	422656	AI870435	Hs.1569	LIM homeobox protein 2	9.3
	449318	AW236021	Hs.78531	Homo saplens, Similar to RIKEN cDNA 5730	9.3
	414175	AI308876	Hs.103849	hypothetical protein DKFZp761D112	9.3
	415279	F04237	Hs.1447	glial fibrillary acidic protein	9.2
C 0	428784	Y12851	Hs.193470	purinergic receptor P2X, ligand-gated to	9.2
60	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	9.2
	424641	AB001106	Hs.151413	glia maturation factor, beta	9.1
	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	9.1
	449448	D60730	Hs.57471	ESTs	9.1
65	408508	AI806109	Hs.135736	KIAA1580 protein	9.0
05	452785 448986	AL359942 H42169	Hs.296434 Hs.18653	erythrold differentiation and denucleati hypothetical protein FLJ14627	9.0 8.9
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	8.9
	433800	AJ034361	Hs.135150	lung type-I cell membrane-associated gly	8.9
	408926	AF217525	Hs.49002	Down syndrome cell adhesion molecule	8.B
70	449625	NM_014253	Hs.23796	odz (odd Oz/ten-m, Drosophila) homolog 1	8.8
	400292	AA250737	Hs.72472	ESTs	8.7
	417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	8.7
	420345	AW295230	Hs.25231	ESTs	8.7
75	429927	NM_001115	Hs.2522	adenylate cyclase 8 (brain)	8.7
75	437528	N59646	Hs.169745	crumbs (Drosophila) homolog 1	8.7
	440152	AB002376	Hs.7006	KIAA0378 protein	8.7
	451099 400780	R52795	Hs.25954	interleukin 13 receptor, alpha 2	8.6
	434891	AA814309	Hs.123583	ESTs	8.6 8.6
80	449277	AA001064	Hs.172976	ESTs	8.6
	415709	AA649850	Hs.278558	ESTs	8.5
	439947	AB006627	Hs.6788	astrotactin	8.5
	447197	R36075		gb:yh86b01.s1 Soares placenta Nb2HP Homo	8.5

					0.4
	433042			Homo sapiens cDNA FLJ11660 fis, clone HE	8.4 8.4
	416370			ESTs, Weakly similar to 138022 hypotheti ESTs, Weakly similar to T09052 hypotheti	8.4
	452786 415796	R61362 R87548		ATPase, Na+fK+ transporting, beta 2 poly	8.3
5	426271	AF026547		chondroitin sulfate proteoglycan 3 (neur	8.3
_	408947	AL080093	Hs.49117	Homo sapiens mRNA; cDNA DKFZp564N1662 (f	8.3
	419863	AW952691		Homo saplens mRNA; cDNA DKFZp761D191 (fr	8.3
	433447	U29195		neuronal pentraxin II	8.3 8.3
10	431467	N71831		Homo sapiens mRNA; cDNA DKFZp434E0528 (f	8.3
10	409327 414300	L41162 Al304870	Hs.53563 Hs.188680	collagen, type IX, alpha 3 ESTs	8.2
	407728	AW071502	Hs.175931	ESTs	8.2
	422798	R92347	Hs.34574	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.2
	419704	AA429104	Hs.45057	ESTs	8.2
15	429007	D80642		gb:HUM092E09B Human fetal brain (TFujiwa	8.1 8.1
	442710	AI015631	Hs.23210	ESTs	8.1
	425048	H05468	Hs.164502 Hs.197962	ESTs ESTs, Weakly similar to I38022 hypotheti	8.0
	429149 445740	AW193360 T78281	Hs.13226	Homo sapiens done 25181 mRNA sequence	8.0
20	418771	AA807881	Hs.25329	ESTs	7.9
	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	7.9
	425984	AW836277	Hs.165636	hypothetical protein DKFZp761C07121	7.9
	448408	AA322866	Hs.21107	neuroligin	7.9 7.9
25	455364	H72176	Hs.4273	hypothetical protein FLJ13159 secreted phosphoprotein 1 (osteopontin,	7.9
23	446619 435501	AU076643 AW051819	Hs.313 Hs.129908		7.8
	423600	A1633559	Hs.310359	ESTs	7.8
	450625	AW970107	***************************************	gb:EST382188 MAGE resequences, MAGK Homo	7.8
	415314	N88802	Hs.5422	glycoprotein M6B	7.7
30	420036	R60336	Hs.52792	Homo sapiens mRNA; cDNA DKFZp586i1823 (f	7.7 7.7
	427687	AW003867	Hs.1570	histamine receptor H1	7.7
	449328	Al962493	Hs.197647 Hs.89768	ESTs gamma-aminobutyric acid (GABA) A recepto	7.7
	419249 407896	X14767 D76435	Hs.41154	Zic family member 1 (odd-paired Drosophi	7.7
35	419103	Z40229	Hs.96423	hypothetical protein FLJ23033	7.6
	438779	NM_003787	Hs.6414	nucleolar protein 4	7.6
	433532	AW975367		gb:EST387475 MAGE resequences, MAGN Homo	7.6
	448555	A1536697	Hs.159863	ESTs	7.5 7.5
40	439662	H97552	Hs.269060	ESTs Horno saplens mRNA; cDNA DKFZp586P1124 (f	7.5 7.5
40	448543 410099	AW897741 AA081630	Hs.21380 Hs.169387	KIAA0036 gene product	7.5
	431592	R69016	Hs.213194	hypothetical protein MGC10895	7.4
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	7.4
	405819				7.4
45	407886	AW969688	Hs.100826	ESTs	7.4 7.4
	437416	AL359605	Hs.283851	Homo sapiens mRNA; cDNA DKFZp547G036 (fr	7.4 7.4
	437698	R61837	Hs.7990 Hs.21925	ESTs, Moderately similar to 184505 calci ESTs	7.4
	408604 418506	D51408 AA084248	Hs.85339	G protein-coupled receptor 39	7.3
50	447499	AW262580	Hs.147674		7.3
	454036	AA374756	Hs,93560	Homo sapiens mRNA for KIAA1771 protein,	7.3
•	409746	NM_004794		RAB33A, member RAS oncogene family	7.2 7.2
	410037	AB020725	Hs.58009	KIAA0918 protein	7.2 7.2
55	419318	AW969742 AL110203	Hs.291005 Hs.138411		7.2
55	424051 442026	Al243749	Hs.8074	brain-specific angiogenesis inhibitor 3	7.2
	448243	AW369771	Hs.52620	integrin, beta 8	7.2
	436281	AW411194	Hs.85195	myeloid leukemia factor 1	7.2
	426429	X73114	Hs.169849		7.2
60	407182	AA312551	Hs.230157	ESTs	7.1 7.1
	415293	R49462	Hs. 106541 Hs. 47522	ESTs ESTs	7.1
	422764 451592	A1767727 A1805416	Hs.213897		7.1
	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	7.0
65	415734	NM_014747	Hs.78748	KIAA0237 gene product	7.0
	434149	Z43829	Hs.19574	hypothetical protein MGC5469	7.0
	436726	AA324975	Hs.128993		7.0 7.0
	417632	R20855	Hs.5422	glycoprotein M6B	6.9
70	422421	AA325138 N23797	Hs.235873 Hs.110114		6.9
70	435267 437117	AL049256	Hs.122593		6.9
	445523		Hs.293788		6.9
	445900		Hs.13429	Homo sapiens clone 24787 mRNA sequence	6.9
ne	445745	AB007924	Hs.13245		6.9
75	424085			6 replication factor C (activator 1) 2 (40	6.9 6.8
	428588		Hs.185701 Hs.300711		6.8
	421723 447342		Hs.19322		6.7
	443297		Hs.13302		6.7
80	443992		Hs.32292	2 ESTs	6.7
	453096				6.7
	453857		Hs.35861		6.7 6.6
	443761	Al525743	Hs.16060	3 ESTs	0.0

	429609	AF002246	Hs.210863	cell adhesion molecule with homology to	66
	435056	AW023337	Hs.5422	glycoprotein M6B	6.6 6.5
	453431	AF094754	Hs.32973	glycine receptor, beta	6.5
_	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	6.5
5	418110	R43523	Hs.217754	hypothetical protein FLJ22202	6.5
	413988	M81883	Hs.324784	glutamate decarboxylase 1 (brain, 67kD)	6.5
	420805 429125	L10333	Hs.99947 +		6.4
	435256	AA446854 AF193766	Hs.271004 Hs.13872	ESTs, Weakly similar to 138022 hypotheti cytokine-like protein C17	6.4 6.4
10	407866	AW088232	Hs.89506	paired box gene 6 (antirdia, keratitis)	6.3
	440700	AW952281	Hs.296184	guanine nucleotide binding protein (G pr	6.3
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	6.3
	422949	AA319435		gb:EST21657 Adrenal gland tumor Homo sap	6.2
15	445102	AW204610	Hs.22270	ESTs	6.2
15	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	6.2
	435538	AB011540	Hs.4930	low density lipoprotein receptor-related	6.2
	410102 416871	AW248508 H98716	Hs.279727	Homo sepiens cDNA FLJ14035 fis, clone HE gb:yx13d08.s1 Soares melanocyte 2NbHM Ho	6.2 6.1
	416702	AA186428	Hs.85591	ESTs	6.1
20	419347	C15944	Hs.90005	superiorcervical ganglia, neural specifi	6.1
	424997	AL138167	Hs.96920	ESTs	6.1
	438660	U95740	Hs.6349	Homo sapiens, clone IMAGE:3010666, mRNA,	6.1
	453649	Y07494	Hs.34114	ATPase, Na+/K+ transporting, alpha 2 (+)	6.1
25	449444	AW818436	Hs.23590	solute carrier family 16 (monocarboxylic	6.1
23	414117	W88559	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	6.0
	425517 427457	AF121179 AW779105	Hs.164682	gb:AF121179 Homo sapiens liver (Chang L- ESTs	6.0 6.0
	437034	AA742643	115.104002	gb:ny91c01.s1 NCI_CGAP_GCB1 Homo saplens	6.0
	444170	AW613879	Hs.102408	ESTs	6.0
30	457183	H91882	Hs.118569	Dvl-binding protein IDAX (inhibition of	6.0
	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	6.0
	454048	H05626	Hs.6921	ESTs	6.0
	439772	AL365406	Hs.10268	Homo sapiens mRNA full length insert cDN	5.9
35	448944	AB014605	Hs.22599	alrophin-1 interacting protein 1; activi	5.9
33	410011	AB020641	Hs.57856	PFTAIRE protein kinase 1	5.9
	415486 438993	H12214 AA828995	Hs.13284	ESTs, Weakly similar to 2109260A B cell gb:od77b08.s1 NCI_CGAP_Ov2 Homo sapiens	5.9 5.9
	447350	Al375572	Hs.172634	ESTs	5.9
	451783	R42554	Hs.210862	T-box, brain, 1	5.9
40	447101	N72185	Hs.44189	ESTs	5.9
	440492	R39127	Hs.21433	hypothetical protein DKFZp547J036	5.9
	440274	R24595	Hs.7122	scrapie responsive protein 1	5.9
	438461	AW075485	Hs.286049	phosphoserine aminotransferase	5.9
45	418064	BE387287	Hs.83384	S100 calcium-binding protein, beta (neur	5.8
73	437036 412225	Al571514 AW902042	Hs.133022	ESTs gb:QV0-NN1022-170400-193-c02 NN1022 Homo	5.7 5.7
	426342	AF093419	Hs.169378	multiple PDZ domain protein	5.7
	444218	AF070641	Hs.10684	Horno sapiens clone 24421 mRNA sequence	5.7
	445828	F05802	Hs.81907	ESTs	5.7
50	447198	D61523	Hs.283435	ESTs	5.7
	427897	NM_017413	Hs.303084	apelin; peptide ligand for APJ receptor	5.7
	448499	BE613280	Hs.77550	hypothetical protein MGC1780	5.7
	443672 412155	AA323362 R38167	Hs.9667 Hs.12449	butyrobetaine (gamma), 2-oxoglutarate di Homo sapiens transmembrane protein HTMP1	5.6 5.6
55	435718	R06569	Hs.269534	ESTs	5.6
	449340	AW235786	Hs.195359	hypothetical protein MGC10954	5.6
	424481	R19453	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	5.6
	451996	AW514021	Hs.245510	ESTs	5.6
60	422411	AW749443	Hs.22511	ESTs	5.6
60	438328	AI492261 AB040943	Hs.32450 Hs 271285	ESTs	5.6
	433244 435191	R15912	Hs.4817	KIAA1510 protein Horno sapiens clone 24461 mRNA sequence	5.6
	418677	S83308	Hs.87224	SRY (sex determining region Y)-box 5	5.5 5.5
	400859	000000	110.07 22 1	over foot accomming region 1/ box o	5.5
65	413625	AW451103	Hs.71371	ESTs	5.5
	421863	AI952677	Hs.108972	Homo saptens mRNA; cDNA DKFZp434P228 (fr	5.5
	434933	R91095	Hs.4276	KIAA1701 protein	5.5
	438702	AI879064	Hs.54618	ESTs	5.5
70	452055 430979	A1377431	Hs.141693 Hs.129010	hypothetical protein MGC10858 ESTs	5.5
,,	412709	A1479755 AL022327	Hs.74518	KIAA0027 protein	5.5 5.5
	439920	H05430	Hs.288433	neurotrimin	5.5 5.5
	424343	AW956360	Hs.4748	adenylate cyclase activating polypeptide	5.4
	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	5.4
75	419235	AW470411	Hs.288433	neurotrimin .	5.4
	418030	BE207573	Hs.83321	neuromedin B	5.4
	410330	AW023630	Hs.46786	ESTS	5.4
	410781 420658	Al375672 AW965215	Hs.165028 Hs.336656	ESTs ESTs	5.4 5.4
80	421308	AA687322	Hs.192843	leucine zipper protein FKSG14	5.4
	443740	R56434	Hs.21062	ESTs	5.4
	426457	AW894667	Hs.169965	chimerin (chimaerin) 1	5.4
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	5.4

					5.4
				DP-ribosylation factor domain protein 1 /GF nerve growth factor inducible	5.4 5.4
				rotocadherin 10	5.4
			Hs.198308 t	ryptophan rich basic protein	5.4
5	443785			pasic-helix-loop-helix-PAS protein	5.4 5.4
	436282	R91913	Hs.272104 1	ESTs, Moderately similar to ALU1_HUMAN A	5.3
	404584 430091	AB032958	Hs.233023	KIAA1132 protein	5.3
	439845	AL355743		Homo sapiens EST from clone 41214, full	5.3 5.3
10	424001	W67883		paternally expressed 10 solute carrier family 6 (neurotransmitte	5.3
	425073 426625	W39609 178300	Hs.22003 Hs.300642	serologically defined colon cancer antig	. 5.3
	428137	AA421792	Hs 170999	ESTs	5.3 5.3
	428679	AA431765		gb:zw80c03.st Soares_testis_NHT Homo sap	5.3
15	438176	AW138970		ESTs hypothetical protein FLJ10201	5.3
	440138 451018	AB033023 AW965599	Hs.247324	mitochondrial ribosomal protein S14	5.3
	416340	N31772	Hs.79226	fasciculation and elongation protein zet	5.3 5.3
20	435244	N77221	Hs.187824	ESTs Sam68-like phosphotyrosine protein, T-ST	5.3
20	446035 424624	NM_006558 AB032947	Hs.13565 Hs.151301	Ca2+-dependent activator protein for sec	5.3
	407748	AL079409	Hs.38176	KIAA0606 protein; SCN Circadian Oscillat	5.3 5.3
	430437	AI768801	Hs.169943	Homo sapiens cDNA FLJ13569 fis, clone PL	5.2
25	414825	X06370	Hs.77432 Hs.36820	epidermal growth factor receptor (avian Bloom syndrome	5.2
25	453941 424998	U39817 U58515	Hs.154138	chitinase 3-like 2	5.2
	423419	R55336	Hs.23539	ESTs	5.2 5.2
	424922	BE386547	Hs.217112	hypothetical protein MGC10825 adenylate kinase 5	5.2
30	447359 408206	NM_012093 AF041853	Hs.18268 Hs.43670	kinesin family member 3A	5.2
50	421013	M62397	Hs.1345	mutated in colorectal cancers	5.2 5.2
	429443	AB028967	Hs.202687	potassium voltage-gated channel, Shal-re	5.2 5.2
	434367	AB020700	Hs.3830 Hs.76118	KIAA0893 protein ubiquitin carboxyl-terminal esterase L1	5.2
35	444861 446142	R46789 A1754693	Hs.145968	ESTs	5.2
55	448816	AB033052	Hs.22151	KIAA1226 protein	5.2 5.2
	451050	AW937420	Hs.69662	ESTs v-myc avian myelocytomatosis viral relat	5.2
	451106 439285	BE382701 AL133916	Hs.25960 Hs.172572	hypothetical protein FLJ20093	5.2
40	416737	AF154335	Hs.79691	LIM domain protein	5.2 5.2
	424800	AL035588	Hs.153203	MyoD family inhibitor	5.2 5.2
	443695	AW204099	Hs.337720 Hs.27513	ESTs, Weakly similar to AF126780 1 retin ESTs	5.2
	415257 433929	F03016 A1375499	Hs.27379	ESTs	5.1
45	415651	Al207162	Hs.3815	stathmin-like-protein RB3	5.1 5.1
	451027	AW519204	Hs.40808	ESTs ESTs	5.1
	409172 423343	Z99399 AA324643	Hs.118145 Hs.246106	ESTS	5.1
	429172	AA447417	Hs.285491	ESTs	5.1 5.1
50	437268	AI754847	Hs.227571	regulator of G-protein signalling 4	5.1
	451270	AW341392 AL157581	Hs.235795 Hs.30957	ESTs Homo sapiens mRNA; cDNA DKFZp434E0626 (f	5.1
	452904 420560	AW207748	Hs.59115	ESTs	5.1
	418097	R45137	Hs.21868	ESTs	5.1 5.1
55	442910		Hs.11307 Hs.8053	ESTs, Weakly similar to T19326 hypotheti ESTs	5.1
	434849 413554		Hs.75426	secretogranin II (chromogranin C)	5.1
	414217		Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	5.1 5.0
60	412068		Hs.73133	metallothionein 3 (growth inhibitory fac B ESTs	5.0
60	413627 418661		Hs.246973 9 Hs.1189	E2F transcription factor 3	5.0
	422438		Hs.27089	S ESTs, Moderately similar to Z195_HUMAN Z	5.0 5.0
	423728	AW891294			5.0
65	431431 435087		Hs.25295 Hs.23567	ESTs	5.0
05	452097				5.0
	410434	AF051152	Hs.63668		4.9 4.9
	408692		Hs.34074 Hs.27978		4.9
70	40780 41894		Hs.28851	3 Human DNA sequence from clone RP5-899C14	4.9
,,	42597		Hs.16557	Homo sapiens clone 25052 mRNA sequence	4.9 4.9
	42681				4.9
	44711		Hs.7154 Hs.17537	ESTs 73 ESTs	4.9
75	44957 45365				4.9
	42386	9 BE409301	Hs.1340	2 C1q-retated factor	4.9 4.9
	41324		Hs.2143 Hs.1980		4.9
	44917 44845			gb:UI-H-Bi0p-abh-g-09-0-Ui.s1 NCI_CGAP_S	4.8
80	40260	4			4.8 4.8
	43603				4.8
	44876 42367		Hs.3817 7 Hs.7847	·	4.8
	. 42301			16	1

	439451	AF086270	Hs.278554	heterochromatin-like protein 1	4.8
	425870	R13406	Hs.56782	ESTs	4.8
	408777 413409	U71204 Al638418	Hs.47626 Hs.78580	Ric (Drosophila)-like, expressed in neur DEAD/H (Asp-Gtu-Ala-Asp/His) box polypep	4.8 4.8
5	413623	AA825721	Hs.246973	ESTs	4.8
-	417246	A1760098	Hs.21411	ESTs	4.8
	420900	AL045633	Hs.44269	ESTs	4.8 4.8
	424153 443539	AA451737 Al076182	Hs.141496 Hs.134074	MAGE-fike 2 ESTs, Moderately similar to ALU6_HUMAN A	4.8 4.8
10	448750	U95020	Hs.21903	calcium channel, voltage-dependent, beta	4.8
	454030	AW021429	Hs.231980	ESTs	4.8
	424458	M29273	Hs.1780	myelin associated glycoprotein	4.8 4.8
	444119 407792	R41231 A1077715	Hs.184261 Hs.39384	ESTs, Weakly similar to T26686 hypotheti putative secreted ligand homologous to f	4.8
15	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	4.7
	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	4.7
	429956 435060	Al374651 Al422719	Hs.22542 Hs.233349	ESTs ESTs, Wealdy similar to fork head like p	4.7 4.7
	436203	BE384982	Hs.5076	Homo sapiens cDNA: FLJ22128 fis, clone H	4.7
20	448475	BE613134	Hs.247474	hypothetical protein FLJ21032	4.7
	422222	AI699372	Hs.193247	hypothetical protein DKFZp434A171	4.7 4.7
	431733 449353	AW298410 AA001220	Hs.21475 Hs.271369	ESTs	4.7
	452022	AW072330	Hs.293875	ESTs	4.7
25	454269	AI961060	Hs.129908	KIAA0591 protein	4.7
	404541	4.4.0.4.0.20	11- 40007	ECT-	4.7 4.7
	428189 409125	AA424030 R17268	Hs.46627 Hs.259873	ESTs exonal transport of synaptic vesicles	4.7
	458435	Al418718	Hs.144121	ESTs, Weakly similar to T46916 hypotheti	4.6
30	425745	U44060	Hs.14427	Homo sapiens cDNA: FL121800 fis, clone H	4.6
	413492	D87470	Hs.75400	KIAA0280 protein KIAA0888 protein	4.6 4.6
	419629 407638	AB020695 AJ404672	Hs.91662 Hs.334483	hypothetical protein FLJ23571	4.6
	436140	W87355	Hs.269587	ESTs	4.6
35	439169	Al912122	Hs.41095	ESTs	4.6
	443150	A1034467 A1758905	Hs.34650 Hs.206063	ESTs ESTs	4.6 4.6
	451073 451659	BE379761	Hs.14248	ESTs	4.6
40	452106	Al141031	Hs.21342	ESTs	4.6
40	451407	AA131376	Hs.326401	fibroblast growth factor 12B	4.6
	448765 430147	R15337 R60704	Hs.21958 Hs.234434	Homo saptens mRNA; cDNA DKFZp547D086 (fr hairy/enhancer-of-split related with YRP	4.6 4.6
	437204	AL110216	Hs.12285	ESTs, Weakly similar to I55214 salivary	4.6
4.5	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	4.5
45	422175	N79885	Hs.6382	ESTs, Highly similar to T00391 hypotheti	4.5 4.5
	407889 419343	R34556 AA456245	Hs.30800 Hs.85603	ESTs, Weakly similar to S65657 alpha-1C- down-regulated by Ctnnb1, a	4.5
	421790	AW896201	Hs.22654	sodium channel, voltage-gated, type I, a	4.5
50	429399	AA452244	Hs.16727	ESTs	4.5
50	450149	AW969781	Hs.132863 Hs.252757	Zic family member 2 (odd-paired Drosophi ESTs	4.5 4.5
	453118 443455	AW195849 AB001025	Hs.9349	ryanodine receptor 3	4.4
	442613	Al004002	Hs.130522	Kv channel-interacting protein 1	4.4
55	429643	AA455889	Hs.167279	FYVE-finger-containing Rab5 effector pro	4.4 4.4
33	416209 418845	AA236776 AA852985	Hs.79078 Hs.89232	MAD2 (mitotic arrest deficient, yeast, h chromobox homolog 5 (Drosophila HP1 alph	4.4
	435202	AI971313	Hs.170204	KIAA0551 protein	4.4
	437496	AA452378	Hs.170144	Homo sapiens mRNA; cDNA DKFZp547J125 (fr	4.4
60	451254	AI571016	Hs.172967	ESTs ESTs	4.4 4.4
00	439039 439979	AI656707 AW600291	Hs.48713 Hs.6823	hypothetical protein FLJ 10430	4.4
	441607	NM_005010	Hs.7912	neuronal cell adhesion molecule	4.4
	424983	A1742434	Hs.169911		4.4 4.4
65	410611 402605	AW954134	Hs.20924	KIAA1628 protein	4.4
05	409248	AB033035	Hs.51965	KIAA1209 protein	4.4
	442222	AI061301	Hs.164773		4.4
	454027	R40192	Hs.21527	Human DNA sequence from clone GS1-115M3 ESTs, Moderately similar to HK61_HUMAN H	4.4 4.4
70	454293 442832	H49739 AW206560	Hs.134013 Hs.253569		4.4
	407304	AA565832		gb:nj32b03.s1 NCI_CGAP_AA1 Homo sapiens	4.4
	423279	AW959861	Hs.290943		4.3 4.3
	427194 419723	AA399018 AL120193	Hs.250835 Hs.92614	ESTs longevity assurance (LAG1, S. carevisiae	4.3
75	445810	AW265700	Hs.155660		4.3
. =	409734	BE161664	Hs.56155	hypothetical protein	4.3
	410389	AW954049	Hs.8177	ESTs, Weakly similar to PIHU86 salivary	4.3 4.3
	411571 433024	AA122393 AA573847	Hs.70811 Hs.26549	hypothetical protein FLJ20516 KIAA1708 protein	4.3
80	453202	AW085781	Hs.26270	hypothetical protein FLJ11588	4.3
	425264	AA353953	Hs.20369	ESTs, Wealthy similar to gonadotropin ind	4.3 4.3
	416427 431789	BE244050 H19500	Hs.79307 Hs.269222	Rac/Cdc42 guanine exchange factor (GEF) mitogen-activated protein kinase 4	4.3
	-01103	11.5000	1 1000000		

				ov	4.3
				STs ypothetical protein FLJ20093	4.3
				U3A protein	4.3
_	425256	BE297611	Hs.155392 c	ollapsin response mediator protein 1	4.3 4.2
5	410358			ST's, Weakly similar to unnamed protein CGI-49 protein	4.2
	430291 433597			STs	4.2
	444127	N63620	Hs.13281 1	STs	4.2 4.2
10	448507			Homo sapiens mRNA; cDNA DKFZp566N1047 (f	4.2 4.2
10	413589	AW452631 H50572	Hs.313803 Hs.19515	ESTs, Highly similar to AF157833 1 noncl ESTs, Highly similar to NRG3_HUMAN PRO-N	4.2
	408577 409719	AI769160	Hs.108681	Homo sapiens brain tumor associated prot	4.2
	428536	A1143139	Hs.2288	visinin-like 1	4.2 4.2
1.5	429118	H20669		ESTs, Highly similar to unnamed protein ESTs, Wealdy similar to 138022 hypotheti	4.2
15	432865 447138	AI753709 AI439112	Hs.152484 Hs.93828	ESTs, Weakly similar to 2109260A B cell	4.2
	450648	A1703366	Hs.26766	ESTs	4.2
	451459	AI797515		ESTs, Moderately similar to ALU7_HUMAN A	4.2 4.2
20	421686	AB011156	Hs.106794 Hs.13522	KIAA0584 protein ESTs, Weakly similar to 138022 hypotheti	4.2
20	452776 436421	AA194540 Al678031	Hs.122813	ESTs, Weakly similar to ZN22_HUMAN ZINC	4.2
	423858	AL137326	Hs.133483	Homo sapiens mRNA; cDNA DKFZp434B0650 (f	4.2 4.2
	434001	AW950905	Hs.3697	serine (or cysteine) proteinase inhibito	4.2 4.2
25	437380	AL359577 Al572739	Hs.112198 Hs.195471	Homo sapiens mRNA; cDNA DKFZp547M073 (fr 6-phosphofructo-2-kinase/fructose-2,6-bi	4.1
23	432328 439607	BE540565	Hs.159460	ESTs	4.1
	424028	AF055084	Hs.153692	Homo sapiens cDNA FLJ14354 fis, clone Y7	4.1 4.1
	446936	H10207	Hs.47314	ESTs calcium/calmodulin-dependent protein kin	4.1
30	424240 412446	AB023185 Al768015	Hs.143535 Hs.92127	ESTs	4.1
30	409953	AA332277	Hs.57691	cadherin 18, type 2	4.1
	416220	N49776	Hs.170994	hypothetical protein MGC10946	4.1 4.1
	419683	AA248897	Hs.48784 Hs.163835	ESTs ESTs	4.1
35	426071 428743	AW138057 AL080060	Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (fr	4.1
55	432809	AA565509	Hs.131703	ESTs	4.1 4.1
	440105	AA694010	Hs.6932	Homo sapiens clone 23809 mRNA sequence	4.1
	452039	A1922988 AB032959	Hs.172510 Hs.318584	ESTs novel C3HC4 type Zinc finger (ring finge	4.1
40	425905 457561	AA331517	Hs.286055	chimerin (chimaerin) 2	4.1
10	429038	AL023513	Hs.194766	seizure related gene 6 (mouse)-like	4.1 4.1
	433932	AW954599	Hs.169330	neuronal protein ESTs	4,1
	436637 439231	Al783629 AW581935	Hs.26766 Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	4.1
45	450530	NM_006668	Hs.25121	cytochrome P450, subfamily 46 (cholester	4.1
	407721	Y12735	Hs.38018	dual-specificity tyrosine-(Y)-phosphoryl	4.1 4.1
	407881	AW072003	Hs.40968 Hs.69233	heparan sulfate (glucosamine) 3-0-sulfot zinc finger protein	4.0
	410486 413916	AW235094 N49813	Hs.75615	apolipoprotein C-II	4.0
50	438703	Al803373	Hs.31599	ESTs	4.0 4.0
	424726	AK001007	Hs.138760	Homo sapiens cDNA FLJ10145 fis, clone HE	4.0
	405771 418841	NM_002332	Hs.89137	low density lipoprotein-related protein	4.0
	421764	Al681535	Hs.148135	serine/threonine kinase 33	4.0
55	424176	AL137273	Hs.142307		4.0 4.0
	425773	N21279	Hs.237749 Hs.163853		4.0
	427304 428882		Hs.131748		4.0
	452834	A1638627	Hs.105685	KIAA1688 protein	4.0 4.0
60	453745	1100001	Hs.63908	hypothetical protein MGC14726 oxidative 3 alpha hydroxysteroid dehydro	4.0
	405239 413801		Hs.11958 Hs.35406	FSTs. Highly similar to unnamed protein	4.0
	429698		Hs.26339	ESTs, Weakly similar to S21348 probable	4.0 4.0
	435854		Hs.4996	putative ankyrin-repeat containing prote	4.0
65	439199		Hs.26299 Hs.12530	ESTs I ESTs	4.0
	439450 446782		Hs.14400	S ESTs	4.0
	419687		Hs.22769	ESTs, Weakly similar to T2D3_HUMAN TRANS	3.9 3.9
70	40240		Hs.10737	5 ESTs	3.9
70	45336: 41421:		Hs.75823		3.9
	42057		Hs.99034	GTP-binding protein Rho7	3.9
	42501	0 T16837	Hs.4241	ESTs	3.9 3.9
75	44423		Hs.14606 9 Hs.16979		3.9
13	44173 41895		Hs.89508		3.9
	40631	1			3.9 3.9
	40846				3.9
80	41065 41469			synuclein, alpha (non A4 component of am	3.9
	41884	19 AW47454	7 Hs.5356	Homo sapiens PIG-M mRNA for mannosyltran	3.9 3.9
	42947			ESTS 59 ESTS .	3.9
	43376	6 AA60923	4 Hs.1126	59 ESTs .	

	436190	AK001059 ·		gb:Homo sapiens cDNA FLJ10197 fis, clone	39
	447891 450221	R41754 AA328102	Hs.6496 Hs.24641	ESTs cytoskeleton associated protein 2	3.9 3.9
-	404283	NACOTOL	110.27071	oj walaan aaaaa ka aa	3.9
5	453919	AW959912	Hs.7076	KIAA1705 protein	3.9 3.9
	429656 412754	X05608 AW160375	Hs.211584 Hs.74565	neurofilament, light polypeptide (68kD) amyloid beta (A4) precursor-like protein	3.9
	445314	A1689948	Hs.65489	Homo sapiens cDNA: FLJ21517 fis, clone C	3.9
10	435652	N32388	Hs.334370	uncharacterized hypothalamus protein HBE	3.9 3.9
10	407378 438054	AA299264 AA776626	Hs.57776 Hs.62183	ESTs, Moderately similar to I38022 hypot ESTs	3.9
	436420	AA443966	Hs.31595	ESTs	3.9
	445133	AW157646	Hs.153506	ESTs	3.9 3.9
15	432590 453331	A1609273 A1240665	Hs.110783 Hs.8895	ESTs ESTs	3.9
	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	3.8
	424635	AA420687	Hs.115455	Homo sapiens cDNA FLJ14259 fis, clone PL amyloid beta (A4) precursor protein-bind	3.8 3.8
	451489 447247	NM_005503 AW369351	Hs.26468 Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	3.8
20	448302	AI480208	Hs.182906	Homo sapiens mRNA for KIAA1872 protein,	3.8
	415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito	3.8 3.8
	417355 446727	D13168 AB011095	Hs.82002 Hs.16032	endothelin receptor type B KIAA0523 protein	3.8
25	424340	AA339036	Hs.7033	ESTs	3.8
25	423346	AJ267677	Hs.127416	synaptojanin 1 ESTs	3.8 3.8
	412788 404593	AA120960	Hs.198416	2018	3.8
	416856	N27B33	Hs.269028	ESTs, Wealdy similar to 138022 hypotheti	3.8
30	429896	AA460367	Hs.224223 Hs.58595	ESTs, Moderately similar to 138022 hypot ESTs, Wealdy similar to 138022 hypotheti	3.8 3.8
30	439619 439634	AW975998 W79377	Hs.167	microtubule-associated protein 2	3.8
	440322	AA879430		gb:of91d08.s1 Soares_NFL_T_GBC_S1 Homo s	3.8
	447761	AF061573	Hs.19492	protocadherin 8 gb:QV-BT009-101198-051 BT009 Homo sapien	· 3.8 3.8
35	452453 439671	AI902519 AW162840	Hs.6641	kinesin family member 5C	3.8
50	447937	AL109716	Hs.20034	Homo sapiens mRNA full length insert cDN	3.8
	459278	AW294659	Hs.34054 Hs.167257	Homo sapiens cDNA: FLJ22488 fis, clone H brain link protein-1	3.8 3.8
	447028 449458	AI973128 AI805078	Hs.208261	ESTs	3.8
40	445888	AF070564	Hs.13415	Homo sapiens clone 24571 mRNA sequence	3.8
	407385	AA610150	Hs.272072 Hs.104935	ESTs, Weakly similar to 138022 hypotheti ESTs	3.8 3.8
	428841 430643	Al418430 AW970065	Hs.287425	MEGF10 protein	3.8
4.5	422263	AA307639	Hs.129908	KIAA0591 protein	3.8 3.8
45	451625 439236	R56793 BE160952	Hs.106576 Hs.247117	atanine-glyoxylate aminotransferase 2-li ESTs, Moderately similar to ALUF_HUMAN !	3.8
	441928	Al370188	Hs.211454	ESTs	3.8
	441797	AI936933	Hs.214635	ESTs	3.7 3.7
50	414922 425588	D00723 F07396	Hs.77631 Hs.46751	glycine cleavage system protein H (amino ESTs	3.7
50	437007	AA741300	Hs.202599		3.7
	435793	AB037734	Hs.4993	KIAA1313 protein	3.7 3.7
	443682 425741	AI383061 AF052152	Hs.47248 Hs.159412	ESTs, Highly similar to similar to Cdc14 Homo sapiens clone 24628 mRNA sequence	3.7
55	418211	BE244746	Hs.247474	hypothetical protein FLJ21032	3.7
	440080	AW051597	Hs.143707	ESTs ESTs	3.7 3.7
	452898 435575	AA814497 AF213457	Hs.78792 Hs.44234	triggering receptor expressed on myeloid	3.7
	409234	AI879419	Hs.27206	ESTs	3.7
60	420489	AA815089	Hs.193513 Hs.41294	ESTs ESTs	3.7 3.7
	426890 438849	AA393167 W28948	Hs.10762	ESTs	3.7
	441869	NM_003947	Hs.8004	huntingtin-associated protein interactin	3.7
65	448796 459318	AA147829 NM_000038	Hs.301431	endothelial zinc finger protein Induced ab:Homo sapiens adenomatosis polyposis c	3.7 3.7
05	459518	Al937419	Hs.294069	· · · · · · · · · · · · · · · · · · ·	3.7
	434444	AI765276	Hs.101257		3.7 3.7
	421183 410555	AL135740 U92649	Hs.102447 Hs.64311	TSC-22-like a disintegrin and metalloproteinase doma	3.7
70	421637	AF035290	Hs.106300	Homo sapiens clone 23556 mRNA sequence	3.7
	418522	AA605038	Hs.7149	Homo saplens cDNA: FLJ21950 fis, clone H	3.7 3.7
	420807 449961	AA280627 AW265634	Hs.57846 Hs.13310		3.7
	422634	NM_016010	Hs.11882	I CGI-62 protein	3.7
75	421030		Hs.101174		3.7 3.7
	427099 452355		Hs.17356 Hs.29202		3.7
	440483	AI200836	Hs.15038	6 ESTs	3.7
80	429597		Hs.2442	a disintegrin and metalloproteinase doma gb:od71a09.s1 NCI_CGAP_Ov2 Homo sapiens	3.7 3.6
OV.	423756 425187		Hs.22509	ESTs .	3.6
	434859	BE255080	Hs.29931	5 collapsin response mediator protein-5; C	3.6 3.6
	413199	M52843	Hs.75236	ÉLAV (embryonic lethal, abnormal vision,	3.6

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					Days C M Locath Lacard a DM	3.6
		H21066	Hs.13223	Homo abreo1	sapiens mRNA full length insert cDN 4h02.s1 Soares adult brain N2b5HB5	3.6
		H46739 AA448419	Hs.45209	ESTs		3.6 3.6
_	419086	NM_000216	Hs.89591	Kallma ESTs	nn syndrome 1 sequence	3.6
5	446659	Al335361 AW205640	Hs.226376 Hs.158206	ESTs		3.6
	426757 418819	AA228776	Hs.191721	ESTs	•	3.6 3.6
	458332	A1000341	Hs.220491	ESTs	sapiens clone HB-2 mRNA sequence	3.6
10	408826 410343	AF216077 AA084273	Hs.48376 Hs.76561	ESTs	Weakly similar to S47072 finger pr	3.6 3.6
10	410507	AA355288	Hs.40834	transi	ional epithelia response protein	3.6
	422977	AA631498	Hs.155572	Hum	83h04.s1 NCI_CGAP_Thy1 Homo saplens in clone 23801 mRNA sequence	3.6
	425305 428002	AA363025 AA418703	RS. 100072	qb:zv	98c03.s1 Soares_NhHMPu_S1 Homo sapi	3.6 3.6
15	428505	AL035461	Hs.2281		nogranin B (secretogranin 1)	3.6
	430530	AA480870	Hs.47660 Hs.318725	EST	rz protein	3.6
	436425 438078	AI913146 AI016377	Hs.131693	EST:		3.6 3.6
	442927	A1024347	Hs.131519	EST		3.6
20	446242	N66336 Al080123	Hs.7360 Hs.22182		finger protein 23 (KOX 16)	3.6
	448831 450474	AW872844	Hs.201919	FST		3.6 3.6
	452198	A1097560	Hs.61210	EST	s, Weakly similar to 138022 hypotheti o sapiens cDNA FLJ13047 fis, clone NT	3.6
25	455800 436443	R22479 AW138211	Hs.167073 Hs.128746	EST	S	3.6
23	426514	BE616633	Hs.170195	bon	e morphogenetic protein 7 (osteogenic	3.6 3.6
	456038	AA203285	Hs.294141 Hs.5510	EST	s, Weakly similar to alternatively sp	3.6
	408902 442950	AW014869 Al500417	Hs.46764	EST	'g	3.6 3.6
30	423905	AW579960	Hs.135150		type-I cell membrane-associated gly	3.6
	425478	AB007953	Hs.268840 Hs.36232		s A0186 gene product	3.6
	453884 404721	AA355925	H\$.JUZJZ			3.6 3.6
	408453	AI369838	Hs.45127		ndroitin sulfate proteoglycan 5 (neur no sapiens cDNA FLJ 14459 fis, clone HE	3.5
35	440553	AA889416	Hs.29536 Hs.14945	2 Ho	g fatty acyt-CoA synthetase 2 gene	3.5
	446372 413999	AB020644 N46124	Hs.34460	ES	Ts	3.5 3.5
	421458	NM_003654			bohydrate (keratan sulfate Gal-6) sul	3.5
40	425017	AL119305 H98180	Hs.28840 Hs.11797			3.5
40	435958 415101	R45531	Hs.14453	4 ES	iTs	3.5 3.5
	451320	AW118072			ncylglycerol kinase, zeta (104kD) STs	3.5
	430290 416836	A1734110 D54745	Hs.13635 Hs.80247		olecystokinin	3.5
45	414821	M63835	Hs.7742	4 Fo	fragment of IgG, high affinity la, re	3.5 3.5
	419412			7 sy na ⊔	nuclein, beta omo sapiens cDNA: FLJ23165 fis, clone L	3.5
	437860 452689		Hs.2841		ensferrin	3.5 3.5
	416661			_	F-II mRNA-binding protein 3	3.5
50	427491		Hs.2257 Hs.8923	iń n	STs, Weakly similar to 138022 hypotheti otassium intermediate/small conductance	3.5
	428037 444584		113.0320	g	b:ok30e11.x1 Soares_NSF_F8_9W_OT_PA_P_S	3.5 3.5
	40829	AL117452		55 C	KFZP586G1517 protein aplication factor C (activator 1) 4 (37	3.5
55	453779 41265			76 d	lfactomedin related ER localized protei	3.5
))	42907		3 Hs.2352	2 8	denylate cyclase 2 (brain)	3.5 3.5
	43688	7 AW95315			ypothetical protein DKFZp547D155 SSTs	3.5
	45078 44682				STs	3.5 3.5
60	43643	4 N50465	Hs.929	27	outative 47 kDa protein	3.5
	41277				ESTS bHLH protein DEC2	3.5
	43647 40860		Hs.861	22	omtein A	3.4 3.4
	42940	1 AW2961			ESTs, Weakly similar to S32567 A4 protei	3.4
65	44842 41873				ESTs ESTs	3.4
	4517		25 Hs.312	2469	ESTS	3.4 3.4
	4359	10 Al08415			ESTs, Weakly similar to ALU7_HUMAN ALU S Homo sapiens cONA: FLJ22487 fis, clone H	3.4
70	4345) 4145				king type-i cell membrane-associated gly	3.4
, ,	4396		02 Hs.29	076	hynothetical protein FLJ21841	3.4 3.4
	4132	93 AL0474			GTP-binding protein homologous to Saccha Homo sapiens mRNA; cDNA DKFZp564H1663 (f	3.4
	4239 4262		.		nucleoporin-like protein 1	3.4 3.4
7:	5 4269	68 U07616	Hs.17	3034	amphiphysin (Stiff-Mann syndrome with br nuclear cap binding protein subunit 2, 2	3.4
	4303			10770 33944	FSTs	3.4
	4350 452				COC7 (cell division cycle 7, S. cerevisi	3.4 3.4
_	449	714 AB033	015 Hs.23		KIAA1189 protein ESTs	3.4
8				93420 58311	Musashi (Drosophila) homolog 1	3.4
		337 NM_01	3280 Hs.1	2523	filmnectin leucine rich transmembrane p	3.4 3.4
		493 BE206	854 Hs.4	6039	phosphoglycerate mutase 2 (muscle)	3.7
					165	

	432731	R31178	Hs.287820	Shannoolin 1	3.4
	448758	AB018311	Hs.21917	fibronectin 1 KIAA0768 protein	3.4
	432613	AW081698	Hs.80712	KIAA0202 protein	3.4
_	434164	AW207019	Hs.148135	serine/threonine kinase 33	3.4
5	425294	AF033827	Hs.155553	HNK-1 sulfotransferase	3.4
	410108 406815	AA081659 AA833930	Hs.318775 Hs.288036	OSBP-related protein 6 tRNA isopentenylpyrophosphate transferas	3.4 3.4
	402855			u a cooperació por opriospriosa a silvación co	3.3
10	422170	AI791949	Hs.112432	anti-Mullerian hormone	3.3
10	445034 -	AW293376	Hs.143659	ESTs	3.3
	424378 423611	W28020 AB011163	Hs.167988 Hs.129908	neural cell adhesion molecule 1 KIAA0591 protein	3.3 3.3
	435593	R88872	Hs.4964	DKFZP586J1624 protein	3.3
1.5	404819			·	3.3
15	436607	AW661783	Hs.211061	ESTs	3.3
	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	3.3
	452693 454996	T79153 AW850180	Hs.48589	zinc finger protein 228 gb:lL3-CT0219-271099-022-C09 CT0219 Homo	3.3 3.3
	406927	M26460		gb:Homo saplens (clone 104) retinoblasto	3.3
20	409045	AA635062	Hs.50094	Homo sapiens mRNA; cDNA DKFZp43400515 (f	· 3.3
	415238	R37780	Hs.21422	ESTs	3.3
	417845 421192	AL117461 AA833718	Hs.82719 Hs.204529	Homo saplens mRNA; cDNA DKFZp586F1822 (f	3.3 3.3
	426695	AW118191	Hs.112729	KIAA1806 protein ESTs	3.3 3.3
25	438885	A1886558	Hs.184987	ESTs	3.3
	451762	AF222980	Hs.26985	disrupted in schizophrenia 1	3.3
	452103	R42764	Hs.339654	ESTs, Weakly similar to I38022 hypotheti	3.3
	453590 453616	AF150278 NM_003462	Hs.33578 Hs.33846	KIAA0820 protein dynein, exonemal, light intermediate pol	3.3 3.3
30	457285	AI038858	Hs.130522	Ky channel-interacting protein 1	3.3
-	436045	AB037723	Hs.5028	DKFZP564O0423 protein	3.3
	437470	AL390147	Hs.134742	hypothetical prolein DKFZp547D065	3.3
	448520	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	3.3 3.3
35	436480 432656	AJ271643 NM_000246	Hs.87469 Hs.3076	putative acid-sensing ion channel MHC class II transactivator	3.3 3.3
55	443898	AW804296	Hs.9950	Sec61 gamma	3.3
	423582	BE000831	Hs.23837	Homo sapiens cDNA FLJ11812 fis, clone HE	3.3
	445953	Al612775	Hs.145710	ESTs	3.3
40	427940	AA417812	Hs.38775	ESTs	3.3 3.3
40	414683 428484	\$78296 AF104032	Hs.76888 Hs.184601	hypothetical protein MGC12702 solute carrier family 7 (cationic amino	3.3
	420649	A1866964	Hs.124704	ESTs, Moderately similar to S65657 alpha	3.3
	419498	AL036591	Hs.20887	hypothetical protein FLJ10392	3.3
15	457579	AB030816	Hs.36761	HRAS-like suppressor	3.3
45	436556 424369	AI364997	Hs.7572 Hs.26714	ESTs KIAA1831 protein	3.2 3.2
	457065	R87622 AI476318	Hs.192480	ESTs	3.2
	440210	AW674562	Hs.125296	ESTs	3.2
50	444513	AL120214	Hs.7117	glutamate receptor, lonotropic, AMPA 1	3.2
50	434353	AA630863	Hs.131375	ESTs, Moderately similar to ALUB_HUMAN !	3.2 3.2
	414430 439924	A)346201 A)985897	Hs.76118 Hs.125293	ubiquilin carboxyl-terminal esterase L1 ESTs	3.2
	411505	AF155659	Hs.70565	molybdenum cofactor synthesis 2	3.2
<i></i>	423175	W27595	Hs.18653	hypothetical protein FLJ14627	3.2
55	415115	AA214228	Hs.127751	hypothetical protein	3.2
	407878 410274	D87468 AA381807	Hs.40888 Hs.61762	activity-regulated cytoskeleton-associat hypoxia-inducible protein 2	3.2 3.2
	437762	178028	Hs.154679	synaptotagmin I	3.2
60	438944	AA302517	Hs.92732	KIAA1444 protein	3.2
60	450313	Al038989	Hs.332633	Bardet-Biedi syndrome 2	3.2
	409459 410953	D86407 AW811766	Hs.54481 Hs.334858	low density lipoprotein receptor-related hypothetical protein MGC12250	3.2 3.2
	418527	AA450386	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	3.2
	420081	AW510776	Hs.94958	tubulin tyrosine ligase-like 1	3.2
65	429496	AA453800	Hs.192793	ESTs	3.2
	430099 434928	AW194988 AW015595	Hs.20537 Hs.4267	hypothetical protein FLJ13942 Homo sapiens clones 24714 and 24715 mRNA	3.2 3.2
	435532	AW291488	Hs.117305	Homo sepiens, clone IMAGE:3682908, mRNA	3.2
	438306	AW188266	Hs.163645	ESTs	3.2
70	439274	AF086092	Hs.48372	ESTs	3.2
	440847	AA907511	Hs.130178	ESTs	3.2
	447750 455350	AJ422234 AW901809	Hs.143434	contactin 1 qb:QV0-NN1020-170400-195-h02 NN1020 Homo	3.2 3.2
	430890	X54232	Hs.2699	glypican 1	3.2
75	420568	F09247	Hs.247735	protocadherin alpha 10	3.2
	410768	AF038185	Hs.66187	Homo sapiens clone 23700 mRNA sequence	3.2
	427450 430456	AB014526 AA314998	Hs.178121 Hs.241503	KIAA0626 gene product hypothetical protein	3.2 3.2
	430181	AF065314	Hs.234785		3.2
80	418512	AW498974	Hs.89981	diacytytycerol kinase, zeta (104kD)	3.2
	419912	AF249745	Hs.6066	Rho guarine nucleotide exchange factor (3.2
	450689 424899	Al369275 Al119387	Hs.243010 Hs.119062		3.2 3.2
	747033	AL 13307	110.113002	Loro	3.2

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	436277			ESTs	3.2 3.2
	451455 445078	A1937227 A1869975		hepcidin antimicrobial peptide junctophilin 3	3.2
_	447746	AW015920	Hs.161359	ESTs	3.2
5	435458	F11872		Homo saplens clone 24841 mRNA sequence	3.2 3.2
	427729 417417	AB033100 F05745	Hs.300646 Hs.89512	KIAA protein (similar to mouse paladin) ATPase, Ca↔ transporting, plasma membra	3.1
	438810	AW897846	Hs.6421	hypothetical protein DKFZp761N09121	3.1
10	439570	179925	Hs.269165	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.1 3.1
10	432527 416801	AW975028 X98834	Hs.102754 Hs.79971	ESTs sal (Drosophila)-like 2	3.1
	421988	AW450481	Hs.161333	ESTs	3.1
	426509	M31166	Hs.2050	pentaxin-related gene, rapidly induced b	3.1
15	408786	AA773187	Hs.294027	ESTS	3.1 3.1
13	433494 412723	AB029396 AA648459	Hs.3353 Hs.335951	beta-1,3-glucuronyltransferase 1 (glucur hypothetical protein AF301222	3.1
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	3.1
	439456	AI752409	Hs.109314	hypothetical protein FLJ20980	3.1 3.1
20	428832 452780	AA578229 BE171598	Hs.324239 Hs.13522	ESTs, Moderately similar to ZN91_HUMAN Z ESTs, Weakly similar to I38022 hypotheti	3.1
20	438192	AI859065	Hs.337620	Homo sapiens AFG3L1 isoform 1 mRNA, part	3.1
	424939	AK000059	Hs.153881	Homo sapiens NY-REN-62 antigen mRNA, par	3.1
	403053	R58624	Hs.2186	eukaryotic translation elongation factor	3.1 3.1
25	404299 407864	AF069291	Hs.40539	chromosome 8 open reading frame 1	3.1
	410181	AI46B210	Hs.261285	pleiotropic regulator 1 (PRL1, Arabidops	3.1
	418852	BE537037	Hs.273294	hypothetical protein FLJ20069	3.1 3.1
	449101 453240	AA205847 A1969564	Hs.23016 Hs.166254	G protein-coupled receptor hypothetical protein DKFZp5661133	3.1
30	440486	BE243513	Hs.7212	hypothetical protein PP1044	3.1
	408096	BE250162	Hs.83765	dihydrofolate reductase	3.1 3.1
	439864 414706	AI720078 AW340125	Hs.291997 Hs.76989	ESTs, Weakly similar to A47582 B-cell gr KIAA0097 gene product	3.1
	436315	BE390513	Hs.27935	hypothetical protein MGC4837	3.1
35	426855	AL117427	Hs.172778	Homo sapiens mRNA; cDNA DKFZp566P013 (fr	3.1
	425683	AB037813	Hs.159200 Hs.169387	hypothetical protein DKFZp762K222 KIAA0036 gene product	3.1 3.1
	410126 435312	BE169274 AJ243396	Hs.4865	voltage-gated sodium channel beta-3 subu	3.1
40	425491	AA883316	Hs.255221	ESTS	3.1
40	456273	AF154846	Hs.1148	zinc finger protein	3.1 3.1
	412140 445255	AA219691 NM_014841	Hs.73625 Hs.12477	RAB6 interacting, kinesin-like (rabkines synaptosomal-associated protein, 91 kDa	3.1
	432154	AJ701523	Hs.112577	ESTs	3.1
15	453128	AW026516	Hs.31791	acylphosphatase 2, muscle type	3.1 3.1
45	438458 448616	AW975186 AF035621	Hs.21611	gb:EST387294 MAGE resequences, MAGN Homo kinesin family member 3C	3.0
	429281	AA830856	Hs.29808	Homo saplens cDNA: FLJ21122 fis, clone C	- 3.0
	443906	AA348031	Hs.7913	ESTs	3.0 3.0
50	417318 452619	AW953937 AW298597	Hs.12891 Hs.61884	ESTs Homo sapiens, clone IMAGE:4298026, mRNA,	3.0
50	444153	AK001610	Hs.10414	hypothetical protein FLJ10748	3.0
	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	3.0
	426327	W03242	Hs.44898 Hs.293663	Homo sapiens clone TCCCTA00151 mRNA sequ ESTs, Moderately similar to 138022 hypot	3.0 3.0
55	451468 422758	AW503398 AF152329	Hs.284180		3.0
	421633	AF121860	Hs.106260		3.0
	428361	NM_015905		transcriptional intermediary factor 1 cadherin 4, type 1, R-cadherin (retinal)	3.0 3.0
	418932 416805	L34059 F13271	Hs.89484 Hs.79981	Human clone 23560 mRNA sequence	3.0
60	419518	U79289	Hs.90798	Human clone 23695 mRNA sequence	3.0
	422709	AA315331	Hs.153485		3.0 3.0
	423135 424901	N67655 Z11933	Hs.26411 Hs.182505	ESTs POU domain, class 3, transcription facto	3.0
	426617	W58006	Hs.266258	endonuclease G-like 1	3.0
65	427386	AW836261	Hs.337717		3.0 3.0
	429859 435071	NM_007050 D60683	Hs.225952 Hs.35495	protein tyrosine phosphatase, receptor t ESTs	3.0
	435092	AL137310	Hs.4749	Homo sapiens mRNA; cDNA DKFZp761E13121 (3.0
70	436211	AK001581	Hs.334828		3.0 3.0
70	436936 445855	AL134451 BE247129	Hs.197478 Hs.145569		3.0
	452294		Hs.11789	5 ESTs, Moderately similar to A47582 B-cel	3.0
	433980	AA137152	Hs.286049	phosphoserine aminotransferase	3.0
75	430228		Hs.6382 Hs.157493	ESTs, Highly similar to T00391 hypotheti cer-d4 (mouse) homolog	3.0 3.0
13	451026 435232			cyclin-dependent kinase inhibitor 2C (p1	3.0
	439566	AF086387		gb:Homo sapiens full length insert cDNA	3.0
	425782		Hs.15952: Hs.14144		3.0 3.0
80	416586 416874		Hs.42568	ESTs	3.0
	410388	W26187	Hs.3327	Homo sapiens cDNA: FLJ22219 fis, clone H	3.0
	411411		Hs.55950 Hs.11246		3.0 3.0
	424066	Z99348	110.11240	Early Moon) animal wiscone in position	

	404048	4 4 DO #700		-t00-40-4 Comm NG. 7 000 04 Nove -	3.0
	429163 454117	AA884766 BE410100	Hs.40368	gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s adaptor-related protein complex 1, sigma	3.0 3.0
	418196	AI745649	Hs.26549	KIAA1708 protein	3.0
5	434131	Al858275	Hs.143659	ESTs	3.0
•	441255	R06350	Hs.171635	ESTs	29
	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU S	29
	453905	NM_002314	Hs.36566	LIM domain kinase 1	29
• •	416602	NM_006159	Hs.79389	nel (chicken)-like 2	2.9
10	431173	AW971198	Hs.294068	ESTs	2.9
	425599	AW366745	Hs.214140	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.9
	436401	A1087958	Hs.29088	ESTS	2.9
	422960	AW890487	Hs.63984	cadherin 13, H-cadherin (heart)	2.9
15	451558 412490	NM_001089 AW803564	Hs.26630 Hs.288850	ATP-binding cassette, sub-family A (ABC1	2.9 2.9
15	433149	8E257672	Hs.42949	Homo saplens cDNA: FLJ22528 fis, clone H hypothetical protein HES6	2.9 2.9
	434811	AW971205	Hs.114280	ESTs	2.9
	425897	AA935315	Hs.48965	Homo sepiens cDNA: FLJ21693 fis, clone C	29
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	2.9
20	453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	2.9
	411124	AW196937	Hs.53929	ESTs, Weakly similar to ALUB_HUMAN IIII	2.9
	419227	BE537383	Hs.89739	cholinergic receptor, nicotinic, beta po	2.9
	427651	AW405731	Hs.18498	Homo sapiens cDNA FLJ12277 fis, clone MA	2.9
25	441707	R42637	Hs.21963	hypothetical protein DKFZp76180514	2.9
25	435741	AI240668	Hs.113099	ESTs	2.9
	437273	AL137451	Hs.120873	ESTs, Highly similar to T46266 hypotheti	2.9
	422939 439376	AW394055 AA883521	Hs.98427 Hs.222064	ESTs, Weakly similar to I38022 hypotheti ESTs	2.9 2.9
	439935	875105	Hs.301676	glutamate receptor, ionotropic, kainate	2.9
30	437267	AW511443	Hs.258110	ESTs	2.9
50	453740	AL120295	Hs.311809	ESTs, Moderately similar to PC4259 femi	2.9
	400250				2.9
	400992				2.9
	408814	N62499	Hs.176227	hypothetical protein FLJ11155	29
35	411849	AW964970	Hs.18861	ESTs, Moderately similar to KiAA1276 pro	2.9
	414853	U31116	Hs.77501	sarcoglycan, beta (43kD dystrophin-assoc	2.9
	423751	AW235633	Hs.46525	ESTs	2.9
	426910	AA470023	Hs.190089	ESTs, Moderately similar to ALU1_HUMAN A	2.9
40	450203	AF097994	Hs.301528	L-kynurenine/alpha-aminoadipate aminotra	2.9 2.9
40	459311 425304	R40192 AA463844	Hs.21527 Hs.31339	Human DNA sequence from clone GS1-115M3	2.9
	428500	AI815395	Hs.184641	fibroblast growth factor 11 fatty acid desaturase 2	2.9
	421641	A1638184	Hs.106334	Homo sapiens clone 23836 mRNA sequence	2.9
	421141	AW117261	Hs.125914	ESTs	29
45	407870	AB032990	Hs.40719	hypothetical protein KIAA1164	2.9
	456723	Z43902	Hs.4748	adenylate cyclase activating polypeptide	2.9
	436456	AW292677	Hs.248122	G protein-coupled receptor 24	2.9
	421483	NM_003388	Hs.104717	hypothetical protein MGC11333	2.9
50	412190	R16180	Hs.274461	ESTs	2.9
50	446131	NM_000929	Hs.290	phospholipase A2, group V	2.9
	441668	AI611973	Hs.127525	ESTs	2.9 2.9
	437387 423420	Al198874 Al571364	Hs,28847 Hs,128382	AD026 protein Homo sapiens mRNA; cDNA DKFZp76111224 (f	2.9
	427958	AA418000	Hs.98280	potassium intermediate/small conductance	2.9
55	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	2.9
	447067	R42098	Hs.21964	ESTs	2.9
	430887	N66801	Hs.260287	KIAA1841 protein	2.9
	441824	AB007871	Hs.7977	KIAA0411 gene product	2.9
60	424126	AA335635	Hs.96917	ESTs	2.9
60	408739	W01556	Hs.238797	ESTs, Moderately similar to I38022 hypot	29
	447422	BE618703	Hs.98258	orthopedia (Drosphila) homolog	29
	435615	Y15065	Hs.4975	potassium voltage-gated channet, KQT-lik	29 29
	446997 433573	AA383439 AF234887	Hs.16758 Hs.57652	Sgir-1 protein cadherin, EGF LAG seven-pass G-type rece	2.9
65	408447	AK002089	Hs.45080	Homo sapiens cDNA FLJ11227 fls, clone PL	2.9
U	419586	AI088485	Hs.144759	ESTs, Wealdy similar to I38022 hypotheti	2.8
	417022	NM_014737	Hs.80905	Res association (RalGDS/AF-6) domain fam	2.8
	408432	AW195262		gb:xn67b05.x1 NC1_CGAP_CML1 Homo sapiens	2.8
	420320	AB002361	Hs.96633	KIAA0363 protein	2.8
70	425241	AA324624	Hs.155247	aldolase C, fructose-bisphosphate	2.8
	428670	AA431682	Hs.134832		2.8
	424415	NM_001975	Hs.146580		2.8
	409185	AW961601	Hs.252406		2.8
75	411555	AF113537	Hs.70669	HMP19 protein 5. hydroxytymine (serotonia) recentor	2.8 2.8
, 5	426847 458809	S78723 AW972512	Hs.298623 Hs.20985	5-hydroxytryptamine (serotonin) receptor sin3-associated polypeptide, 30kD	2.8
	420071	AB028985	Hs.94806	ATP-binding cassette, sub-family A (ABC1	2.8
	424572	M19650	Hs.150741		2.8
	444670	H58373	Hs.332938		2.8
80	411089	AA456454	Hs.183418		2.8
	416111	E18EE0AA	Hs.79018	chromatin assembly factor 1, subunit A (2.8
	440637	AW900115	Hs.7309	Homo sapiens clone 23741 mRNA sequence	2.8
	408554	AA836381	Hs.315111	nuclear receptor co-repressor/HDAC3 comp	2.8

					2.8
				ukaryotic translation elongation factor ESTs	2.8
			Hs.142634 z	tinc finger protein	2.8
_	429006			sypothetical protein FLJ13842	2.8 2.8
5	434981			ESTs hypothetical protein DKFZp762H1311	2.8
	437435 442748			ESTs	2.8
	443312	N52025	Hs.46616	ESTs	2.8 2.8
10	450940			ESTs, Wealdy similar to I38022 hypotheti	2.8
10	452738			hypothetical protein MGC12435 ESTs	2.8
	409182 439793	AA018825		Kruppel-like factor 4 (guf)	2.8
	432683	AW995441		ESTs	2.8 2.8
1.5	434269	AK001991	Hs.3781	similar to murine leucine-rich repeat pr hexabrachion (tenascin C, cytotactin)	2.8
15	429500	X78565 R20077	Hs.289114 Hs.302185	Homo saplens clone 23618 mRNA sequence	2.8
	433290 434276	AF123659	Hs.93605	leucine zipper, putative lumor suppresso	2.8
	435977	AL138079	Hs.5012	brain-specific membrane-anchored protein	2.8 2.8
20	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4 gb:yq37d04.s1 Soares fetal liver spieen	28
20	425168 428180	R96366 Al129767	Hs.182874	quanine nucleotide binding protein (G pr	2.8
	409348	Al401535	Hs.146090	ESTs	2.8
	409887	AL137534	Hs.56876	Homo sapiens mRNA; cDNA DKFZp434H1419 (f	2.8 2.8
25	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat ESTs, Weakly similar to ALU1_HUMAN ALU S	2.8
25	430039 417642	BE253012 BE302665	Hs.153400 Hs.105461	hypothetical protein FLJ20357	2.8
	419169	AW851980	Hs.262346	ESTs, Wealdy similar to S72482 hypotheti	2.8
	434008	AA740878	Hs.112982	ESTs	2.8 2.8
20	446776	AW293417	Hs.156455 Hs.40369	ESTs ESTs	2.8
30	408838 422565	A1669535 BE259035	Hs.118400	singed (Drosophila)-like (sea urchin fas	2.8
	447397	BE247676	Hs.18442	E-1 enzyme	2.8
	412530	AA766268	Hs.266273	hypothetical protein FLI13346	2.8 2.8
25	424330	AW073953	Hs.333396 Hs.170953	Homo sapiens cDNA FLJ13596 fis, clone PL ESTs	2.8
35	446377 458924	AW014022 BE242158	Hs.24427	DKFZP566O1646 protein	2.8
	447710	Al420523	Hs.328241	ESTs	2.8 2.8
	404049			gb:RC1-DT0001-031299-011-a11 DT0001 Homo	2.8 2.8
40	416913 426400	AW934714 M78361	Hs.169743	Homo sapiens clone 25121 neuronal olfact	2.8
+0	413264	W26456	Hs.134757	hypothetical protein FLJ20033	2.8
	458997	AW937420	Hs.69662	ESTS	2.7 2.7
	422864	AA318323	11-040407	gb:EST20390 Retina II Homo sapiens cDNA G protein-coupled receptor, family C, gr	2.7
45	430526 452023	AF181862 AB032999	Hs.242407 Hs.27566	KIAA1173 protein	2.7
43	432022	AL162042	Hs.272348	Homo sapiens mRNA; cDNA DKFZp761L1212 (f	2.7
	452438	BE514230	Hs.29595	JM4 protein	2.7 2.7
	435408	H07897	Hs.4302 Hs.194628	ESTs, Weakly similar to T29299 hypotheti ESTs	2.7
50	418791 438821	AA935633 AA826425	Hs.291829	ESTs	2.7
-	423464	NM_016240		CSR1 protein	2.7 2.7
	442091	AW770493	Hs.182874	guanine nucleotide binding protein (G pr Homo sapiens cDNA: FLJ23285 fis, clone H	2.7
	442242 412436	AV647908 AA665089	Hs.90424	gb:nu76d01.s1 NCI_CGAP_Alv1 Homo sapiens	2.7
55	432821	BE170702	Hs.279005		2.7
•	416404	AA180138	Hs.107924		2.7 2.7
	441364	AW450466	Hs.126830 Hs.34145	ESTs, Weakly similar to YD38_YEAST HYPOT ESTs, Weakly similar to 849647 GTP-bindi	2.7
	450202 426304	AW969756 AA374532	Hs.124673		2.7
60	428722		Hs.190787	tissue inhibitor of metalloproteinase 4	2.7
	449701		Hs.129908		2.7 2.7
	420372 410318		Hs.293660 Hs.269259		2.7
	414603		Hs.25119	ESTs, Weakly similar to YEX0_YEAST HYPOT	2.7
65	416096		Hs.88974	cytochrome b-245, beta polypeptide (chro	2.7 2.7
	420896			Homo sapiens cDNA: FLJ22165 fis, clone H ESTs, Weakly similar to ZN43_HUMAN ZINC	2.7
	424856 436304		Hs.9521 Hs.10888		2.7
	441027		Hs.12644	4 ESTs	2.7
70	452545	N31940	Hs.14434		2.7 2.7
	454201		Hs.44131 Hs.23213	KIAA0974 protein ESTs	2.7
	448560 426807		Hs.15668	2 ESTs	2.7
	42582	5 Al929508	Hs.15959	0 tymphocyte antigen 6 complex, locus H	2.7
75	44035	1 AF030933	Hs.7179	RAD1 (S. pombe) homolog 4 protein tyrosine phosphatase, non-recept	2.7 2.7
	42539 42762		Hs.15611 Hs.24895		2.7
	42641			gb:EST90805 Synovial sarcoma Homo sapien	2.7
00	42249	1 AA338548	Hs.11754		2.7 2.7
80			Hs.15055 Hs.28901		2.7
	43241 41486				2.7
•	41582		Hs.23079		2.7

	445568	H00918	Hs.268744	KIAA1796 protein	2.7
	433315	R95754	Hs.239706	GRB2-associated binding protein 1	2.7
	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	2.7
_	447959	Al452784	Hs.270270	ESTs, Wealdy similar to 2109260A B cell	2.7
5	426420 436899	BE383808 AA764852	Hs.322430 Hs.291567	NDRG family, member 4 ESTs	2.7 2.7
	444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	27
	426501	AW043782	Hs.293616	ESTs	2.7
10	449092	U91641	Hs.22985	alpha2,8-sialyltransferase	2.7
10	427311 453313	AB020672 BE005771	Hs.175411 Hs.153746	KIAA0865 protein hypothetical protein FLJ22490	27 27
	404029	82003771	FIS. 133740	Hypothetical protest r Cazzaso	27
	416289	W26333	Hs.337438	EST ₈	27
1.5	439108	AW163034	Hs.6467	synaptogyrin 3	2.6
15	418746	A1955289	Hs.300759	ribosomai protein L36	2.6 2.6
	412046 435040	Y07847 A1932350	Hs.73088 Hs.152825	RAS-related on chromsome 22 ESTs	2.6 2.6
	453083	U87223	Hs.31622	contactin essociated protein 1	2.6
00	428167	AA770021	Hs.16332	ESTs	2.6
20	420028	AB014680	Hs.8786	carbohydrate (N-acetytglucosamine-6-O) s	2.6 2.6
	443715 421247	AI583187 BE391727	Hs.9700 Hs.102910	cyclin E1 general transcription factor IIH, polype	2.6
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	2.6
~-	415056	AB004662	Hs.77867	adenosine A1 receptor	2.6
25	451697	AW449774	Hs.296380	POM (POM121 rat homolog) and ZP3 fusion	2.6
	433701 457358	AW445023 AI479755	Hs.15155 Hs.129010	ESTs ESTs	2.6 2.6
	430347	NM_002039	Hs.239706	GRB2-associated binding protein 1	26
	418027	AB037807	Hs.83293	hypothetical protein	2.6
30	440491	R35252	Hs.24944	ESTs, Weakly similar to 2109260A B cell	2.6
	425171	AW732240	Hs.16365	ESTs	26 26
	459335 425402	AW298545 Al215881	Hs.250726 Hs.24970	EST ESTs, Weakly similar to B34323 GTP-bindi	26
	453169	AB037815	Hs.32156	KIAA1394 protein	2.6
35	433647	AA603367	Hs.222294	ESTs	2.6
	450414	A1907735	Hs.21446	KIAA1716 protein	2.6 2.6
	446233 415446	Al282028 F08898	Hs.25205 Hs.66075	ESTs ESTs	2.6 2.6
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-l	2.6
40	413012	D83777	Hs.75137	KIAA0193 gene product	2.6
	428671	BE297851	Hs.189482	zinc finger protein 179	26
	427158	AA935603	Hs.166231 Hs.49476	ESTs Horno sapiens clone TUA8 Cri-du-chat regi	2.6 2.6
	408988 459516	AL119844 Al049662	Hs.246858	EST	26
45	402693		. 4.2	 -	2.6
	408039	AA131424	Hs.50340	ESTs	2.6
	422896	AW961489	Hs.154116	ESTs	2.6 2.6
	423130 438796	AW897586 W67821	Hs.21213 Hs.109590	ESTs genethonin 1	2.6
50	439871	R88518	Hs.46736	hypothetical protein FLJ23476	2.6
	440192	AA872282	Hs.190596	ESTs	2.6
	419708	AK000753	Hs.92374 Hs.279307	hypothetical protein hypothetical protein DKFZp434l2117	2.6 2.6
	449436 436870	AA860329 AW204219	Hs.155560	calnexin	2.6
55	448424	AW009892	Hs.31924	ESTs	2.6
	401324				2.6
	414136	AAB12434	Hs.119023	SMC2 (structural maintenance of chromoso	2.6 2.6
	433943 428001	AA992805 H97428	Hs.44865 Hs.219907	lymphoid enhancer-binding factor 1 ESTs, Moderately similar to Transforming	2.6
60	429139	F09092	Hs.66087	ESTs	2.6
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	26
	448966	AW372914	Hs.86149	phospholnosital 3-phosphate-binding prot	2.6
	444001	A1095087 N53437	Hs.152299 Hs.18268	ESTs, Moderately similar to S65657 alpha adenylate kinase 5	2.6 2.6
65	412049 441783	BE313412	Hs.7961	Homo saplens clone 25012 mRNA sequence	2.6
	425287	R88249	Hs.155524	peanut (Drosophila)-like 2	2.6
-	432149	AW614326	Hs.157022	ESTs, Weakly similar to T34549 probable	2.6
	452234	AW084176	Hs.223296	ESTs, Weakly similar to 138022 hypotheti	2.6 2.6
70	453478 418962	AF083898 AA714835	Hs.33021 Hs.271863	neuro-oncological ventral antigen 2 ESTs	2.6
, ,	418858	AW961605	Hs.21145	hypothetical protein RG083M05.2	2.6
	443257	AJ334040	Hs.11614	HSPC065 protein	2.6
	428748	AW593206	Hs.98785	Ksp37 protein	2.6 2.6
75	444984	H15474	Hs.132898 Hs.102720	fatty acid desaturase 1 ESTs	26
, ,	433404 434779	T32982 AF153815	Hs.50151	potassium inwardly-rectifying channel, s	2.6
	420582	BE047878	Hs.99093	Homo saplens chromosome 19, cosmid R2837	2.6
	452856	AF034799	Hs.30881	protein tyrosine phosphatase, receptor t	26
80	436440	AI471862	Hs.196008		26 26
30	438527 433216	A1969251 AF217412	Hs.115325 Hs.47320	neuroligin 3	26
	435380		Hs.192221		2.6
	428966	AF059214	Hs.194687		2.6

					2.6
	439653 419304	AW021103 AJ271326		hypothetical protein FLJ20373 ESTs, Weakly similar to T45070 protein k	2.6
	422991	H10940	Hs.48965	Homo sapiens cDNA: FLI21693 fis, clone C	2.6
_	448548	R13209		solute carrier family 12, (potassium-chl	2.6 2.6
5	435370 408875	AI964074 NM_015434		ESTs DKFZP434B168 protein	2.5
	457005	AJ007421	Hs.172597	sal (Drosophila)-like 3	2.5
	430154	AW583058	Hs.234726	serine (or cysteine) proteinase inhibito trinucleotide repeat containing 3	2.5 2.5
10	438549 427951	BE386801 AI826125	Hs.21858 Hs.43546	ESTs	2.5
10	411800	N39342	Hs.103042	microtubule-associated protein 18	2.5
	457683	AI821877	Hs.140002	ESTs, Moderately similar to ALU7_HUMAN A erythrocyte membrane protein band 4.1-li	2.5 2.5
	451422 430713	AB002336 AA351647	Hs.26395 Hs.2642	eukaryotic translation elongation factor	2.5
15	428826	AL048842	Hs.194019	attractin	2.5
	428963	AW382682	Hs.258208	Homo sapiens, clone MGC:15606, mRNA, com solute carrier family 11 (proton-coupled	2.5 2.5
	428141 429550	D50402 AW293055	Hs.182611 Hs.119357	ESTs	2.5
	429550 438662	AA223599	Hs.6351	cleavage and polyadenylation specific fa	2.5
20	435760	AF231922	Hs.213004	chromosome 21 open reading frame 62	2.5 2.5
	427513	AI476318	Hs.192480 Hs.230188	ESTs KIAA1396 protein	2.5
	430061 435923	AB037817 BE301930	Hs.5010	Homo sapiens done 24672 mRNA sequence	2.5
25	417123	BE326521	Hs.159450	ESTs ALLIA CONTACTOR ALLIA CONTACTOR A	2.5 2.5
25	439699	AF086534 AI815750	Hs.187561 Hs.20977	ESTs, Moderately similar to ALU1_HUMAN A hypothetical protein MGC3129 similar to	2.5 2.5
	412980 427209	H06509	Hs.92423	KIAA1566 protein	2.5
	424327	AA431707	Hs.31209	ESTs	2.5 2.5
20	436340	R42246	Hs.21606	ESTs hypothetical protein MGC3295	2.5
30	450650 439444	T65617 A)277652	Hs.101257 Hs.54578	ESTs, Weakly similar to I38022 hypotheti	2.5
	400777	74217002			2.5 2.5
	439478	AF049460	Hs.6574	deformed epidermal autoregulatory factor gamma-aminobutyric acid (GABA) A recepto	2.5
35	450407 450385	NM_000810 Al631024	Hs.24969 Hs.24948	synuclein, alpha interacting protein (sy	2.5
	432558	R97268	Hs.177269	ESTs	2.5
	400860	DE001001	11- 00004	guanylate binding protein 1, interferon-	2.5 2.5
	410361 416063	BE391804 BE047699	Hs.62661 Hs.93454	ESTs	2.5
40	414998	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin	2.5
	452823	AB012124	Hs.30696	transcription factor-like 5 (basic helix	2.5 2.5
	417791 418079	AW965339 R40058	Hs.111471 Hs.6911	ESTs ESTs	2,5
	408495	W68796	Hs.237731	ESTs	2.5
45	442104	L20971	Hs.188	phosphodiesterase 4B, cAMP-specific (dun Homo sapiens mRNA; cDNA DKFZp547D023 (fr	2.5 2.5
	437370 429803	AL359567 W81489	Hs.161962 Hs.223025		2.5
	424959	NM_005781	Hs.153937	activated p21cdc42Hs kinase	2.5 2.5
50	427413		Hs.177781		2.5
50	408955 415261	BE315170 T40928	Hs.8087 Hs.8346	NAG-5 protein ESTs	2.5
	415716	N59294	Hs.179662	nucleosome assembly protein 1-like 1	2.5 2.5
	417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430 Homo sapiens cDNA FLJ11364 fis, clone HE	2.5 2.5
55	418388 421002	R72332 AF116030	Hs.29258 Hs.100932		2.5
55	423244	AL039379	Hs.209602	FSTs. Weakly similar to ubiquitous TPR m	2.5 2.5
	423553		Hs.96854	ESTs, Weakly similar to DYLX_HUMAN CYTOP	2.5 2.5
	427961 428301	AW293165 AW628666	Hs.143134 Hs.98440	ESTs, Weakly similar to I38022 hypotheti	2.5
60	428508		Hs.184668	R SBRI31 prolein	2.5 2.5
	428858		Hs.37636	gb:zv67d11.r1 Soares_total_fetus_Nb2HF8_ ESTs, Weakly similar to KIAA1392 protein	2.5
	428943 432427		Hs.6638	Homo sapiens cDNA FLJ11602 fis, clone HE	2.5
	435347			3 ESTs	2.5 2.5
65	437949		Hs.41654 Hs.65379		2.5
	438208 440286		Hs.7138	cholinergic receptor, muscarinic 3	2.9
	441523				2.5 2.5
70	441805		Hs.30191 Hs.12925		2
70	442337 442789			1 ESTs, Wealdy similar to ALU7_HUMAN ALU S	2.
	445556	6 Al910241	Hs.12887	actin-related protein 3-beta	2. 2.
	449086		Hs.20803	17 ESTs ab:IL-BT152-080399-004 BT152 Hamo sapien	2
75	45958	3 A1907673		Annual to the annual and the transfer and the	
, 5	TABLE	8B:		A t A - Million accombined	
	Pkey:		Inique Eos prol Sene cluster nu	oeset identifier number rober	
_	Acces		ene crusier no Senbank acces		
80				_	
	Pkey 40843	CAT Num 2 1058667	ber Accessio 1 AW1952	in 62 R27868 AW811262	
	41222			42 N77591	
				171	

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412436
                                            AA665089 AA135130 AA484059 AA102419 AW877765
                                            H46739 H51513 H19779
H98716 N90792 N24283
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1626761_1
             416871
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  5
             422864
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             422949
                           223184_1
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                           223410_1
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                                            AW853758 H56414
                                            AA828125 AA834883 AA330555
R96366 AL133929 AA351636 H78818 AA477084 Z28957 H80194
AF121179 BE162736 AA358827
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                           231725_1
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                                            AA436760 AW237453 BE327496 N47347 N56967
D80642 AA443145 AL119015 AW904500
AA884766 AW974271 AA592975 AA447312
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                            41555_1
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AW975186 AA807807 D29548
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467651_1
                                             AA828995 AA834879 AI926361
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              439566
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                                             AA879430 BE070262 BE070493 BE070272 BE070484 BE070397 BE070395 BE070201 BE070198 BE070404 BE070270 BE070400 A1168422 D80113 T59074
                                             AF086387 W77884 W72711
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25
              444584
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              447197
                           711623_1
                            764066_1
                                             AW015994 R39898 AW000978 Al598202 Al521706
              448451
                                             AW970107 AA513951 AA010406
AI902519 AI902518 AI902516
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                            918300 1
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 30
                                             AW850180 AW850326
                            1248640 1
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                            1283853_1
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              455350
              TABLE BC:
                                     Unique number corresponding to an Eos probeset
              Pkey:
Ref:
 35
                                     Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA
                                      sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
                                      Indicates DNA strand from which exons were predicted.
              Strend:
              Nt_position:
                                      Indicates nucleotide positions of predicted exons.
 40
                                                              Nt_position
                              Ref
                                              Strand
               Pkev
               400777
                              8131663
                                                              70745-71121
               400780
                              8131663
                                              Minus
                                                             118372-118619
91888-92018,98131-98294,99474-99570
              400859
400860
                              9757499
                                              Minus
                                                              151830-152104,152649-152744
                              9757499
                                              Minus
 45
                              8096828
                                                               140390-140822
               400992
                                              Plus
                                                              234057-234174 110326-110491
               401324
                               9863791
               402408
402604
                              9796239
                                              Minus
                                                              20393-20767
                              9909420
                                              Plus
                               9909420
                                                              47680-47973
               402605
                                              Minus
  50
               402693
                               8569863
                                                              82366-82515
                                              Minus
                                                              59763-59909
108716-111112
               402855
                               9662953
                                              Minus
               404029
404048
                               7671252
                                              Plus
                                                              54421-56808
                               3688074
                                              Minus
               404049
                               3688074
                                                               75765-78155
                                               Minus
  55
                404283
                               2276311
                                              Minus
                                                               99460-99564
                                                               3826-4025
               404299
404541
                               5738652
                                              Minus
                               8318559
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                                              Plus
               404584
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                                                              74922-75788
173763-174294
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  60
               404721
404819
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                                              Minus
                                                               16223-16319,16427-16513,16736-16859,16941-17075,17170-17287,17389-17529,18261-18357,18443-18578
                               4678240
                                               Plus
                                                               51728-51836
                405238
                               7249119
                                               Minus
                                                              91191-91254,91510-91589
                405771
                               7018349
                                               Plus
                405819
                               4007557
                                               Plus
                                                               2830-2967
  65
                                                               137114-139033
                                               Minus
                406311
                               9211559
                TABLE 9A:ABOUT 1202 GENES UP-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT CENTRAL NERVOUS SYSTEM (CNS)
                TABLE 9A-ABOUT 1202 GENES UP-REGULATED IN GLOBLASTOMA COMPARED TO NORMAL ADULT CENTROL NERVOUS STSTEM (CNS). These were selected from 59680 probesets on the Affymetrix Eos Hu03 Gene Chip array such that the ratio of "average" glioblastoma to "average" normal adult CNS tissues was greater than or equal to 2.0. The "average" glioblastoma lavel was set to the 75th percentile amongst various glioblastoma tumors. The "average" normal adult CNS tissue level was set to the 95th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues.
   70
                subtracted from both the numerator and the denominator before the ratio was evaluated.
                                       Unique Eos probeset identifier number

Exemplar Accession number, Genbank accession number
                Pkey:
   75
                ExAcon:
                Unigenel D:
                                        Unigene number
                                       Unigene gene title
Ratio of 75th percentile turnor to 95th percentile normal adult nervous system tissue
                Unigene Title:
                R1:
   80
                                                UnigenelD
                Pkey
                                                               Unigene Title
                              ExAccn
                 452461
                              N78223
                                               Hs.108106
                                                               transcription factor
                                                                                                                                             20.1
                                                               carbonic anhydrase XII
                 436895
                              AF037335
                                                Hs.5338
                                                Hs.36820
                              U39817
                                                               Bloom syndrome
                453941
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PCT/US02/29560

				44 4 44 1904	12.4
				-Myc target JPO1 matrix metalloproteinase 7 (matrilysin,	12.4
	428330 447342			Homo sapiens, Similar to RIKEN cDNA 2010	11.7
	422163			prominin (mouse)-like 1	11.4
5	439451			heterochromatin-like protein 1	11.2 10.2
	424800			MyoD family inhibitor chromatin assembly factor 1, subunit A (10.0
	416111 444190			cysteine and glycine-rich protein 2	9.9
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	9.9
10	449340			hypothetical protein MGC10954	9.8 9.4
	409731	AA125985 BE139460	Hs.56145 Hs.124673	thymosin, beta, identified in neuroblast Homo sapiens cDNA FLJ11477 fis, clone HE	8.9
	439978 411411	AA345241	Hs.55950	ESTs, Weakly similar to KIAA1330 protein	8.9
	456516	BE172704		KIAA1610 protein	8.2
15	420092	AA814043	Hs.88045	ESTs	7.9 7.9
	422631	BE218919	Hs.118793 Hs.32964	hypothetical protein FLJ10688 SRY (sex determining region Y)-box 11	7.9
	453392 438527	U23752 Al969251	Hs.115325	RAB7, member RAS oncogene family-like 1	7.9
	427581	NM_014788	Hs.179703	KIAA0129 gene product	7.8
20	418661	NM_001949	Hs.1189	E2F transcription factor 3	7.8 7.8
	440684	AI253123	Hs.127356 Hs.167279	ESTs, Highly similar to S21424 nestin (H FYVE-finger-containing Rab5 effector pro	7.7
	429643 409638	AA455889 AW450420	Hs.21335	ESTs	7.5
	444665	BE613126	Hs.47783	B aggressive lymphoma gene	7.5
25	456759	BE259150	Hs.127792	delta (Drosophila)-like 3	7.5 7.4
	412777	Al335773	Hs.270123 Hs.211061	ESTs ESTs	7.3
	436607 432058	AW661783 AW665996	Hs.130729	ESTs, Weakly similar to ALU1_HUMAN ALU S	7.3
	417061	A1675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	7.3
30	428976	AL037824	Hs.194695	ras homolog gene family, member I	7.2 7.1
	433244	AB040943	Hs.271285 Hs.128993	KIAA1510 protein ESTs, Weakly similar to T00079 hypotheti	7.1
	436726 408432	AA324975 AW195262	NS. 120333	gb:xn67b05.x1 NCI_CGAP_CML1 Homo sapiens	7.1
	434164	AW207019	Hs.148135	serine/threonine kinase 33	7.0
35	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-l	7.0 7.0
•	439726	AW449893	Hs.293707 Hs.3076	ESTs, Weakly similar to 138598 zinc fing MHC class II transactivator	6.8
	432656 431117	NM_000246 AF003522	Hs.250500	delta (Drosophila)-like 1	6.8
	453387	AJ990741	Hs.252809	ESTs	6.8
40	418821	AA436002	Hs.183161	ESTs	6.6 6.6
	437034	AA742643	Un coppo	gb:ny91c01.s1 NCI_CGAP_GCB1 Homo sapiens MD-2 protein	6.5
	411252 424687	AB018549 J05070	Hs.69328 Hs.151738	matrix metalloproteinase 9 (gelatinase B	6.4
	452953	Al932884	Hs.271741	ESTs, Weakly similar to A46010 X-linked	6.3
45	433532	AW975367		gb:EST387475 MAGE resequences, MAGN Homo	6.3 6.3
	420311	AW445044	Hs.38207	Human DNA sequence from clone RP4-530I15	6.2
	418097 407304	R45137 AA565832	Hs.21868	ESTs gb:nj32b03.s1 NCI_CGAP_AA1 Homo sapiens	6.2
	435256	AF193766	Hs.13872	cytokine-like protein C17	6.1
50	449448	D60730	Hs.57471	ESTs	6.1 6.0
	403790	AE404470		gb:AF121179 Homo sapiens liver (Chang L-	6.0
	425517 420674	AF121179 NM_000055	Hs,1327	butyrytcholinesterase	6.0
	435542	AA687376	Hs.269533	ESTs	5.9
55	418216	AA662240	Hs.283099		5.8 5.8
	439086	AF085947 AW271720	Hs.42233	gb:Homo sapiens full length insert cDNA hypothetical protein FLJ10300	5.7
	408037 412225	AW902042	113.42230	gb:QV0-NN1022-170400-193-c02 NN1022 Homo	5.7
	436109	AA922153	Hs.132760	hypothetical protein MGC15729	5.7
60	435005	U80743	Hs.306094	trinucleotide repeat containing 12	5.7 5.7
	429149	AW193360	Hs.197962 Hs.83484	ESTs, Weakly similar to 138022 hypotheti SRY (sex determining region Y)-box 4	5.6
	418113 405558	Al272141	113,00404	ON JOA COURSING TO GOT TO COME	5.6
	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	5.6
65	442547	AA306997	Hs.217484		5.6 5.5
	413063		Hs.75184 Hs.59115	chitinase 3-like 1 (cartilage glycoprote ESTs	5.5
	420560 408096		Hs.83765		5.5
	443539		Hs.13407	4 ESTs, Moderately similar to ALU6_HUMAN A	5.4
70	426318		Hs.14711		5.4 5.3
	429115		Hs.28902		5.3
	453900 444168			gb:RC1-HT0256-081199-011-f01 HT0256 Homo	5.3
	432789		Hs.3104	KIAA0042 gene product	5.3
75	437036	AI571514	Hs.13302		5.2 5.2
	421247		Hs.10291		5.2 5.2
	441523 451108				5.1
	451106 457211			ESTs, Weakly similar to S51797 vasodilal	5.1
80	454157	7 AW162906	Hs.31248	11 ESTs, Weakly similar to \$66668 hydrogen	5.1
	423343				5.1 5.1
	425292 406679			gb:zm66b07.r1 Stratagene neuroepithelium	5.1
	10007	, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,		172	

	442671	AJ005668	Hs.134779	EST	5.1
	433001 418819	AF217513	Hs.279905	clone KQ0310 PRO0310p1	5.0
	432946	AA228776 U60899	Hs.191721 Hs.279854	ESTS	5.0
5	420730	NM_002691	Hs.99890	mannosidase, alpha, class 2B, member 1 polymerase (DNA directed), della 1, cata	4.9
•	441217	Al922183	Hs.213246	ESTs	4.9 4.9
	453385	AW296101	Hs.252806	ESTs	4.8
	418203	X54942	Hs.83758	CDC28 protein kinase 2	4.7
	450813	AI739625	Hs.203376	ESTs	4.7
10	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	4.7
	412530	AA766268	Hs.266273	hypothetical prolein FLJ13346	4.7
	431070	AW408164	Hs.249184	transcription factor 19 (SC1)	4.7
	429786	AL080232	Hs.220696	Homo sapiens mRNA; cDNA DKFZp586A061 (fr	4.7
15	405771	41470040	11- 400 400		4.6
13	457065	AJ476318 AK001059	Hs.192480	ESTs	4.6
	436190 400859	WWW 1099		gb:Homo sapiens cDNA FLJ10197 fis, clone	4.6
	435267	N23797	Hs.110114	ESTs	4.6
	443454	AI057494	Hs.133421	ESTs	4.6
20	452811	AA937079	Hs.118983	hypothetical protein FLJ12150	4.5 4.5
	437267	AW511443	Hs.258110	ESTs	4.5
	435020	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8	4.5
	454269	AJ961050	Hs.129908	KIAA0591 protein	4.5
25	422106	D84239	Hs.111732	Fc fragment of IgG binding protein	4.5
25	422765	AW409701	Hs.1578	bacutoviral IAP repeat-containing 5 (sur	4.5
	456534	X91195	Hs.100623	phospholipase C, beta 3, neighbor pseudo	4.5
	423756	AA828125		gb:od71a09.s1 NCI_CGAP_Ov2 Horno sapiens	4.5
	417308	H60720	Hs.81892	KIAA0101 gene product	4.5
30	422170	AI791949	Hs.112432	anti-Mullerian hormone	4.4
50	429500 406568	X78565 AF088886	Hs.289114 Hs.11590	hexabrachion (tenascin C, cytotactin)	4.4
	426812	AF105365	Hs.172613	cathepsin F solute carrier family 12 (potassium/chlo	4.4
	402516	A 100000	113.172010	adible carrier farmly 12 (polassiumento	4.4 4.4
	432865	AJ753709	Hs.152484	ESTs, Weakly similar to 138022 hypotheti	4.4
35	413625	AW451103	Hs.71371	ESTs	4.4
	436098	R20597	Hs.9739	glycerol-3-phosphate dehydrogenase 1 (so	4.4
	418333	W92113		gb:zh48e01.r1 Soares_fetal_liver_spleen_	4.4
	416933	BE561850	Hs.80506	small nuclear ribonucleoprotein polypept	4.4
40	438192	AI859065	Hs.337620	Homo sapiens AFG3L1 isoform 1 mRNA, part	4.3
40	457374	AA493662		gb:nh05d12.s1 NCI_CGAP_Thy1 Homo sapiens	4.3
	433159	AB035898	Hs.150587	kinesin-like protein 2	4.3
	444386	BE065183	LI- 20070	gb:RC1-BT0314-020200-012-c04 BT0314 Homo	4.3
	453202 441020	AW085781 W79283	Hs.26270	hypothetical protein FLJ11588	4.3
45	414733	BE514535	Hs.35962 Hs.77171	ESTs minichromosome maintenance deficient (S.	4.3
1.5	407902	AL117474	Hs.41181	Homo saplens mRNA; cDNA DKFZp727C191 (fr	4.3 4.3
	405701	/12:17:47	113.41101	Tionio aspena militari, como bra epi 27 0131 (il	4.3
	451659	BE379761	Hs.14248	ESTs	4.3
	418845	AA852985	Hs.89232	chromobox homolog 5 (Drosophila HP1 alph	4.2
50	433323	AA805132	Hs.30701	ESTs	4.2
	439811	AA135332	Hs.71608	ESTs	4.2
	415406	T26510		gb:AB282F8R Infant brain, LLNL array of	4.2
	436282	R91913	Hs.272104	ESTs, Moderately similar to ALU1_HUMAN A	4.1
55	441269	AW015206	Hs.178784	ESTS	4.1
55	418727 433006	AA227609	Hs.94834	ESTs Medanataki almilar ta T20285 humak	4.1
	436480	BE242758 AJ271643	Hs.190223	ESTs, Moderately similar to T29285 hypot	4.1
	430786	A3271043 AA486144	Hs.87469 Hs.31293	putative acid-sensing ion channel ESTs	4.1 4.1
	445372	N36417	Hs.144928	ESTs	4.1 4.1
60	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	4.0
	457465	AW301344	Hs.122908	DNA replication factor	4.0
	422094	AF129535	Hs.272027	F-box only protein 5	4.0
	442029	AW956698	Hs.14456	neural precursor cell expressed, develop	4.0
65	459321	AW044477	Hs.299538	ESTs	4.0
65	421308	AA687322	Hs.192843	leucine zipper protein FKSG14	4.0
	420567	AK000812	Hs.98874	similar to proline-rich protein 48	4.0
	447004	AW296968	Hs.157539	ESTS	4.0
	448295	AI381911	Hs.334859	KIAA1814 protein	3.9
70	439699 440704	AF086534 M69241	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A insulin-like growth factor binding prote	3.9
, ,	453096	AW294631	Hs.162 Hs.11325	ESTs	3.9 3.9
	457026	AA397620	Hs.48692	ESTs	3.9
	404642				3.9
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	3.9
75	430132	AA204686	Hs.234149	hypothetical protein FLJ20647	3.9
	437718	AI927288	Hs.196779	ESTs	3.9
	438490	AW593272	Hs.301299	ESTs	3.9
	429919	AA460692	Hs.278945	hypothetical protein FLJ23024	3.9
QΛ	413604	R51767		gb:yg73g11.r1 Soares Infant brain 1NIB H	3.9
80	425599	AW366745	Hs.214140	ESTs, Wealthy similar to ALU1_HUMAN ALU S	3.9
	448796	AA147829	Hs.301431	endothelial zinc finger protein induced	3.9
	449300 452203	A1656959 X57522	Hs.222165	EST8	3.8
	-DEEDS	rwi dek	Hs.158164	transporter 1, ATP-binding cassette, sub	3.8

	425769	U72513	Hs.159486	Huma	n RPL13-2 pseudogene mRNA, complete	3.8
	404295					3.8 3.8
			Hs.62661 Hs.191381	hynn	ylate binding protein 1, interferon- thetical protein	3.8
5	428728 409142	NM_016625 AL136877	Hs.50758	SMC	4 (structural maintenance of chromoso	3.8 3.8
,	430172	AA468591	Hs.161889	EST:	1	3.8
	447499	AW262580	Hs.147674	proto	cadherin beta 16	3.8
	405884	AM127017	Hs.244353	EST	5	3.7
10	437236 418883	AW137817 BE387036	Hs.1211	acid	ohosobatase 5. tartrate resistant	3.7 3.7
10	444143	AW747996	Hs.160999	EST	s, Moderately similar to A56194 throm	3.7
	425529	NM_014656	Hs.158282	EST	A0040 gene product	3.7
	425502	R98895 NM_007019	Hs.125823 Hs.93002	ubio	uitin carrier protein E2-C	3.7
15	419741 402424	MMCOOLOIS	1,0.0000			3.7 3.7
1.5	429469	M64590	Hs.27	glyc	ine dehydrogenase (decarboxylating; no sapiens PRO1082 mRNA, complete cds	3.7
	434072	H70854	Hs.283059 Hs.77513	HOL	X10 (yeast) homolog, cytochrome c oxid	3.7
	414872 426071	U82010 AW138057	Hs.163835	ES.	īs —	3.7 3.7
20	419078	M93119	Hs.89584	inst	ulinoma-associated 1	3.7 3.7
	428037	N47474	Hs.89230	pot	assium intermediate/small conductance Ts, Wealdy similar to PC4259 ferritin	3.7
	416547	H62914 AA764852	Hs.268946 Hs.291567	ES	Te	3.6
	436899 436722	AW975977	113.201001	gb:	EST388086 MAGE resequences, MAGN Homo	3.6 3.6
25	440652	Al216751	Hs.143977	ES		3.6
	428450	NM_014791	Hs.184339 Hs.339654	KV	AA0175 gene product Ts, Weakly similar to 138022 hypotheti	3.6
	452103 409048	R42764 H59990	Hs.37699	E9	Ts.	3.6
	439546	AF088056	12.2.	gb	:Homo sapiens full length insert cDNA	3.6 3.6
30	443544	AI076315	Hs.16359	ES	iTs clin-dependent kinase inhibitor 2A (me	3.6
	418478	U38945	Hs.1174 Hs.269901		STS	3.6
	435889 420301	A1249107 AA767526	Hs.22030	pa	ired box gene 5 (B-cell lineage specif	3.6 3.6
	438078	AI016377	Hs.131693	E	STS	3.6
35	408420	NM_006915	Hs.44766	re	tinitis pigmentosa 2 (X-linked recessi c:yx13d08.s1 Soares melanocyte 2NbHM Ho	3.5
	416871 424085	H98716 NM_002914	Hs.13922	R TE	ofication factor C (activator 1) 2 (40	3.5
	446291	BE397753	Hs.14623	in	terferon, gamma-inducible protein 30	3.5 3.5
	432281	AK001239	Hs.27426	3 h	ypothetical protein FLJ10377 STs, Highly similar to unnamed protein	3.5
40	436123	AA057484 AW834039	Hs.35406		h-CVC-TT0010-091199-053-e09 1 10010 Homo	3.5
	411256 419239		Hs.18459	ΩĹ	tomo egniens cDNA: FLJ23241 fis, clone U	3.5 3.5
	435065			_ 9	b:RC4-BT0310-110300-015-b08 BT0310 Homo lomo sapiens, clone IMAGE:3682908, mRNA	3.5
4.5	435532		Hs.11730 Hs.44189		STs	3.5
45	447101 410530		Hs.6417		TPage H+ transporting, lysosomal (vacu	3.5 3.5
	422156			,	nb.vv56d10_s1 Soares_multiple_sclerosis_	3.5 3.5
	453616			6 (dynein, axonemal, light intermediate pol Homo sapiens mRNA full length insert cDN	3.5
50	439743 453884		Hs.2838 Hs.3623	2	KIAAO186 gene product	3.5
50	424954				tumor protein p53 (Li-Fraumeni syndrome)	3.5 3.5
	42072	AA927802		71	ZAP3 protein ESTs, Weakly similar to ALUC_HUMAN !!!!	3.4
	426764 42064			na	FSTs. Moderately similar to S65657 alpha	3.4
55	44883			2	zinc finger protein 23 (KOX 16)	3.4 3.4
	44437	1 BE540274	Hs.239		forkhead box M1	3.4
	40260		4 Hs.323	-3	mitogen-activated protein kinase kinase	3.4
	44240 41,430				ESTs	3.4 3.4
60	44467	0 H58373	Hs.332	938	hypothetical protein MGC5370 gb:601159567T1 NIH_MGC_53 Homo sapiens c	3.4
	41455			420	ESTs	3.4
	45221 41441				hypothetical protein MGC2721	3.4 3.4
	44996				ESTs gb:PM3-BT0584-260300-002-g05 BT0584 Homo	3.4 3.4
65				e4	gb:PM3-B10584-250300-002-g03-B1050-4-10000 DKFZP586E1621 protein	3.4
	4538 4174				nleckstrin homology-like domain, family	3.4
	4228		34 Hs.150	33	neutrophil cytosolic factor 1 (47kD, chr	3.4 3.4
70	4461		Hs.21		ESTs ESTs	3.4
70					ESTs Moderately similar to \$65657 alpha	3.4
	4536 4082				Homo saniens cDNA: FLJ22785 fis, clone K	3.4 3.3
	4557	78 BE0887	46	045	gb:CM2-BT0693-210300-123-d09 BT0693 Homo	3.3
7	5 4175				ESTs endothelial cell growth factor 1 (plate)	3.3
7:) 4124 4541			0	gb:1L3-ST0141-131099-017-A02 ST0141 Homo	3.3
	454	294 AB0007	34 Hs.50		IAK hinding protein	3.3 3.3
	457	131 AC0023			Human Chromosome 16 BAC clone CIT987SK-A Homo sapiens cDNA FLJ14035 fis, clone HE	3.3
8	O 410			19727 19657	ESTs	3.3
0	U 449 436			34828	hynothetical protein FLJ10719; KIAA1794	3.3 3.3
	453	746 AL1206	i11	. 9300	gb:DKFZp761H119_r1 761 (synonym: harny2)	3.3
	452	799 Al9488	29 Hs.2	13786	ESTS	

175

	435380	AA679001	Hs.192221	ESTs	3.3
	426746	J03626	Hs.2057	undine monophosphate synthetase (orotat	3.3
	453362	H14988 Al202788	Hs.107375	ESTs	3.3
5	456473 416426	AA180256	Hs.25682 Hs.210473	Homo sapiens mRNA for KIAA1863 protein,	3.3 3.3
,	445777	AI580371	Hs.145384	Homo saplens cDNA FLJ14872 fis, clone Pt. ESTs	3.3
	423757	AL049337	Hs.132571	Homo sapiens mRNA; cDNA DKFZp564P016 (fr	3.3
	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone CO	3.3
	404299	72.000100		Total deposits object to be seen as a deposit of	3.3
10	404108			•	3.3
	425189	H16622		gb:ym26c07.r1 Soares Infant brain 1NIB H	3.3
	449318	AW236021	Hs.78531	Homo saptens, Similar to RIKEN cDNA 5730	3.3
	450193	Al916071	Hs.15607	Homo sapiens Fanconi enemia complementat	3.2
1.5	427725	U56839	Hs.180533	mitogen-activated protein kinase kinase	3.2
15	424051	AL110203	Hs.138411	Homo saplens mRNA; cDNA DKFZp586J1922 (f	3.2
	418968	NM_000078	Hs.89538	cholesteryl ester transfer protein, plas	3.2
	449248	M33782	Hs.23391	Homo saplens, Similar to transcription f	3.2
	439416	W58294	Hs.56254	ESTs	3.2
20	401596	AA172106	Hs.110950	Rag C protein .	3.2 3.2
20	408380 450325	AF123050 AI935962	Hs.44532 Hs.26289	diubiquitin ESTs	3.2
	430325	AA625947	Hs.25750	ESTS	3.2
	457536	AA305233	Hs.278712	eukaryotic translation initiation factor	3.2
	426836	N41720	Hs.172684	vesicle-associated membrane protein 8 (e	3.2
25	442710	AJ015631	Hs.23210	ESTs	3.2
	435232	NM_001262	Hs.4854	cyclin-dependent kinase inhibitor 2C (p1	3.2
	430970	AI018210	Hs.144083	ESTs	3.2
	416192	NM_005036	Hs.998	peroxisome proliferative activated recep	3.2
	446676	H09380	Hs.300965	ESTs	3.2
30	451459	AI797515	Hs.270560	ESTs, Moderately similar to ALU7_HUMAN A	3.2
	407603	AW955705	Hs.62604	Homo sapiens, clone IMAGE:4299322, mRNA,	3.2
	413840	AL301558	Hs.146381	RNA binding motif protein, X chromosome	3.2
	448751	BE551203	Hs.201792	ESTs	3.2
25	432593	AW301003	Hs.51483	ESTs, Weakly similar to hypothetical pro	3.2
35	458786	Al457098	Hs.280848	ESTs	3.2
	455909	BE156417	Hs.278798	ESTs	3.2
	419311	AA689591		gb:nv66a12.s1 NCI_CGAP_GCB1 Homo sapiens	3.2
	439710	AF086543		gb:Homo sapiens full length insert cONA	3.2 3.1
40	434559	AF147315	Hs.167073	gb:Homo saplens full length insert cDNA Homo saplens cDNA FLJ13047 fis, clone NT	3.1
70	455800 436703	R22479 AW880614	Hs.146381	RNA binding motif protein, X chromosome	3.1
	414799	A1752416	Hs.77326	insulin-like growth factor binding prote	3.1
	437860	AA333063	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	3.1
	434182	W20309	Hs.118520	G-protein gamma-12 subunit	3.1
45	417900	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevi	3.1
	434769	AA648884	Hs.134278	Homo sapiens cDNA FLJ12676 fis, clone NT	3.1
	414825	X06370	Hs.77432	epidermal growth factor receptor (avian	3.1
	426413	AA377823		gb:EST90805 Synovial sarcoma Homo sapien	3.1
	447959	Al452784	Hs.270270	ESTs, Weakly similar to 2109260A B cell	3.1
50	404589				3.1
	421764	AI681535	Hs.148135	serine/threonine kinase 33	3.1
	419986	Al345455	Hs.78915	GA-binding protein transcription factor,	3.1
	416941	BE000150	Hs.48778	niban protein	3.1
55	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	3.1
22	449611	A1970394	Hs.197075	ESTs	3.1 3.1
	434746 434274	AA648368	Hs.295368	ESTs Moderately similar to ALU1_HUMAN A	3.1
	427899	AA528539 AA829286	Hs.116252 Hs.332053	serum amyloid A1	31
	427699	BE302665	Hs.105461	hypothetical protein FLJ20357	3.1
60	452472	AW957300	Hs.294142	ESTs, Weakly similar to C55663 oligodend	3.1
	446131	NM_000929	Hs.290	phospholipase A2, group V	3.1
	440052	AI633744	Hs.195648	ESTs, Weakly similar to 138022 hypotheti	3.1
	426531	AA381071		gb:EST94100 Activated T-cells XII Homo s	3.1
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	3.1
65	406267				3.1
	447039	AV661798	Hs.282915	ESTs	3.1
	404802				3.1
	406927	M26460		gb:Homo sapiens (clone 104) retinoblasto	3.1
70	419314	AW971924	Hs.87280	ESTs	3.0
70	435894	AI076667	Hs.188011	ESTs	3.0
	432140	AK000404	Hs.272688	hypothetical protein FLJ20397	3.0
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	3.0
	425202	AW962282	Hs.152049	ESTs, Weakly similar to 138022 hypotheti	3.0
75	407047	X65965	Un 1140	gb:H.sapiens SOD-2 gene for manganese su LIM domain only 1 (rhombotin 1)	3.0 3.0
15	418241	M26682 797832	Hs.1149 Hs.15476	differentially expressed in FDCP (mouse	3.0
	446599 412950	Z97832 BE018581	Hs.15476 Hs.245342	hypothetical protein FLJ14642	3.0
	428670	AA431682	Hs.134832	ESTs	3.0
	446975	BE246446	Hs.16695	ubiquitin-ectivating enzyme E1-like	3.0
80	437756	AA767537	Hs.197096	ESTs	3.0
	416084	L16991	Hs.79006	deoxythymidylate kinase (thymidylate kin	3.0
	402374	AL135225	Hs.301865	dopachrome tautomerase (dopachrome della	3.0
	443885	H91806	Hs.15284	ESTs	3.0

	434008	AA740878	Hs.112982	ESTs		3.0 3.0
	452568	AA805634	Hs.300870		o sapiens mRNA; cDNA DKFZp547M072 (fr	3.0
	414239 421013		Hs.182330 Hs.1345	ESTs mutat	ted in colorectal cancers	3.0
5	424635	AA420687	Hs.115455		o sapiens cDNA FL114259 fis, clone PL	3.0 3.0
	410276	A1554545 N29862	Hs.68301 Hs.44104	EST:		3.0
	433865 406028	N23002	110.77101			3.0 3.0
10	401626	Morco	Un 21601	EST	2	3.0
10	415949 418583	H10562 AA604379	Hs.21691 Hs.86211	hypo	othetical protein	3.0 3.0
	417933	X02308	Hs.82962	thyn	nidylate synthelase no saplens cDNA: FLI22487 fis, clone H	3.0
	434577	R37316 Al768801	Hs.179769 Hs.169943	Horr	no sapiens cDNA FLJ13569 fis, clone PL	3.0
15	430437 427940	AA417812	Hs.38775	EST	's	2.9 2.9
	456060	C14904	Hs.45184		no sapiens cONA FLJ12284 fis, clone MA	2.9
	421988 448775	AW450481 AB025237	Hs.161333 Hs.388	EST nud	ix (nucleoside diphosphate linked moi	2.9
	438598	AI805943	Hs.326067	hyp	othetical protein MGC5178	2.9 2.9
20	429612	AF062649	Hs.252587 Hs.40905	pitu ES	itary tumor-transforming 1 re	2.9
	451189 401558	AA016019	MS.40500	EJ	13	2.9 2.9
	426207	BE390657	Hs.30026	HS	PC182 protein	29
25	404721					2.9
25	401384 417288	A)984792	Hs.108812	hyp	pothetical protein FLJ22004	2.9 2.9
	427648	A1376722	Hs.180062		deasome (prosome, macropain) subunit,	29
	435928	H64345 N75450	Hs.183961 Hs.183412	E9	Ts Ts, Moderately similar to AF116721 67	2.9
30	431740 428242	H55709	Hs.2250	leu	rkemia inhibitory factor (cholinergic	2.9 2.9
•	439972	AI348100	Hs.124662 Hs.144553		TTs TS, Wealdy similar to unnamed protein	2.9
	433112 423751	AA973801 AW235633	Hs.46525		STS	29 29
	406748	AW339106	Hs.21749		nexin A2	29
35	422154	T79045	Hs.12692	, E	STs	2.9
	405588 440911	AA909536	Hs.14356	2 E	STs	29 29
	412420	AL035668	Hs.73853		one morphogenetic protein 2 STs	2.9
40	445043 410114	AW014413 AW590540	Hs.19606 Hs.27128	Λ E	QTe	2.9
40	419217	AA504571		9	b:aa60e12.r1 NCI_CGAP_GCB1 Homo sapiens	2.9 2.9
	415849		Hs.6806 Hs.20450	_	STs ICM-like membrane protein precursor	2.9
	448140 453331	AF146761 Al240665	Hs.8895	F	STs	2.9 2.9
45	432065	AA401039	Hs.2903	9	orotein phosphatase 4 (formerly X), cata chondroitin sulfate proteoglycan BEHAB/b	2.9
	438380 454377		Hs.6194		p:7B03C12 Chromosome 7 Fetal Brain cDNA	2.9
	421491		Hs.4273	6 I	ESTs	2.9 2.8
50	452291		Hs.2885 Hs.6607	5 1	CDC7 (cell division cycle 7, S. cerevisi ESTs	2.8
50	415446 439516		115.0001		gb:zd60d04.r1 Soares_fetal_heart_NbHH19W	2.8 2.8
	427221	L15409	Hs.1740		von Hippel-Lindau syndrome hypothetical protein FLJ13158	2.8
	422493 41945		3 Hs.2501 Hs.9053		syntaxin binding protein 2	2.8
55	44878		Hs.2205	<u>i1</u>	hypothetical protein MGC15548	2.8 2.8
_	42412				ESTs ESTs, Weakly similar to 138022 hypotheti	2.8
	45869 41897				ESTs	2.8 2.8
	44047	1 AA88614	6 Hs.307		ESTs transcription factor 3 (E2A immunoglobul	2.8
60	42101 43364				FSTs	2.8
	41581		Hs.788	67	protein tyrosine phosphatase, receptor-t	2.8 2.8
	42172				sodium channel, voltage-gated, type III, ESTs	2.8
65	43496 43202				Homo sapiens mRNA; cDNA DKFZp761L1212 (f	2.8 2.8
0.5	4005	17 AF24238	8 Hs.149		lengsin thrombospondin 1	2.8
	4330: 4487:				Homo sapiens mRNA; cDNA DKFZp564H1916 (f	2.8
	4067		3 Hs.18	2426	ribosomal protein S2	2.8 2.8
70			64 Hs.19 Hs.12		BANP homolog, SMAR1 homolog ESTs	2.8
	4401 4039		(13.12		•	2.8 2.8
	4251	93 AW9656			ESTs Homo saplens cDNA FLJ20653 fis, clone KA	2.8
75	4252				EQTe	2.8
/ -) 4402 4123		710		gb:RC0-MT0004-130300-011-e07 MT0004 Homo	2.8 2.8
	4487	769 N66037		173	ESTs gb:QV2-CT0261-201099-011-f01 CT0261 Homo	2.8
	4110 438			2224	ESTs. Wealdy similar to ALU5_HUMAN ALU S	2.8 2.8
80) $\widetilde{457}$	578 AA5780)27		gb:nt20h01.s1 NCI_CGAP_HSC1 Homo sapiens	2.8
		510 AA4220 769 AW873		13640 20831	Homo sapiens cDNA FLJ14597 fis, clone NT	2.8
		769 AW8/3 701 AA411		13886	nuclear autoantigenic sperm protein (his	2.8
	-				177	

	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	2.8
	439662	H97552	Hs.269060	ESTS	28
	425694	U51333	Hs.159237	hexakinase 3 (white cell) centromere protein F (350/400kD, mitosin	28 28
5	414747 414598	U30872 A1094221		tung type-I cell membrane-associated gly	28
•	447752	M73700		lactotransferrin	2.8
	408761	AA057264		ESTs, Weakly similar to (define not ava	2.8 2.7
	453350	AI917771	Hs.61790 Hs.279789	hypothetical protein FLJ23338 histone deacetylase 3	2.7
10	456629 439538	AW891965 AA837323	Hs.164047	ESTs	27
10	458814	A1498957	Hs.170861	ESTs, Wealdy similar to Z195_HUMAN ZINC	2.7
	456029	BE255990	Hs.218329	hypothetical protein	27
	451129	BE072881	11- 200776	gb:RC2-BT0548-200300-012-e09 BT0548 Homo	2.7 2.7
15	456412 453536	AW749617 AA137000	Hs.280776 Hs.62578	tankyrase, TRF1-interacting ankyrin-rela ESTs	2.7
13	438378	AW970529	Hs.86434	hypothetical protein FLJ21816	2.7
	425745	U44060	Hs.14427	Homo septens cDNA: FLJ21800 fis, clone H	27
	446322	N23033	Hs.155814	ESTs	2.7 2.7
20	451592 429466	AI805416 M85835	Hs.213897 Hs.12827	ESTs ESTs	2.7
20	429747	M87507	Hs.2490	caspase 1, apoptosis-related cysteine pr	2.7
	455514	AW983871		gb:RC1-HN0003-220300-021-h07 HN0003 Homo	2.7
	414732	AW410976	Hs.77152	minichromosome maintenance deficient (S.	2.7 2.7
25	444207	AI565004 AA402414	Hs.79572 Hs.3059	cathepsin D (lysosomal aspartyl protease coatomer protein complex, subunit beta	2.7
23	427421 449655	AJ021987	Hs.59970	ESTs	2.7
	422648	D86983	Hs.118893	Melanoma associated gene	2.7
	428494	AA233439	Hs.184634	hypothetical protein FLJ20005	27
20	406895	X60648	Hs.172550	polypyrimidine tract binding protein (he Horno sapiens, clone IMAGE:3605822, mRNA	2.7 2.7
30	453255	AA278167 NM_014137	Hs.19215 Hs.177258	PRO0650 protein	2.7
	427348 435370	AI964074	Hs.225838	ESTs	2.7
	407862	BE548267	Hs.50724	Homo sapiens cDNA FLJ10934 fis, clone OV	2.7
~ -	411874	AA096106	Hs.20403	EST8	2.7 2.7
35	421192	AA833718	Hs.204529	KIAA1806 protein	2.7
	435899	W89093 R58394	Hs.189914 Hs.25119	ESTs ESTs, Weakly similar to YEX0_YEAST HYPOT	2.7
	414603 453462	AL037291	Hs.236605	ESTs, Moderately similar to ALU4_HUMAN A	2.7
	436554	AI985810	Hs.301173	ESTs	2.7
40	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	2.7 2.7
	403881	A110774470	11- 000574	analisaaminin C I	2.7
	431779 404984	AW971178	Hs.268571	apolipoprotein C-I	27
	448275	BE514434	Hs.20830	kinesin-like 2	2.7
45	446839	BE091926	Hs.16244	mitotic spindle coiled-coil related prof	2.7
	411927	BE274009	Hs.772	glycogen synthase 1 (muscle)	2.7 2.7
	404756 447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	2.7
	422176	H80977	113.772.0	gb:yu89a11.s1 Soares fetal liver spleen	2.7
50	439627	BE621702	Hs.29076	hypothetical protein FLJ21841	2.7
	436532	AA721522		gb:nv54h12.r1 NCI_CGAP_Ew1 Homo saptens	2.7 2.7
	412833	AW960547	Hs.298262 Hs.204579	ribosomal protein S19 ESTs	2.7
	457245 446861	Al745498 Al696519	Hs.14427	Homo saplens cDNA: FLJ21800 fis, clone H	2.7
55	453263	R91778	Hs.99369	ESTs	2.7
	459385	BE380047		gb:601159362F2 NIH_MGC_53 Homo saplens c	2.7
	438764	AA824524	Hs.336452	ESTs ESTs, Wealdy similar to (38022 hypotheti	2.7 2.7
	429285 424853	AI971081 BE549737	Hs.20432 Hs.132967		2.7
60	430037	BE409649	Hs.227789		2.7
	449892	N73608	Hs.50309	ESTs	2.7
	454201	AB023191	Hs.44131	KIAA0974 protein	2.7 2.7
	452279	AA286844	Hs.61260	hypothetical protein FLJ13164 metzxin 1	2.7
65	427954 400371	J03060 U80740	Hs.247551	(IREGALII I	2.7
05	452449	AW068658	Hs.20943	ESTs	2.7
	431114	AA492400	Hs.291015		2.7
	417088	M54915	Hs.81170	pim-1 oncogene	2.7 2.7
70	447674	BE270640	Hs.19192	cyclin-dependent kinase 2	27
70	403680 454679	AW813110		ab:CM4-ST0189-051099-021-05 ST0189 Homo	2.7
	411968	Al207410	Hs.69280	Homo sapiens, clone IMAGE:3636299, mRNA,	2.6
	422240		Hs.29002	KIAA1706 protein	2.6
75	424368		Hs.146085	5 KIAA1345 protein	26 26
75	405808		Hs.92357	galactokinase 1	26
	419700 435972		Hs.11419		26
	453568		Hs.557	adrenergic, alpha-10-, receptor	2.6
90	443725	AW245680		growth arrest and DNA-damage-inducible,	2.6 2.6
80	444156		Hs.86437 Hs.98947		2.6 2.6
	428209 437640				2.6
	453948		Hs.64859		2.6
				450	

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				44.4 to 400 above out to both	2.6
	415402			mannosyl (alpha-1,3-)-glycoprotein beta- topolsomerase (DNA) II alpha (170kD)	26 26
	425397 418228	J04088 AA962181		ESTs, Moderately similar to ALU1_HUMAN A	26
	401324	ACCOUNT	10.11(210	CO13, 110001010) C	2.6
5	425234	AW152225	Hs.165909	ESTs, Weakly similar to 138022 hypotheti	2.6
	443210	AI692649	Hs.9451	hypothetical protein MGC13168	2.6
	457244	AA581385	Hs.162473	ESTs, Wealdy similar to 138022 hypotheti	2.6 2.6
	417144	AA382104	Hs.81337	lectin, galactoside-binding, soluble, 9 Homo saplens clone TCCCIA00164 mRNA sequ	2.6
10	433933 437437	AI754389 AA226869	Hs.133494 Hs.16520	hypothetical protein DKFZp762L0311	2.6
10	434206	AW136973	Hs.288516	ESTs, Wealty similar to \$69890 mitogen i	2.6
	400992	,,			2.6
	455530	AW984744		gb:RC1-HN0015-040400-011-d03 HN0015 Homo	2.6
	436139	AA765786	Hs.120936	ESTs	2.6
15	448330	AL036449	Hs.207163	ESTs	2.6 2.6
	412942	AL120344	Hs.75074 Hs.336938	mitogen-activated protein kinase-activat Homo sapiens PRO0593 mRNA, complete cds	2.6
	432753 433430	NM_014075 AI863735	Hs.186755	ESTs	2.6
	436693	AW973223	Hs.303197	B-cell CLL/lymphoma 7C	2.6
20	429482	AF076974	Hs.203952	transformation/transcription domain-asso	26
	432715	AA247152	Hs.200483	ESTs, Weakly similar to KIAA1074 protein	2.6
	414217	Al309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	2.6 2.6
	434165	AA971328	Hs.95361	myosin VIIA (Usher syndrome 1B (autosoma	26
25	414835	AA156720 T48851	Hs.185342 Hs.149250	ESTs O-siglec precursor,	2.6
25	424489 436496	AA281959	Hs.5210	glia maturation factor, gamma	2.6
	403797	74 40 1000	7.2.0	3	2.6
	434573	AW372340	Hs.159717	ESTs	26
	418841	NM_002332	Hs.89137	low density lipoprotein-related protein	2.6
30	415785	R82419	Hs.23603	ESTs, Moderately similar to ALU8_HUMAN A	2.6 2.6
	450608	AA010365	Hs,193229 Hs.31339	ESTs fibroblast growth factor 11	2.6
	425304 432268	AA463844 BE311856	Hs.274230	3'-phosphoadenosine 5'-phosphosulfate sy	2.6
	410507	AA355288	Hs.40834	transitional epithelia response protein	2.6
35	427343	AI880044	Hs.176977	protein kinase C binding protein 2	2.6
	420917	AW135716	Hs.117330	ESTs	2.6
	414399	L47345	Hs.155202	transcription elongation factor B (SIII)	2.6 2.6
	446089	AI860021	Hs.270651 Hs.7446	ESTs, Moderately similar to A47582 B-cel chromosome 6 open reading frame 5	2.6
40	440829 408475	AF136407 AA315514	Hs.47986	hypothetical protein MGC10940	2.6
70	450946	AA374569	Hs.127698	ESTs, Moderately similar to 2109260A B c	2.6
	421462	AF016495	Hs.104624	aquaporin 9	2.6
	434846	AW295389	Hs.119768	ESTs	2.6
15	422887	AI751848	Hs.49215	ESTs	2.6 2.6
45	417435	NM_005181	Hs.82129 Hs.271586	carbonic anhydrase III, muscle specific hypothetical protein DKFZp762M115	2.5
	437389 408981	AL359587 AW500797	Hs.49427	Gem-interacting protein	2.5
	432180	Y18418	Hs.272822	Ruv8 (E coli homolog)-like 1	2.5
	418079	R40058	Hs.6911	ESTs	2.5
50	437820	AA769062	Hs.323836	ESTs. Weakly similar to alternatively sp	2.5
	439685	AW956781	Hs.293937	ESTs, Weakly similar to FXD2_HUMAN FORKH	2.5 2.5
	425681	AB018297 Al018174	Hs.159183 Hs.42936	KIAA0754 protein ESTs	2.5
	435177 437323	AA371145	Hs.226627		2.5
55	422114	AW194851	Hs.111801		2.5
	448478	Al523218	Hs.203456		2.5
	426623	AA382826	Hs.132793		2.5 2.5
	448764	A1568607	Hs.182112		2.5 2.5
60	458385	AI051489 N28939	Hs.246214 Hs.13434	Homo sapiens clone 24418 mRNA sequence	2.5
OU	403726 444888	AI651039	Hs.148559		2.5
	456179	H75490	Hs.271930		2.5
	424840	D79987	Hs.153479		2.5
15	406273	NM_000919		peptidylglycine alpha-amidating monooxyg	2.5 2.5
65	418054	NM_002318		lysyl oxidase-like 2	2.5 2.5
	445936		Hs.61478	hypothetical protein FLJ22329 gb:lL3-CT0214-150200-074-E06 CT0214 Homo	2.5
	454967 442303	AW848276 AA989289	Hs.129169		2.5
	456583		Hs.10410		2.5
70	434263		Hs.44648	ESTs	2.5
	416892	L24498	Hs.80409	growth arrest and DNA-damage-inducible,	2.5
	424528		Hs.23895		2.5 2.5
	406038		Hs.88219 Hs.31517		2.5
75	413495 423098		Hs.20468		2.5
13	410817		Hs.93659		2.5
	439841		Hs.6710	mannose-P-dolichol utilization defect 1	2.5
	453828		Hs.29382		2.5
00	445034				2.5 2.5
80	449620		Hs.23794		25 25
	406876 412370		Hs.18084	gb:RC2-ET0021-280400-011-c05 ET0021 Homo	2.5
	423642			- 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	2.5

	420257	AUA076700	11- 40000T	FCT-	
	430357	AW976789	Hs.165607	ESTs	2.5
	414853	U31116	Hs.77501	sarcoglycan, beta (43kD dystrophin-assoc	2.5
	416097	BE387371	Hs.118964	hypothetical protein FLJ20085	2.5
5	428619	AK002140	Hs.187378	hypothetical protein FLJ11278	2.5
,	413976	BE295452	Hs.75655	procollagen-proline, 2-oxoglutarate 4-di	2.5
	445223	AW291553	Hs.254983	ESTs	25
	423926	X03833	Hs.1722	interteukin 1, atpha	2.5
	410165	BE560228	Hs.71869	apoptosis-associated speck-like protein	2.5
10	406474				2.5
10	433908	AW298141	Hs.157975	ESTs	2.5
	439755	AW748482	Hs.77873	B7 homolog 3	2.5
	437528	N59646	Hs.169745	crumbs (Drosophila) homolog 1	2.5
	420734	AW972872	Hs.293736	ESTs	25
1.5	415346	Z43108		gb:HSC13E071 normalized infant brain cDN	25
15	419337	AW291112	Hs.209978	ESTs	25
	444606	R09478	Hs.18041	ESTs	2.5
	430061	AB037817	Hs.230188	KIAA1396 protein	2.5
	413407	AJ356293	Hs.75339	inositol polyphosphate phosphatase-like	2.5
~~	411965	BE467339	Hs.280115	ESTs	2.5
20	409278	AA346683	Hs.52763	anaphase-promoting complex subunit 7	2.5
	403142			, , , ,	2.5
	401714				2.5
	425081	X74794	Hs.154443	minichromosome maintenance deficient (S.	2.5
	416505	H66470	Hs.16004	ESTs	2.5
25	431518	AA743462	Hs.165337	ESTs	2.5
	448623	BE613468	Hs.107515	ESTs, Wealdy similar to T00329 hypotheti	25
	428301	AW628666	Hs.98440	ESTs, Weakly similar to 138022 hypotheti	2.5
	404366			, ···, ···	2.5
	449733	R74546	Hs.29438	Homo sapiens cDNA FLJ12094 fis, clone HE	2.5
30	459583	Al907673		gb:IL-BT152-080399-004 BT152 Homo sapten	2.5
50	402856	AW939659		gb:RC0-DT0076-110100-031-c09 DT0076 Homo	2.5
	420751	J03019	Hs.99913	adrenergic, beta-1-, receptor	2,4
	436805	AA731533	Hs.270751	ESTs	2.4
	420285	AA258124	Hs.293878	ESTs, Moderately similar to ZN91_HUMAN Z	2.4
35	453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	2.4
55	453853	AL040600	Hs.188083	ESTs	2.4
	407909	AW103986	18.10000	gb:xd63e06.x1 NCI_CGAP_Ov23 Homo sapiens	2.4
	454630	BE142075		gb:CM3-HT0137-170999-012-f02 HT0137 Homo	2.4
	451026	AA013218	Hs.157492	cer-d4 (mouse) homolog	2.4
40	420779	L12398	Hs.99922	dopamine receptor D4	2.4
70	438322	AA804170	Hs.221349	ESTs	2.4
	455908	BE156306	13.221343	gb:QV0-HT0367-150200-114-h04 HT0367 Homo	24
	419625	U91616	Hs.91640	nuclear factor of kappa light polypeptid	2.4
45	440773	AA352702	Hs.332541	Homo sapiens, Similar to RIKEN cDNA 2700	2.4
73	450823	T81223	Hs.22011	complement-c1q tumor necrosis factor-rel	2.4
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	2.4
	429109	AL008637	Hs.196352	neutrophil cytosofic factor 4 (40kD)	2.4
	451802	Al817711	Hs.209374	ESTS	2.4
50	419417	R92491	Hs.39429	ESTs	2.4
50	407094	AF000574	Hs.22405	teukocyte immunoglobulin-like receptor,	2.4
	423567	BE252949	Hs.69331	hypothetical protein FLJ 13633	2.4
	427501	Al369280	Hs.131743	ESTs	2.4
	451773	Z42044	Hs.26996	KIAA1278 protein	2.4
55	436845	AA732297	Hs.113928	ESTS	24
55	431584	AW296121	Hs.266263	Homo sapiens cDNA FLJ14115 fis, clone MA	24
	440614	AA781530	Hs.127236	hypothetical protein FLJ12879	24
	423721	AF176911	Hs.132004	cardiotrophin-like cytokine; neurotrophi	24
	452125	BE312642	Hs.28077	GDP-mannose pyrophosphorylase B	2.4
60	419508	AW997938	Hs.90786	ATP-binding cassette, sub-family C (CFTR	2.4
UU	453446	BE299996	11- 40000-	gb:600944574F1 NIH_MGC_17 Homo saplens c	24
•	419792	AA250890	Hs.190037	ESTs	2.4
	452786	R61362	Hs.106642		2.4
	410447	AW816134		gb:MR3-ST0220-290100-016-e04 ST0220 Homo	2.4
65	438662	AA223599	Hs.6351	cleavage and polyadenylation specific fa	2.4
65	402408				2.4
	443950	NM_001425	Hs.9999	epithelial membrane protein 3	24
	414625	AA335738	Hs.76686	glutathione peroxidase 1	2.4
	403048				2.4
70	432088	AA525454		gb:ni85c09.s1 NCI_CGAP_Pr20 Homo saptens	2.4
70	431692	AL021331	Hs.267749	unc93 (C.elegans) homolog A	24
	455023	AW850907		gb:IL3-CT0220-310100-065-H11 CT0220 Homo	24
	426249	F05422	Hs.168352	nucleoporin-like protein 1	24
	446795	AI797713	Hs.156471	ESTs	2.4
75	414774	X02419	Hs.77274	plasminogen activator, urokinase	24
75	414252	AA346483	Hs.126191	ESTs	2.4
	417918	AA209205	Hs.163754	hypothetical protein FLJ12606	2.4
	427550	BE242818	Hs.179606	nuclear RNA helicase, DECD variant of DE	2.4
	404020				2.4
00	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	2.4
80	417222	A1525424	Hs.42053	hypothetical protein MGC2383	. 24
	443839	BE269042	Hs.9661	proteasome (prosome, macropain) subunit,	24
	452706	AW449390	Hs.257150	ESTs, Moderately similar to SUR1_HUMAN S	2.4
	401676			•	24

				COT. AL-J V. W. A. ALLET BUILDARD A	2.4
	428882	AA436915 R88520		ESTs, Moderately similar to ALU7_HUMAN A ESTs	24
	436277 426271	AF026547		chondroitin sulfate proteoglycan 3 (neur	24
	405353	AI 020541	113.103047	onormount sanda protosgrjasti o frios.	2.4
5	409193	AA131483		gb:zo08e05.r1 Stratagene neuroepithelium	2.4
	431431	AL096711		Human DNA sequence from clone RP3-403A15	24
	407889	R34556	Hs.30800	ESTs, Weakly similar to S65657 alpha-1C-	2.4 2.4
	453335	AW857376 AW297288	Hs.169238 Hs.55918	fucosyttransferase 3 (galactoside 3(4)-L hypothetical protein FLJ11354	2.4
10	450621 419652	AU157485	Hs.91973	hypothetical protein	2.4
10	421151	BE174431	Hs.63386	ESTs	2.4
	437846	AA773866	Hs.244569	esophagus cancer-related gene-2	2.4
	420681	AA847602	Hs.106510	ESTs, Moderately similar to ALU2_HUMAN A	2.4
1.0	405288				2.4
15	453527	R49570	Hs.180236	ESTS	2.4 2.4
	429875	A1091815	Hs.136754	gb:qa58b06.s1 Soares_NhHMPu_S1 Homo sapi ESTs	24
	436360 418592	A1962796 X99226	Hs.284153	Fanconi anemia, complementation group A	2.4
	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	2.4
20	449539	W80363	Hs.58446	ESTs	2.4
	419870	AW403911	Hs.266175	phosphoprotein associated with GEMs	2.4
	404584			FOT	2.4 2.4
	454276	AW294996	Hs.255374 Hs.132370	ESTs NADPH oxidase 1	2.4
25	423746 415558	AW361817 AA885143	Hs.125719	ESTs	2.4
23	428141	D50402	Hs.182611	solute carrier family 11 (proton-coupled	2.4
	406953	L36847		gb:Human (clone p17/90) rearranged iduro	2.4
	444471	AB020684	Hs.11217	KIAA0877 protein	2.4
20	451031	Al360187	Hs.4254	ESTs	2.4 2.4
30	455302	AW997641	Un 000E47	gb:RC6-BN0052-170200-011-D06 BN0052 Homo Homo sapiens, clone IMAGE:2905978, mRNA,	2.4
	449063 401048	A1627352	Hs.236547	Horio sapiers, done invoc.2500570, mides,	2.4
	434420	AA688278	Hs.194864	hypothetical protein FLJ22578	2.4
	425848	BE242709	Hs.159637	valyI-IRNA synthetase 2	2.4
35	449086	AI628357	Hs.208037	ESTs	2.4
	415238	R37780	Hs.21422	ESTs	2.4 2.4
	448337	AW206453	Hs.3782	ESTs	23
	416991	N36389 L28824	Hs.141296 Hs.74101	KIAA0226 gene product spleen tyrosine kinase	2.3
40	412600 418385	AW590613	Hs.301040	Homo sapiens, clone IMAGE:3357127, mRNA,	2.3
-10	440769	BE561793	Hs.21446	KIAA1716 protein	2.3
	450437	X13956	Hs.24998	hypothetical protein MGC10471	2.3
	412035	N78559	Hs.293629	hypothetical protein MGC3121	2.3 2.3
45	406739	Al566709	Hs.182426	ribosomal protein S2	2.3
43	418506 410286	AA084248 AI739159	Hs.85339 Hs.61898	G protein-coupled receptor 39 DKFZP586N2124 protein	23
	443740	R56434	Hs.21062	ESTs	2.3
	405605				23
	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	2.3
50	426509	M31166	Hs.2050	pentaxin-related gene, rapidly induced b	2.3 2.3
	445828	F05802	Hs.81907 Hs.196647	ESTs KIAA0527 protein	2.3
	457195 420372	AB011099 AW960049	Hs.293660	Homo sapiens, clone IMAGE:3535476, mRNA,	2.3
	423198	M81933	Hs.1634	cell division cycle 25A	2.3
55	457730	AW753613		gb:RC1-CT0268-060100-013-e01 CT0268 Homo	2.3
	412014	A1620650	Hs.43761	ESTs, Weakly similar to A46010 X-linked	2.3 2.3
	447131	NM_004585		retinolo acid receptor responder (tazaro ESTs	2.3
	446288 436954	AW189209 AA740151	Hs.149708 Hs.130425		2.3
60	411658	AW855598	113,100120	gb:CM1-CT0278-031199-032-e08 CT0278 Homo	2.3
•	404240			•	2.3
	456094	H95091		gb:yw57a09.r1 Soares_placenta_8to9weeks_	2.3
	416951	AA190926	Hs.190785		2.3 2.3
65	406737	Al356586	Un 125005	gb:qy15h09.x1 NCI_CGAP_Bm23 Homo sapien ESTs	2.3
05	458453 452330	Al097452 Al879127	Hs.135095 Hs.191979		2.3
	408523		Hs.314287		2.3
	455470			gb:PM0-MT0011-240300-001-c09 MT0011 Homo	2.3
50	436323		Hs.140963		23
70	450000		Hs.10888	hypothetical protein FLJ21709	2.3 2.3
	416171 419134		Hs.125790 Hs.221771		23
	445933		Hs.293860		2.3
	422089		Hs.10313		2.3
75	449911	Al262106	Hs.12653	ESTs	2.3
	417079	U65590	Hs.81134		2.3 2.3
	411742			eukaryolic translation Initiation factor potassium voltage-gated channel, KQT-lik	2.3 2.3
	435615 423491		Hs.4975 Hs.12967		2.3
80	407182		Hs.23015		2.3
	411448				2.3
	438644	A1126162	Hs.12903	7 ESTs	2.3
	432691	U29725	Hs.3080	mitogen-activated protein kinase 7	2.3

	452198 411125 404054	AI097560 AA151647	Hs.61210 Hs.68877	ESTs, Wealdy similar to 138022 hypotheti cytochrome b-245, alpha polypeptide	2.3 2.3 2.3
_	430458	AA479300	Hs.225706	ESTs, Weakly similar to I38022 hypotheti	2.3
5	440210	AW674562	Hs.125296	ESTs	2.3
	446727	AB011095	Hs.16032	KIAA0523 protein	2.3
	453775 438379	NM_002916 N23018	Hs.35120 Hs.171391	replication factor C (activator 1) 4 (37 C-terminal binding protein 2	2.3 2.3
	449919	AI674685	Hs.200141	ESTs	2.3
10	415293	R49462	Hs.106541	ESTs	2.3
	441126	NM_000429	Hs.323715	methionine adenosyltransferase I, alpha	2.3
	408203	AA053137	Hs.42390	nasopharyngeat carcinoma susceptibility	2.3
	434941	AW073202	Hs.334825	Homo sapiens cDNA FLJ14752 fis, clone NT	2.3
15	450748	A1733093	Hs.130016	ESTs	2.3
13	404185 418327	U70370	Hs.84136	asimal files harmondomain homeoninfine fo	2.3 2.3
	451370	AI791929	Hs.300782	paired-like homeodomain transcription (a ESTs	2.3
	400034	74731323	10.000704	4016	2.3
	407723	AW071161	Hs.252873	ESTs	2.3
20	431320	AW969474	Hs.183070	ESTs	2.3
	429271	AF039850	Hs.198515	dead ringer (Drosophila)-like 1	2.3
	453707 419225	AW003879 U70073	Hs.126522	Homo sapiens, clone MGC:16722, mRNA, com gb:HSU70073 Human Homo sapiens cDNA clon	2.3 2.3
	444556	Al277924	Hs.145199	ESTs	2.3
25	405741	, 42, 102			2.3
	400917				2.3
	432567	AA736777	Hs.293770	ESTs .	2.3
	437949	U78519	Hs.41654	ESTs, Wealdy similar to A46010 X-linked	2.3
30	450514	AC005785	Hs.25059 Hs.301989	A kinase (PRKA) anchor protein 8 KIAA0246 protein	2.3 2.3
30	418400 444019	BE243026 BE173977	Hs.10098	putative nucleotar RNA helicase	2.3
	406326	02173377	113.10030	possito necessa 1444 namase	23
	412077	N51107	Hs.47199	ESTs, Wealthy similar to FLJ00004 protein	2.3
	427647	W19744	Hs.180059	Homo sapiens cDNA FLJ20653 fis, clone KA	2.3
35	414528	AA148950	Hs.188836	ESTs	2.3
	414854	BE546797	Hs.51483	ESTs, Weakly similar to hypothetical pro	2.3
	420352	BE258835 AW292275	Hs.158365	gb:601117374F1 NIH_MGC_16 Homo sapiens c ESTs	2.3 2.3
	439467 402627	A11232213	115.130000	COIS	2.3
40	451711	AK000461	Hs.26890	cat eye syndrome chromosome region, cand	2.3
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	2.3
	423869	BE409301	Hs.134012	C1q-related factor	2.3
	405915				2.3
45	431503	NM_012129	Hs.258576	claudin 12	2.3 2.3
43	423306 443232	W88562 AF161521	Hs.108198 Hs.9081	ESTs phenylatanyl-IRNA synthetase beta-subuni	2.3
	433064	D79991	Hs.30002	SH3-containing protein SH3GLB2; KIAA1848	2.3
	434437	AI912566	Hs.187813	ESTs	2.3
	436191	BE407866	Hs.170253	hypothetical protein FLI23282	2.3
50	420006	H14429	Hs.94300	serologically defined colon cancer antig	2.3
	447942	F12628	Hs.334786	hypothetical protein MGC16040	23 23
	403166 422119	AJ277829	Hs.111862	KIAA0590 gene product	23
	403751	-42110E3	10.111002	terenduce gone product	2.3
55	426451	AI908165	Hs.169946	GATA-binding protein 3	2.3
	427413	BE547647	Hs.177781	hypothetical protein MGC5618	23
	409091	AW970386	Hs.269423	ESTs	2.3
	440491	R35252 AK000123	Hs.24944 Hs.180479	ESTs, Weakly similar to 2109260A B cell hypothetical protein FLJ20116	2.3 2.3
60	427722 405747	ANUU0123	FIS. 100413	hypodieucai protein r Eszo 10	2.3
	438210	AA780519	Hs.311601	EST	2.3
	404652				2.3
	423524	AF055989	Hs.129738	potassium voltage-gated channel, Shaw-re	2.2
65	426793	X89887	Hs.172350	HIR (histone cell cycle regulation defec	2.2
0.5	444424 434031	AI654684 BE384165	Hs.196377 Hs.23723	ESTs pseudouridylate synthase 1	2.2 2.2
	427650	AW501245	Hs.252259	ribasomal protein S3	2.2
	435220	D50030	Hs.104	HGF activator	2.2
	438279	AA805166	Hs.154762	HIV-1 rev binding protein 2	2.2
70	424668	D83702	Hs.151573	cryptochrome 1 (photolyase-like)	2.2
	429961	BE246829	Hs.226770		2.2
	442065 415198	AI831229 AW009480	Hs.128417 Hs.943	hypothetical protein FLJ14009 natural killer cell transcript 4	2.2 2.2
	420536	AL117455	Hs.275438	histone deacetylase 7A	2.2
75	411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-assoc	2.2
	443753	AW367578	Hs.134749		2.2
	423243	AA351938	Hs.23964	sin3-associated polypeptide, 18kD	2.2
	446572	AV659151	Hs.282961	ESTs	2.2
80	412247 421040	AF022375 AA715026	Hs.73793 Hs.135280	vascular endothelial growth factor ESTs	2.2 2.2
30	426212	S71824	Hs.167988		2.2
	455584	BE007420		gb:PM3-BN0142-200300-001-c04 BN0142 Homo	2.2
	406851	AA609784	Hs.180255	major histocompatibility complex, class	2.2

				and the state of t	2.2
	444153			hypothetical protein FLJ10748 topoisomerase (DNA) III alpha	2.2
	419575			ESTs	2.2
	418672 456261		Hs.104157	ESTs, Wealdy similar to KIAA0694 protein	2.2
5	415737		He 118743	ESTs	2.2
_	447554	AJ391598	Hs.36119	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.2 2.2
	405159		11: 044442	ret.	2.2
	442177	AW661820	Hs.211413 Hs.39749	ESTs ESTs	22
10	446139 458339	H77395 AW976853	Hs.172843	ESTs	2.2
10	401876	711313033			2.2
	439566	AF086387		gb:Homo sapiens full length insert cDNA	2.2 2.2
	425079	H09963	Hs.2257	vitronectin (serum spreading factor, som	22
1.5	441837	AA361743	Hs.179881	core-binding factor, beta subunit preproprotactin-releasing peptide	2.2
15	430644	AB015419 AL133990	Hs.247710 Hs.190642	ESTs	2.2
	431474 407739	NM_002285	Hs.38070	lymphoid nuclear protein related to AF4	2.2
	424244	AV647184	Hs.143601	Iwnothetical protein hCLA-iso	2.2
	438057	AW294544	Hs.125785	ESTs, Wealthy similar to CORB MOUSE CORNI	2.2 2.2
20	412715	NM_000947	Hs.74519	primase, polypeptide 2A (58kD)	2.2
	422365	AF035537	Hs.115521	REV3 (yeast homolog)-like, catalytic sub	2.2
	404170 406902	M32074		gb:Human retinoic acid receptor gamma 2	2.2
	437902	AA770599	Hs.144055	ESTs	2.2
25	401012				2.2 2.2
	446502	Al302654	Hs.208024	ESTs	2.2
	442554	AW467376	Hs.129640	ESTs lg superfamily protein	2.2
	443021	AA368546 AW117261	Hs.8904 Hs.125914	ESTs	2.2
30	421141 443070	BE388662	Hs.8984	Homo sapiens chromosome 14 BAC 98L12	2.2
50	446566	H95741	Hs.17914	membrane-spanning 4-domains, subfamily A	2.2
	427695	R88483	Hs.172862	ESTs	2.2 2.2
	426503	AA380153		gb:EST93093 Skin tumor I Homo sapiens cD	2.2 2.2
25	431468	AW248431	Hs.256526 Hs.47367	nuclear prelamin A recognition factor KIAA1785 protein	2.2
35	416185 437319	AW975861 BE410958	Hs.56406	Homo sapiens cDNA FLJ13549 fis, clone PL	2.2
	402064	DC410350	113.50400		2.2
	413335	AI613318	Hs.48442	ESTs	2.2
	408212	AA297567	Hs.43728	hypothetical protein	2.2 2.2
40	406169		05054	interdentia 12 magnitus alpha 2	2.2
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2 Horno sapiens cDNA FLJ13054 fis, clone NT	2.2
	407335	AA631047 W42591	Hs.158761 Hs.23892	ESTs	2.2
	409715 431921	N46466	Hs.58879	ESTs	2.2
45	443823	BE089782	Hs.9877	hypothetical protein	2.2
	432458	AI968598	Hs.78768	malignant cell expression-enhanced gene/	2.2 2.2
	419726	U50330	Hs.1274	bone morphogenetic protein 1 Homo sapiens mRNA; cDNA DKFZp564C142 (fr	2.2
	423178	AI033140 AA903705	Hs.124983 Hs.4190	Homo sapiens cDNA: FLJ23269 fis, clone C	2.2
50	451089 415216	AI825905	Hs.193211		2.2
50	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	2.2
	441830	AA383104	Hs.42954	hypothetical protein DKFZp564D0372	2.2 2.2
	406660	X65371	Hs.172550	polypyrimidine tract binding protein (he proteasome (prosome, macropain) subunit,	2.2
55	443378	AW392550 R97268	Hs.9280 Hs.177269		2.2
"	432558 408146	R45621	Hs.81057	hypothetical protein MGC2718	2.2
	419865	NM_007020		U1-snRNP binding protein homolog (70kD)	22
	439444	AI277652	Hs.54578	ESTs, Wealty similar to 138022 hypotheti	2.2 2.2
۲0	438407	AI457122	Hs.12967		2.2
60	450184 409130		Hs.23761 Hs.75658		2.2
	428844				2.2
	429489		Hs.20403	9 aristatess-like homeobox 3	2.2
	433042	AW193534			2.2 2.2
65	440658		Hs.14303		2.2
	408204 427498		Hs.43666 6 Hs.17872		2.2
	408006		Hs.30334		2.2
	445703			glycine dehydrogenase (decarboxylating;	2.2
70	431446	AW294929	Hs.25538		2.2 2.2
	456660			12 sotute carrier family 30 (zinc transport nuclear transcription factor, X-box bind	2.2
	433099				2.2
	41585 41524		Hs.2725	2 ESTs	2.2
75	44365			gb:yl42f10.s1 Soares fetal liver spleen	2.2
	40252	1 AW501216		15 KIAA0515 protein	2.2
	41481				2.2 2.2
	44653		Hs.2826 Hs.7280		2.2
80	41579 41481		Hs.7736		2.2
00	45302			2 RecQ protein-like 4	2.2
	41213	3 U83460	Hs.7361	4 solute carrier family 31 (copper transpo	2.2 2.2
	40788		3 Hs.4096	8 heparan sulfate (glucosamine) 3-O-sulfot	2.2

			16- 6400	mana a series de la series de l	20
	437033	AW248364 AA577455	Hs.5409 Hs.24937	RNA polymerase I subunit	2.2 2.2
	422732 416388	AI417358	Hs.73677	transformer-2 alpha (htra-2 alpha) ESTs	2.2
	452849	AF044924	Hs.30792	hook2 protein	2.2
5	446615	BE513202	Hs.15589	PPAR binding protein	2.2
•	428361	NM_015905	Hs.183858	transcriptional Intermediary factor 1	2.2
	446279	AA490770	Hs.182382	EST ₈	2.2
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	2.2
10	403969				2.2
10	410423	AW402432	Hs.63489	protein tyrosine phosphatase, non-recept	2.2
	429736	AF125304	Hs.212680	tumor necrosis factor receptor superfami	2.2
	447091	AW089648 NM_003877	Hs.157779 Hs.110776	ESTs, Wealdy similar to CA17_HUMAN COLLA	2.2 2.2
	422017 426728	NM_007118	Hs.171957	STAT induced STAT inhibitor-2 triple functional domain (PTPRF interact	2.2
15	438726	AB033103	Hs.6385	KIAA1277 protein	2.2
13	453315	BE544203	Hs.24831	ESTs	2.2
	423244	AL039379	Hs.209602	ESTs, Wealdy similar to ubiquitous TPR m	2.2
	433610	AA806822	Hs.112547	ESTs	2.2
•	429451	BE409851	Hs.202833 -	heme oxygenase (decycling) 1	2.2
20	417980	R32235		gb:yh67f08.r1 Soares placenta Nb2HP Homo	2.2
	406347				22
	414406	BE297904		gb:601177814F1 NIH_MGC_17 Homo sapiens c	2.2 2.2
	401827	A A 420CEO	Hs.16529	transmanherna A euroceanihi mambas (tatr	2.2
25	446913 452294	AA430650 AI871925	Hs.117895	transmembrane 4 superfamily member (tetr ESTs, Moderately similar to A47582 B-cel	22
23	404084	7407 1323	113.111030	LOTS, INDOCINCIA SULLING BUTTIONE D'OC	2.2
	456786	AK002084	Hs.132851	hypothetical protein FLJ11222	2.2
	435031	AI632091	Hs.116877	ESTs	2.2
	442609	AL020996	Hs.8518	selenoprotein N	2.1
30	439732	AW629604	Hs.167641	hypothetical protein from EUROIMAGE 1703	2.1
	421506	BE302796	Hs.105097	flymidine kinase 1, soluble	2.1
	439253	AF086064	Hs.332252	ESTs	21
	409669	AW177551	Hs.220255	hypothetical protein MGC13098	2.1
35	429574	BE268321	Hs.208912	hypothetical protein MGC861	2.1 2.1
33	437470 408945	AL390147 AW015089	Hs.134742 Hs.4964	typothetical protein OKFZp547D065 DKFZP586J1624 protein	2.1
	447687	A1627947	Hs.150186	hypothetical protein DKFZp566K1946	2.1
	459584	Al910884	Hs.207898	ESTs	21
	439130	AA306090	Hs.124707	ESTs	2.1
40	428180	AI129767	Hs. 182874	guanine nucleotide binding protein (G pr	2.1
. •	442028	AI239437	Hs.48945	ESTs	2.1
	430968	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	2.1
	443609	AV650231	Hs.282941	ESTs, Highly similar to A Chain A, Human	2.1
4.5	417164	AA338283	Hs.81361	heterogeneous nuclear ribonucleoprotein	21
45	444534	AW271626	Hs.42294	ESTs	2.1
	438391	AI262248	Hs.25027	ESTs	2.1 2.1
	442003	AW297497	Hs.201891 Hs.289038	ESTs	2.1
	456278 416976	BE300369 BE243985	Hs.80680	hypothetical protein MGC4126 major vault protein	21
50	417810	D28419	Hs.82609	hydroxymethylbilane synthase	2.1
•	445242	BE156478	Hs.21108	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.1
	452712	AW838616		gb:RC5-LT0054-140200-013-D01 LT0054 Homo	2.1
	434926	BE543269	Hs.50252	mitochondrial ribosomal protein L32	2.1
	421564	AB007864	Hs.105850	KIAA0404 protein	2.1
55	424927	AW973666	Hs.153850	hypothetical protein C321D2.4	2.1.
	432742	AA564453	Hs.162339	ESTs	2.1 2.1
	435958	H98180	Hs.117975	ESTs ESTs	21
	421531 410431	AA713505 BE261320	Hs.291769 Hs.158196	transcriptional adaptor 3 (ADA3, yeast h	21
60	420503	AI570943	Hs.337546	ESTs	21
-	448127	AJ478416	Hs.282883	ESTs, Weatty similar to ALU1_HUMAN ALU S	2.1
	452897	BE066058	Hs.269233	ESTs, Moderately similar to 178885 serin	2.1
	447112	H17800	Hs.7154	ESTS	2.1
-	406577				2.1
65	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	2.1
	451460	AI797550	Hs.209652	ESTs	21
	447402	H54520	Hs.18490	hypothetical protein FLJ20452	21
	435828	AA700705	Hs.13852	ESTs	2.1 2.1
70	436396 420582	AI683487 BE047878	Hs.152213 Hs.99093	wingless-type MMTV integration site fami Homo sapiens chromosoma 19, cosmid R2837	21
,,	452020	AA722012	Hs.255757		21
	415586	245481	,	gb:HSC2QE041 normalized infant brain cDN	2.1
	452620	AA436504	Hs.119286		2.1
	457066	BE244513	Hs.158272		2.1
75	435472	AW972330	Hs.283022	triggering receptor expressed on myeloid	2.1
	431741	AA514783	Hs.191701		2.1
	446840	AW294828	Hs.209203		21
	440818	AJ147060	Hs.146726		2.1 2.1
80	410174	AA306007	Hs.59461	DKFZP434C245 protein	21
50	400822 412760	AW379030	Hs.41324	ESTs	21
	410653	BE383768	Hs.65238	95 kDa retinoblastoma protein binding pr	21
	426925	NM_001196			2.1
	· -				

					2.1
		79 1001 111		nypothetical protein MGC13102 ESTs	2.1 2.1
	452560 456437		Hs.115185	ESTs, Moderately similar to PC4259 ferri	2.1
_	458922	BE501831	Hs.282053 1	ESTs Homo sapiens mRNA; cDNA DKFZp434N079 (fr	2.1 2.1
5	439231		Hs.141480 Hs.90691	nucleophosmin/nucleoplasmin 3	2.1
	419488 411829	AW865749		gb:QV3-SN0021-100500-185-c03 SN0021 Homo	2.1
	457192	AL135682	Hs.22452	Homo sapiens mRNA for KIAA1737 protein, gb:QV0-OT0033-010400-182-a07 OT0033 Homo	2.1 2.1
10	422128	AW881145 W31518		ESTs	2.1
10	452571 423699	H41850		PCAF associated factor 65 alpha	2.1
	406610				2.1 2.1
	453638	AW814996 AA362858		gb:MR1-ST0206-170400-024-h09 ST0206 Homo gb:EST72900 Ovary II Homo sapiens cDNA 5	2.1
15	418856 437623	D63880	Hs.5719	chromosome condensation-related SMC-asso	2.1
10	410908	AA121686	Hs.10592	ESTs	2.1 2.1
	420221	N25991	Hs.43725 Hs.221610	ESTs ESTs	21
	424739 425398	AA346108 AL049689	Hs.156369	hypothetical protein similar to tenascin	21
20	424901	Z11933	Hs.182505	POU domain, class 3, transcription facto	2.1 2.1
	411096	U80034	Hs.68583	mitochondrial intermediate peptidase gb:HSC3JF101 normalized infant brain cDN	2.1
	415635 418181	F13168 U37012	Hs.83727	cleavage and polyadenylation specific fa	2.1
	407103	AA424881	Hs.256301	hypothetical protein MGC13170	2.1 2.1
25	454389	AW752571		gb:IL3-CT0213-170100-055-F02 CT0213 Homo	2.1
	400021 439228	N51700		gb:yy72d01.s1 Soares_multiple_sclerosis_	2.1
	456505	AA504595	Hs.111418	ESTs	2.1 2.1
20	405258		Hs.101654	ESTs	2.1
30	444645 430246	AI184564 AI269069	Hs.109268	hypothetical protein FLJ12552	2.1
	458687	AW024815	Hs.170088	GLUT4 enhancer factor	2.1 2.1
	403857				2.1
35	400258 422221	AA306649	Hs.169370	FYN oncogene related to SRC, FGR, YES	2.1
55	441054	AA913591	Hs.126480	ESTs	2.1 2.1
	452700	AI859390	Hs.288940	five-span transmembrane protein M83 gb:MR4-ST0124-181299-020-b06 ST0124 Horno	2.1
	454606 448954	AW809752 AB014564	Hs.22616	KIAA0664 protein	2.1
40	443148	AI034357	Hs.211194	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.1 2.1
	453486	AL039201	Hs.173554 Hs.192142	ubiquinol-cytochrome c reductase core pr ESTs	2.1
	437695 425449	AA769202 X52056	Hs.157441	spleen focus forming virus (SFFV) provir	2.1
	447270	AC002551	Hs.331	general transcription factor IIIC, polyp	2.1 2.1
45	435677	AA694142	Hs.293726 Hs.250181		2.1
	436382 435837	AW977063 Al689210	Hs.187276		2.1
	458287	AA987556	Hs.12867	ESTs	21 21
50	423794	BE551781	Hs.231895 Hs.74316	ESTs desmoplakin (DPI, DPII)	2.1
50	408049 402721	AW076098	15.74310		2.1
	451999	AW176401	Hs.27424	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	2.1 2.1
	417541	AI992191 AW402389	Hs.180040 Hs.920	hypothetical protein FLJ22439 modulator recognition factor I	2.1
55	414857 435760		Hs.213004		2.1
	428086	AL110193	Hs.224137		2.1 2.1
	447853		Hs.164285 Hs.89555		2.1
	419034 431019			forthead box G18	2.1
60	421064	Al245432	Hs.10138		2.1 2.1
	416435		Hs.17970 Hs.22253		2.1
	437014 459369		110.22200	gb:yd40e03.r1 Soares fetal liver spleen	2.1
	40223	9		4 hypothetical protein DKFZp434E1723	· 2.1
65	41228			A Louis manage A	2.1
	42601 43888		Hs.18498	7 FSTs	2.1
	42607	6 AW962714	ļ	gb:EST374787 MAGE resequences, MAGG Horno	21 21
70	40456		Hs.8858	bromodomain adjacent to zinc finger doma	2.1
70	44293 40817		Hs.19066	hypothetical protein DKFZp667O2416	21
	42386	7 AA331886	i	gb:EST35757 Embryo, 8 week I Homo sapien Sarcolemmal-associated protein	2.1 2.1
	45860		Hs.4007 Hs.2889		2.1
75	40965 40172				2.1
	43367	5 AW97765			2.1 2.1
	45674 41703		Hs.1844 6 Hs.8097		2.1
	4150		Hs.2289	5 hypothetical protein FLJ23548	2.1 2.1
80) 43926	62 AA83233	3 Hs.3330	45 ESTs	2.
	4031 4367		7 Hs.2890)53 hypothetical protein FLJ14733	2.1
	4406				2.
				185	

	409745	AA077391		gb:7B14E12 Chromosome 7 Fetal Brain cDNA	2.1
	453485	BE620712	Hs.33026	hypothetical protein PP2447	2.1
	418177 457292	N44967 AJ921270	Hs.5663 Hs.334882	ESTs hypothetical protein FLJ14251	2.1 2.1
5	454434	AA083558	Hs.261286	ESTs	21
	406085				21
	424441 422726	X14850 U11690	Hs.147097 Hs.1572	H2A histone family, member X laciogenital dysplasia (Aarskog-Scott sy	21 21
	424576	BE154142	Hs.96833	ESTS	21
10	423660	AL045228	Hs.130831	Homo sapiens mRNA; cDNA DKFZp434L137 (fr	2.1
	403509 441940	AF231919 AW298115	Hs.18759 Hs.128152	KIAA0539 gene product - ESTs	2.1 2.1
	439190	AW978693	Hs.293811	ESTs	21
1.5	417791	AW965339	Hs.111471	ESTs	2.1
15	423701 427239	AA329856 BE270447	Hs.143022 Hs.174070	ESTs ubiquitin carrier protein	2.1 2.1
	459642	BE243103	113.117010	gb:TCAAP2E0949 Pediatric acute myelogeno	2.1
	450385	AI631024	Hs.24948	synuclein, alpha interacting protein (sy	2.1
20	425159 425591	NM_004341 AW294734	Hs.154868 Hs.279727	carbamoyl-phosphate synthetase 2, aspart Homo sapiens cDNA FLJ14035 fis, clone HE	2.1 2.1
20	445101	T75202	Hs.12314	Homo sapiens mRNA; cDNA DKFZp586C1019 (f	21
	412811	H06382	Hs.21400	ESTs	2.1
	426369 435924	AF134157 AW029203	Hs.169487 Hs.191952	Kreisler (mouse) maf-related leucine zip ESTs	2.1 2.1
25	418388	R72332	Hs.29258	Homo sapiens cDNA FLJ11364 fis, clone HE	2.1
	452235	AL039743	Hs.28514	testes development-related NYD-SP21	2.1
	452313 450704	Y00486 H85157	Hs.28914 Hs.40696	adenine phosphoribosyltransferase ESTs	- 21 - 21
	427539	AA405205	Hs.97960	ESTs, Wealdy similar to T51146 ring-box	21
30	402028			•	2.1
	405362 414718	H95348	Hs.107987	ESTs .	21 21
	433424	R68252	Hs.163566	ESTs	2.1
25	444875	AI200759	Hs.44737	ESTs	2.0
35	449523 456072	NM_000579 H54381	Hs.54443	chemokine (C-C motif) receptor 5 gb:yq89a03.s1 Soares fetal liver spleen	2.0 2.0
	436331	AI239495	Hs.120189	ESTs	2.0
	448418	Z43704	Hs.21192	Homo sapiens clone 25155 mRNA sequence	2.0
40	447250 448192	AI878909 R43915	Hs.17883 Hs.4958	protein phosphatase 1G (formerly 2C), ma ESTs	2.0 2.0
70	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	2.0
	408605	AF025374	Hs.46465	T-cell, immune regulator 1	2.0
	410790 436872	AW803357 X15624		gb:IL2-UM0079-090300-050-A08 UM0079 Homo gb:Human H1 RNA	2.0 2.0
45	432238	AL133057	Hs.274135	Homo sapiens mRNA; cDNA DKFZp434K1815 (f	2.0
	446307	T50083	Hs.9094	ESTs	2.0
	436588 452487	AA759233 AW207659	Hs.126506 Hs.6630	ESTs Homo sapiens cDNA FLJ13329 fis, clone OV	2.0 2.0
	430420	AW140027	Hs.26373	Homo sapiens cDNA: FLJ23449 fis, clone H	2.0
50	432036	AF224266	Hs.272373	interleukin 20	2.0
	414450 433507	L00727 AI817336	Hs.898 Hs.191791	dystrophia myotonica-protein kinase ESTs	2.0 2.0
	427964	AA418082	Hs.98286	ESTs, Weakly similar to T20655 hypotheti	2.0
55	443108	W86975	Hs.203707	ESTs	2.0 2.0
22	434504 454310	AI887341 AW818390	Hs.121590 Hs.175613	hypothetical protein FLJ 12827 homolog of Xenopus Claspin	2.0
	443566	AI290284	Hs.159872	ESTs	2.0
	449722	BE280074	Hs.23960	cyclin B1	2.0 2.0
60	452682 412362	AA456193 AW945484	Hs.9071 Hs.184252	progesterone membrane binding protein ESTs, Weakly similar to ALU8_HUMAN ALU S	2.0
••	429341	X73874	Hs.2393	phosphorylase kinase, alpha 1 (muscle)	2.0
	435863	AF255346	Hs.62919 Hs.2186	Jun dimerization protein p21SNFT eukaryotic translation elongation factor	2.0 2.0
	400774 453944	R58624 AW975369	Hs.292570	Homo sapiens, clone IMAGE:3502107, mRNA,	20
65	419227	BE537383	Hs.89739	cholinergic receptor, nicotinic, beta po	2.0
	448529 443206	T26460 AB011420	Hs.22550 Hs.9075	ESTs serine/threonine kinase 17a (apoptosis-i	2.0 2.0
	439360	AA448488	Hs.336629		2.0
70	436660	A1658870	Hs.184513	ESTs	2.0
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	408215	BE614290	Hs.43812	syntaxin 10	2.0
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                              Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA
                             sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
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                              Indicates DNA strand from which exons were predicted.
           Nt_position:
                             Indicates nucleotide positions of predicted exons.
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TABLE 10A: ABOUT 582 GENES SIGNIFICANTLY DOWN-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT CNS TISSUES
Table 10A lists about 582 genes significantly down-regulated in glioblastoma compared to normal adult CNS tissues. These were selected from 59680 probesets on the
Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" normal CNS to "average" glioblastoma was greater than or equal to 3. The "average" normal CNS level was set to the 85th percentile amongst various tumor samples. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number

75 ExAcon: Exemptar Accession number, Genbank accession number

UnigenetD: Unigene number Unigene Title: Unigene gene title

R1: Ratio of 75th percentile normal central nervous system tissue to 85th percentile tumor

80	Pkey 453655 417275 430829	ExAcon AW960427 X63578 AW451999		Unigene Title transforming growth factor, beta recepto parvalbumin ESTs	R1 136.7 29.0 25.7
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	410657	AF063228	Hs.65248	dynein, cytoplasmic, intermediate polype	22.6
	419954	D14720	Hs.93883	myelin protein zero (Charcot-Marie-Tooth	21.2
	459247	N46243	Hs.110373	ESTs, Highly similar to T42626 secreted	18.5
_	416133	NM_001683	Hs.89512	ATPase, Ca↔ transporting, plasma membra	15.5
5	416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin t	15.2
	417167 433940	AW206437 H05129	Hs.4290 Hs.7459	ESTs cyclic AMP-regulated phosphoprotein, 21	14.8 13.4
	413324	V00571	Hs.75294	corticotropin releasing hormone	13.1
	439830	AA846666	Hs.151489	ESTs, Weakly similar to XE7_HUMAN PROTEI	12.6
10	408068	AW148652	Hs.167398	ESTs	12.6
	412636	NM_004415	Hs.74316	desmoplakin (DPI, DPII)	12.5 12.2
	429096 412638	AB011106 AA910199	Hs.196012 Hs.203838	KIAA0534 protein ESTs	12.2
	423690	AA329648	Hs.23804	ESTs, Wealdy similar to PN0099 son3 prot	12.1
15	456844	A1264155	Hs.152981	CDP-diacylglycerol synthase (phosphatida	11.9
	418318	U47732	Hs.84072	transmembrane 4 superfamily member 3	10.9
	442593	R39804 Al290919	Hs.31961 Hs.153661	ESTs ESTs	10.8 10.4
	446353 420290	AW977318	Hs.194480	ESTS	10.3
20	414220	BE298094		gb:601118231F1 NIH_MGC_17 Homo sapiens c	10.3
	414290	AI568801	Hs.71721	EŞTs	10.2
	426365	AA376657	Hs.10283	RNA binding motif protein 88	10.0
	414937 419643	R38698 F06066	Hs.12382 Hs.91791	ESTs chromosome 11 open reading frame 25	10.0 9.5
25	407173	T64349	15.31731	gb:yc10d08.s1 Stratagene lung (937210) H	9.5
	412454	R55745	Hs.167330	ESTs	9.5
	439366	AF100143	Hs.6540	fibroblast growth factor 13	9.4
	415315	F12240	Hs.250655	prothymosin, alpha (gene sequence 28)	9.3
30	441790 448117	AW294909 H49129	Hs.132208 Hs.172982	ESTs ESTs	9.2 9.1
50	400661	1143123	NS.172302	2015	9.0
	433558	AA833757	Hs.201769	ESTs, Weakly similar to T24435 hypotheti	9.0
	412453	R20205	Hs.167330	ESTs	9.0
35	408920	AL120071	Hs.48998	fibronectin leucine rich transmembrane p	8.9
33	409031 428106	AA376836 BE620016	Hs.76728 Hs.182470	ESTs PTD010 protein	8.7 8.3
	446544	AI631932	Hs.7047	ESTs, Weakly similar to Unknown [H.sapie	8.2
	423479	NM_014326	Hs.129208	death-associated protein kinase 2	8.2
40	439480	AL038511	Hs.125316	ESTs, Weakly similar to S33990 finger pr	8.2
40	418036	Z37976	Hs.83337	tatent transforming growth factor beta b	8.0 8.0
	456490 410200	U83171 AA082557	Hs.97203 Hs.101915	small inducible cytokine subfamily A (Cy Stargardt disease 3 (autosomal dominant)	8.0
	414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	8.0
	408428	NM_014787	Hs.44896	DnaJ (Hsp40) homolog, subfamily 8, membe	7.9
45	437073	AJ885608	Hs.94122	ESTs	7.9
	408434	AW195317	Hs.107716	hypothetical protein FLJ22344	7.9 7.9
	438150 440209	AA037534 H05049	Hs.79059 Hs.22269	transforming growth factor, beta recepto neurexin 3	7.8
	408119	W26213	Hs.101672	ESTs, Weakly similar to T00331 hypotheti	7.8
50	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	7.8
	410587	AA370706	Hs.86412	chromosome 9 open reading frame 5	7.8 7.7
	429611 405800	AI889077	Hs.211388	Homo sapiens BAC clone CTB-60N22 from 7q	7.7
	421750	AK000768	Hs.107872	hypothetical protein FLJ20761	7.7
55	426356	BE536836	Hs.98682	hypothetical protein FKSG32	7.7
	423440	R25234	Hs.143434	contactin 1	7.7
	445148	AJ214510 D86980	Hs.146304 Hs.79170	ESTs KIAA0227 protein	7.6 7.6
	416294 424087	N69333	Hs.143434	contactin 1	7.6
60	437479	R61866	Hs.101277	ESTs	7.5
	405071				7.5
	421224	AW402154	Hs.125812	ESTs	7.4 7.4
	442025 459476	AW887434 BE185844	Hs.11810	CDA11 protein gb:iL5-HT0731-110500-087-c08 HT0731 Horno	7.2
65	430573	AA744550	Hs.136345		7.1
	401836				7.1
	448958	AB020651	Hs.22653	KIAA0844 protein	7.1
	430152	AB001325 AW968619	Hs.234642 Hs.155849		7.1 7.1
70	419474 401780	A11300013	TS.133043	2318	7.1
	446052	AA358760		gb:EST67699 Fetal tung II Homo sapiens c	7.0
	423605	AF047826	Hs.129887		7.0
	433098	AW190593	Hs.151143		7.0
75	449511 451285	AI436187 AW137912	Hs.296261 Hs.227583		6.9 6.8
, ,	428414	AL049980	Hs.184216		6.8
	419273	BE271180	Hs.293490	ESTs, Weakly similar to i38022 hypotheti	6.8
	443155	R54485	Hs.23772	ESTs	6.8
80	450561 433068	R49674 NM_006456	Hs.25909 Hs.288215	ESTs sialytransferase	6.8 6.8
50	440729	AA904739	Hs.128204		6.8
	448426	BE018315	Hs.280776	tankyrase, TRF1-interacting ankyrin-rela	6.7
	423589	AA328082	Hs.209569	ESTs	6.6

	44004	41370003	Hs.72630 E	STs	6.5
	415681 413510	AI379882 F13044		h:HSC3HH101 normalized infant brain cDN	6.4
	427992		Hs.181353	JDP-Gal:betaGlcNAc beta 1,3-galactosyftr	6.4
_	453344		Hs.44571 1	STs	6.4 6.4
5	450642		Hs.7130 (copine IV	6.4
	432251	AW972983		polycythemia rubra vera 1; cell surface KIAA0231 protein	6.4
	429322	D86984 AW016637		ESTs	6.4
	444927 447482	AB033059		KIAA1233 protein	6.4
10	400332	S66407	He 248032	FI TA	6.3
	440703	AL137663	Hs.7378	Homo sapiens mRNA; cDNA DKFZp434G227 (fr	6.3
	446129	AW244073		ESTs	6.3 6.3
	454076	AW204712		ESTs gb:EST69040 Fetal lung II Homo sapiens c	6.3
1.5	425526	AA359933	Hs.109439	osteoglycin (osteoinductive factor, mime	6.3
15	421913	A1934365 AA913143	Hs.26303	ESTs	6.2
	434273 408480	AI350337	Hs.164568	fibroblast growth factor 7 (keratinocyte	6.2
	451301	AI769514	Hs.209890	EST	6.2
	430754	AW862610	Hs.157068	ESTs	6.2 6.2
20	438356	AA805530	Hs.48527	ESTs	6.2
	422743	BE304678	Hs.119598	ribosomal protein L3 Homo sapiens cDNA FLJ11422 fis, clone HE	6.2
	453355	AW295374	Hs.31412	ESTs	6.2
	426388	AW081394 AI904296	Hs.97103	gb:PM-BT046-220199-285_1 BT046 Homo sapi	6.1
25	452502 402546	Albunzau			6.1
23	457534	AI761307	Hs.232226	ESTs	6.1
	408165	AL137573	Hs.43143	Homo sapiens mRNA; cDNA DKFZp564A2463 (f	6.1 6.1
	404958			At an anniana — Data for KIA A1963 protoin	6.1
20	432501	BE546532	Hs.25682	Homo sapiens mRNA for KIAA1863 protein, ESTs	6.1
30	442979	AW440782	Hs.174743 Hs.113987	lectin, galactoside-binding, soluble, 2	6.0
	422262 408713	AL022315 NM_001248	Hs.47042	ectonucleoside triphosphate diphosphohyd	6.0
	454065	BE394588	110.41412	gb:601311808F1 NIH_MGC_44 Homo sapiens c	6.0
	430004	U27768	Hs.227571	regulator of G-protein signalling 4	5.9
35	401521				5.9 5.9
	425087	R62424	Hs.126059	ESTs	5.9
	445298	AF187813	Hs.14637 Hs.21435	kidney- and liver-specific gene ESTs	5.9
	417761 424806	R13727 AA382523	Hs.105689	MSTP031 protein	5.9
40	441695	T12411	Hs.183745	hypothetical protein FLJ13456	5.9
0	457483	AB034694	Hs.272558	endomucin-1	5.9
	417175	R44558	Hs.94002	ESTs	5.8 5.8
	437483	AL390174	11- 440000	gb:Homo sapiens mRNA; cDNA DKFZp547J184	5.8
45	436427	AI344378	Hs.143399 Hs.146246	ESTs ESTs	5.8
43	411939 459053	A1365585 A1807052	Hs.210361	ESTs	5.7
	411052	AW814950		gb:MR1-ST0206-130400-023-d06 ST0206 Homo	5.7
	431063	Z98949	Hs.326843	hypothetical protein bk125H2.1	5.7 5.7
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	5.7
50	408478	NM_000806		gamma-aminobutyric acid (GABA) A recepto ESTs	5.7
	442676	AI733585 AV659082	Hs.130897 Hs.134228		5.7
	446443 400865	AV659062	NS. 134220		5.7
	459080	AW192083	Hs.290855	ESTs	5.6
55	407952		Hs.88845	ESTs, Highly similar to T50835 hypotheti	5.6
	431984		Hs.272284		5.6 5.6
	425705		Hs.159265		5.6
	442238				5.6
60	422994 457148		Hs.184627		5.6
00	428356		Hs.10338	ESTs	5.6
	415927		Hs.78919	Kell blood group precursor (McLeod pheno	5.5 5.5
	402092				· 5.5
15	440526		Hs.21147		5.5
65	444409		Hs.49265 Hs.86320		5.4
	417877 458231				5.4
	43070		Hs.25065		5.4
	45618		Hs.44940		5.4
70	42742	4 AA402453			5.4 5.4
	43735			6 ESTs gb:CM1-BT0614-160300-149-f02 BT0614 Homo	5.4 5.4
	45561				5.3
	42929				5.3
75	42786 40855		Hs.46362		5.3
,,	44420				5.3
	42283		Hs.33294	3 ESTs	5.3 5.3
	40318	Ю		tur, and binding pentoin & adianada	5.3 5.3
٥٨	41802				5.2
80			Hs.2396 Hs.2729		5.2
	43159 43193				5.2
	43740				5.2
				101	

	438285	AA782845	Hs.22790	ESTs	5.2
	439901	N73885	Hs.124169	ESTs	5.2
	438507	AA809052	Hs.211275	ESTs	5.2
_	449222	AW293984	Hs.197621	ESTs	5.2
5	402834	AK001507	Hs.306084	Homo sapiens clone FL86914 PRO1821 mRNA,	5.2
	419042	T81429	Hs.221065	ESTs	5.2
	436777	AA731199 AI280246	Hs.293130 Hs.149504	ESTs ESTs	5.2 5.1
	445071 408016	AV136827	Hs.256096	ESTS ESTS	5.1 5.1
10	412047	AA934589	Hs.49696	ESTs	5.1
	436953	AW959074	Hs.23648	Homo sapiens cDNA FLJ13097 fis, clone NT	5.1
	436773	AW078629	Hs.82110	PC4 and SFRS1 interacting protein 1	5.1
	409263	AA069573	Hs.50319	ESTs	5.1
	453830	AA534296	Hs.20953	ESTs	5.1
15	459580	AA022888	Hs.176065	ESTs .	5.1
	417616	R07728	Hs.268668	ESTs	5.1
	423457	F08208	Hs.283844	similar to rat tricarboxylate carrier-li	5.1 5.0
	441535 416490	AL135735 AF090116	Hs.7885 Hs.79348	phosphatidylinositot binding clathrin as regulator of G-protein signalling 7	5.0
20	417284	N62889	Hs.107242	Homo sapiens cDNA FLJ12965 fis, clone NT	5.0
	447135	T58148	10.101242	gb:yb98g06.s1 Stratagene lung (937210) H	5.0
	448605	AL109678	Hs.21597	Homo sapiens mRNA full length insert cDN	5.0
	442240	AI791883	Hs.292719	ESTs	4.9
25	459399	BE407712	Hs.153998	creatine kinase, mitochondrial 1 (ubiqui	4.9
25	427972	AA864870	Hs.181304	putative gene product	4.9
	432944	AA570687	Hs.38512	ESTS	4.9 4.9
	440198 444047	BE560093 AI097452	Hs.135095	gb:601345159F1 NIH_MGC_8 Homo sapiens cD ESTs	4.9
	416040	AW819158	Hs.289044	Homo sapiens cDNA FLJ12048 fis, clone HE	4.9
30	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	4.8
-	436670	AI690021	Hs.201536	ESTs	4.8
	448072	AI459306	Hs.24908	ESTs	4.8
	408936	AL138043	Hs.293549	ESTs	4.8
25	412622	AW664708	Hs.171959	ESTs	4.8
35	414943	D80647	Hs. 124193	ESTs	4.8
	429254	H10133	Hs.91846	hypothetical protein DKFZp761C121	4.8
	453567	A1742835	Hs.33368	hypothetical protein FLJ11175 Homo sapiens mRNA; cDNA DKFZp564O1262 (f	4.8 4.8
	407906 441028	AA369665 AI333660	Hs.41185 Hs.17558	Homo sapiens cDNA FLJ14446 fis, clone HE	4.7
40	405130	A333000	113.11300	Tions supris core (to (The list, solid) in	4.7
	455225	AW996689		gb:QV3-BN0046-150400-151-g09 8N0046 Homo	4.7
	446218	AV657159		gb:AV657159 GLC Homo sapiens cONA clone	4.7
	443347	A1052543	Hs.133244	melanoma-derived leucine zipper, extra-n	4.7
4.5	402176				4.7
45	416577	BE063207	Hs.79381	grancalcin	4.7
	435221	AK001781	Hs.296543	Homo sapiens cDNA FLJ10919 fis, clone OV	4.7
	420480	AL137361	Hs.98173	hypothetical protein	4.7 4.6
	400800 435161	Y10262 AF124150	Hs.46925 Hs.272091	eyes absent (Drosophila) homolog 3 ESTs	4.6
50	404793	AF 124130	16.272031		4.6
50	430895	U66581	Hs.248121	G protein-coupled receptor 22	4.6
	438571	AW020775	Hs.56022	ESTs	4.6
	445924	AJ264671	Hs.164166	ESTs	4.6
	444585	AW170015	Hs.6594	ESTs	4.6
55	421044	AF061871	Hs.311736	Human DNA sequence from clone RP1-238D15	4.6
	418274	AI458587	Hs.128677	Human DNA sequence from clone RP1-50O24	4.6
	425475 434311	W56339 BE543469	Hs.107057 Hs.266263	ESTs Homo sapiens cDNA FLJ14115 fis, clone MA	4.6 4.5
	414272	AI651603	Hs.46988	ESTs	4.5
60	445235	AI564022	Hs.138207	ESTs	4.5
	414327	BE408145	Hs.185254	ESTs. Wealthy similar to T24435 hypotheti	4.5
	414630	BE410857		gb:601301177F1 NIH_MGC_21 Homo sapiens c	4.5
	414456	H74314		gb:yu56e10.r1 Soares fetal liver spleen	4.5
45	401024			A Company of the Comp	4.5
65	414699	AJ815523	Hs.76930	synuclein, alpha (non A4 component of am	4.5 4.5
	423449 405138	AI497900	Hs.33067	ESTs	4.5
	413544	BE147225		gb:PM2-HT0225-031299-003-f11 HT0225 Hamo	4.5
	453880	AI803166	Hs.28462	ESTs, Weakly similar to 138022 hypotheti	4.5
70	433521	T66087	Hs.112482		4.4
	441184	AA922009	Hs.150269		4.4
	429876	AB028977	Hs.225974	KIAA 1054 protein	4.4
	445481	AW661846	Hs.148836		4.4
75	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	4.4
75	404769	AMM1033/3	LL 24144	ECT.	4.4 4.4
	444331 429726	AW193342 AW628326	Hs.24144 Hs.27151	ESTs ESTs	4.4 4.4
	449093	AB035356	Hs.22998	neurexin 1	4.4
	451959	AA056203	Hs.27337	hypothetical protein FLJ20623	4.4
80	415716	N59294	Hs.179662	nucleosome assembly protein 1-like 1	4,4
	417888	R23053		gb:yh31a05.r1 Soares placenta Nb2HP Homo	4.4
	419656	AB002314	Hs.92025	KIAA0316 gene product	4.4
	425864	U56420	Hs.159903	olfactory receptor, family 5, subfamily	4.4

					4.4
		AW518888 BE144444	Hs.40937 [STs b:MR0-HT0168-141199-002-109 HT0168 Homo	4.3
	413493 432712		Hs.288031	sterol-C5-desaturase (fungal ERG3, delta	4.3
	459650			ESTs	4.3 4.3
5	404828			COT.	4.3
	423782	A1472209 AA460967		ESTs ESTs	4.3
	426867 426802	AA385182	Hs 46699	ESTs	4.3
	457353	X65633	He 248144	metanocortin 2 receptor (adrenocorticotr	4.3 4.3
10	412112	BE180342		gb:RC3-HT0622-130400-012-a07 HT0622 Homo	4.3
	401522	N47812 Al365384	Hs.306198 Hs.11571	CGI-35 protein Homo sapiens cDNA FLJ11570 fis, clone HE	4.3
	419055 410171	H07892		ESTs	4.3
	419564	U08989	He 91139	solute carrier family 1 (neuronal/epithe	4.3 4.3
15	458789	AL157468	Hs.325825	Homo sapiens cDNA FLJ20848 fis, clone AD gb:QV0-CT0225-100400-187-d08 CT0225 Homo	4.3
	455040	AW852286 AI440266	Hs.170673	ESTs, Weakly similar to T24832 hypotheti	4.3
	438533 459005	AA447679	Hs.144558	ESTs. Weakly similar to ALU1_HUMAN ALU S	4.2
	418489	U76421	Hs.85302	adenosine deaminase, RNA-specific, B1 (h	4.2 4.2
20	433389	AF038171	11- 44500	gb:Homo sapiens clone 23671 mRNA sequenc hypothetical protein from Xq28	4.2
	454356 442339	AW390363 BE299668	Hs.11522 Hs.227591	FSTs Weakly similar to 1901303A Leu zip	4.2
	421249	AA285362	I IDILLI I I I	gb:HTH277 HTCDL1 Homo sapiens cDNA 5/3	4.2
	443998	AI620661	Hs.296276	ESTs	4.2 4.2
25	452197	AW023595	Hs.232048	ESTs ESTs	4.2
	451117	AA015752 AW247252	Hs.205173 Hs.75514	nucleoside phosphorylase	4.2
	404501 410378	R23324	Hs.41693	DnaJ (Hsp40) homolog, subtamily B, membe	4.2
	422528	AB011182	Hs.118087	KIAA0610 protein	4.2 4.1
30	440323	AA970614	Hs.127992	eSTs chromosome 1 open reading frame 7	4.1
	425767	AF054176 AA478486	Hs.159483 Hs.3852	KIAA0368 protein	4.1
	434460 410362	H04811	Hs.93164	proprotein convertase subtilisin/kexin t	4.1
	413121	T96090	Hs.142678	ESTs	4.1 4.1
35	409403	AA668224	Hs.6634	Homo sapiens cDNA: FLJ22547 fis, clone H	4.1
	450235 449754	AA007512 H00820	Hs.17538 Hs.30977	ESTs ESTs, Weakly similar to 834087 hypotheti	4.1
	449754	BE048255	115.503//	gb:tz49b05.y1 NCI_CGAP_Bm52 Homo sapien	4.1
	408496	AI683802	Hs.136182	ESTs	4.1 4.1
40	430261	AA305127	Hs.237225	hypothetical protein HT023	4.1
	434101	AA625205 T92157	Hs.259599 Hs.16970	KIAA1622 protein ESTs	4.1
	451837 411772	BE170301	(15.15570	gb:QV4-HT0536-040500-193-f05 HT0536 Homo	4.1
	437630	AI252782	Hs.153026	SWAP-70 protein	4.1 4.0
45	430212	AA469153		gb:nc67f04.s1 NCI_CGAP_Pr1 Homo sapiens	4.0
	400216	AI537278	Hs.225841	DKFZP434D193 protein	4.0
	429830 453165	S74727	Hs.32042	aspartoacytase (aminoacytase 2, Canavan	4.0
	418047	R37633	Hs.4847	ESTs	4.0 4.0
50	405354	4147000013	Un 495005	ESTs	4.0
	427931 428775	AW206512 AA434579	Hs.186996 Hs.143691		4.0
•	449422	AA001373	Hs.59821	ESTs	4.0
	453864		Hs.21068	hypothetical protein	4.0 4.0
55	456407	AW968614		gb:EST380690 MAGE resequences, MAGJ Horno huntingtin-associated protein interactin	4.0
	441869 420784		Hs.102395		4.0
	425195		Hs.94319	VPS10 domain receptor protein	4.0 4.0
	429628		Hs.13268	ESTs	4.0
60	410087	********	Hs.33257) ESTs gb:UI-HF-BR0p-ajr-c-08-0-UI.r1 NIH_MGC_5	4.0
	409840 452854		Hs.14060	prokineticin 1 precursor	4.0
	419910		Hs.19017	3 ESTs, Weakly similar to A46010 X-linked	4.0 4.0
	427443		Hs.97872		3.9
65	414990		Hs.22165 Hs.11491		3.9
	412678 405629		113.11431	- 2013	3.9
	42029		Hs.15276		3.9
70	45309		Hs.86379	ESTs	3.9 3.9
70	43575		Hs.30317	gb:Homo sapiens growth hormone receptor 2 Homo sapiens mRNA; cDNA DKFZp547G133 (fr	3.9
	44100: 41451:		Hs.13556	io ESTs, Wealthy similar to T43458 hypotheti	3.9
	44225			O Human EST clone 25267 mariner transposon	3.9 3.9
	42256	3 BE299342			3.9
75	40669		Hs.1230 3 Hs.3346		3.9
	44385 41267			4 ESTs	3.9
	42278				3.9
00	40537	7		r FOTo Months similar to 16 7Kd nation I	3.9 3.9
80					3.9
	45334 43196			27 c6.1A	3.9
	41685		Hs.8029		3.9

	400004	AA400117	Hs.125747	COT-	2.0
	427264			ESTs	3.9
	422746	NM_004484	Hs.119651	glypican 3	3.9
	452346	BE243534		gb:TCBAP1D0885 Pediatric pre-B cell acut	3.9
	414666	NM_004466	Hs.76828	glypican 5	3.8
5	418217	AI910647	Hs.13442	ESTs	3.8
	419118	AA234223	Hs.139204	ESTs	
					3.8
	445017	AI205493	Hs.176860	ESTs	3.8
	405867				3.8
	422760	BE409561		gb:601299865F1 NIH_MGC_21 Homo sapiens c	3.8
10	453863	X02544	Hs.572	orosomucoid 1	3.8
	457821	H47166			
			Hs.124322	ESTs, Wealtly similar to A47582 B-cell gr	3.8
	457330	AB013818	Hs.247220	peroxisome biogenasis factor 10	3.8
	435600	AL047034	Hs.119747	ESTs	3.8
	456083	U46922	Hs.77252	fragile histidine triad gene	3.8
15	413341	H78472	Hs.191325	ESTs, Weakly similar to T18967 hypotheti	3.8
13					
	449057	AB037784	Hs.22941	KIAA1363 protein	3.8
	421855	F06504	Hs.27384	ESTs, Moderately similar to ALU4_HUMAN A	3.8
	414764	AW013887	Hs.72047	ESTs	3.8
	404391				3.7
20	433629	R13140	Hs.13359	ESTs	3.7
	424738	AI963740		ESTs	3.7
		M30014U	Hs.46826	E318	
	401315				3.7
	407706	AA191085	Hs.26612	ESTs, Moderately similar to S23650 retro	3.7
	440530	AA888646	Hs.174187	ESTs	3.7
25	433930	AA620338	Hs.273781	ESTs	3.7
	409662	AW452320	Hs.279726	ESTs	3.7
	437268	AJ754847	Hs.227571	regulator of G-protein signalling 4	3.7
	445688	AI248205	Hs.153244	ESTs	3.7
	408593	R19566	Hs. 197617	ESTs	3.7
30	417091	AA193283	Hs.291990	ESTs	3.7
50		AW885606			3.7
	448556		Hs.5064	ESTs	
	423135	N67655	Hs.26411	ESTs	3.7
	400135				3.7
	459150	BE155356		gb:PM1-HT0350-160300-009-d06 HT0350 Homo	3.7
35	457221	AW383197	Hs.218260	ESTs	3.7
"				ESTs	3.7
	451660	AI807927	Hs.249601		
	401600	BE247275	Hs.151787	U5 snRNP-specific protein, 116 kD	3.7
	446818	A1342668	Hs.279765	ESTs .	3.7
	447795	AW295151	Hs.163612	ESTs	3.7
40	427562	R56424	Hs.26534	ESTs	3.6
40					3.6
	412258	AA376768	Hs.324841	hypothetical protein FLJ22622	
	454339	AW381980		gb:QV4-HT0316-091199-028-d05 HT0316 Homo	3.6
	439274	AF086092	Hs.48372	ESTs	3.6
•	452381	H23329	Hs.290880	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.6
45	422897	AA679784	Hs.4290	ESTs	3.6
73					
	429656	X05608	Hs.211584	neurofilament, light potypeptide (68kD)	3.6
	421908	AW935200	Hs.285814	sprouty (Drosophila) homolog 4	3.6
	407978	AW385129	Hs.41717	phosphodiesterase 1A, calmodulin-depende	3.6
	426452	AW614271	Hs.121647	ESTs, Highly similar to AC006014 8 simil	3.6
50	400685				3.6
50		A1074701	LI- 24200	CCT-	
	417154	A1674701	Hs.21388	ESTs	3.6
	447176	Z42549	Hs.160893	ESTs	3.6
	423893	AL031709	Hs.134846	Human DNA sequence from clone 316G12 on	3.6
	449231	BE410360	Hs.298573	KIAA1720 protein	3.6
55	411607	AW853498		gb:RC1-CT0252-170200-025-h02 CT0252 Homo	3.6
J J		~~~~~		Bounds at acted at Acton	
	405977	050000		PAY.	3.6
	441470	BE503874	Hs.301986	ESTs	3.6
	423568	NM_005256	Hs.129818	growth arrest-specific 2	3.6
. -	441235	AI884586	Hs.135570	Homo sapiens cDNA: FLJ21268 fis, clone C	3.6
60	450236	AW162998	Hs.24684	KIAA1376 protein	3.6
					3.6
	425364	AF052150	Hs.155959	Homo sapiens clone 24533 mRNA sequence	
	426775	AA384564	Hs.108829	ESTs	3.6
	414831	M3115B	Hs.77439	protein kinase, cAMP-dependent, regulato	3.6
.	415876	AW501916	Hs.117897	ESTs	3.6
65	400878				3.6
	425153	AW023193	Hs.27046	ESTs	3.6
			ris.27040		
	432222	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	3.5
	415047	F13142		gb:HSC3JD031 normalized infant brain cDN	3.5
	401532				3.5
70	446495	D60923	Hs.153460	ESTs	3.5
. •	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A 8 cell	3.5
	445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	3.5
	455901	BE155527		gb:PM1-HT0350-190400-013-b08 HT0350 Homo	3.5
	416421	AA134006	Hs.79306	eukaryotic translation initiation factor	3.5
75	455697	BE067952		gb:CM0-8T0365-061299-122-g09 8T0365 Homo	3.5
. •	405678			9 goo o - o o o o	3.5
		011000	11	CCT-	
	418207	C14685	Hs.34772	ESTs	3.5
	425383	D83407	Hs.156007	Down syndrome critical region gene 1-lik	3.5
	417027	AA192306	Hs.23926	triadin	3.5
80	408367	AK001178	Hs.44424	homolog of rat orphan transporter v7-3	3.5
		R09935		ESTs	3.5
	417702		Hs.191146		
	445687	W80382	Hs.149297	ESTs	3.5
	408776	AA057365	Hs.63356	ESTs, Wealthy similar to I38022 hypotheti	3.5

		05000404	_	b:MR1-BT0371-050500-009-a12 BT0371 Homo	3.5
	413164 414593	BE068494 BE386764	9	15:MK1-B10371-030500-003-312 51-03111 folia 15:601273249F1 NIH_MGC_20 Homo sapiens c	3.5
	453220	AB033089		Homo sapiens mRNA for KIAA1263 protein,	3.5
_	415621			ESTs	3.5 3.5
5	454437			hypothetical protein MGC12936 ESTs	3.5
	446066 423374		Hs.127656	KIAA1349 protein	3.5
	419347	C15944	Hs.90005	superiorcervical ganglia, neural specifi	3.5 3.5
10	418516			phosphoinositide-3-kinase, catalytic, al hypothetical protein SP192	3.5 3.5
10	451776 432305			insufin-like growth factor binding prote	3.5
	456995	T89832		ESTs	3.5
	403323		45 (003		3.5 3.5
15	425022 439394	M95724 AA149250		centromere protein C 1 ESTs	3.4
13	433803	AI823593		ESTs	3.4
	450715	AI266484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	3.4 3.4
	411474	AW848427	Hs.77890	gb:IL3-CT0214-150200-075-H10 CT0214 Homo guanylate cyclase 1, soluble, beta 3	3.4
20	415076 423826	NM_000857 U20325	Hs.1707	cocaine- and amphetamine-regulated trans	3.4
20	459495	BE544158		gb:601076707F1 NIH_MGC_12 Homo sapiens c	3.4 3.4
	427173	BE255017	Hs.97540	ESTs ESTs	3.4 3.4
	408112 446092	AW451982 N33522	Hs.248613 Hs.145894	ESTS	3.4
25	416868	AI656856	Hs.292597	ESTs	3.4
	458234	BE551408	Hs.127196	ESTS	3.4 3.4
	419555	AA244416 BE312991		gb:nc07d11.s1 NCI_CGAP_Pr1 Homo sapiens gb:601150275F1 NIH_MGC_19 Homo sapiens c	3.4
	414314 400425	AY004252	Hs.287385	PR domain containing 12	3.4
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	434053	AW445136	Hs.134946	ESTs KIAA1829 protein	3.4
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	428006	AA418743	Hs.98306	KIAA1862 protein	3.4
35	424695	U58331	Hs.151899	sarcoglycan, delta (35kD dystrophin-asso	3.4 3.4
	443294 428212	A1733625 AW444451	Hs.133053 Hs.134812	ESTs ESTs	3.4
	457673	AA551569	Hs.272034	hypothetical protein PRO2822	3.4
40	446390	AA233393	Hs.14992	hypothetical protein FLJ11151	3.3 3.3
40	428536	AI143139	Hs.2288 Hs.145601	visinin-like 1 ESTs	3.3
	426597 410366	AA382250 Al267589	Hs.302689	hypothetical protein	3.3
	458258	AW406546	Hs.127971	ESTs	3.3 3.3
45	401738	707.400	11- 50000	small inducible cytokine subfamily A (Cy	3.3 3.3
45	409038 425785	T97490 T27017	Hs.50002 Hs.159528	Homo sapiens clone 24400 mRNA sequence	3.3
	433328	AW298159	Hs.23644	ESTs, Weakly similar to S65824 reverse t	3.3
	414541	BE293116	Hs.76392	aldehyde dehydrogenase 1 family, member	3.3 3.3
50	434998 456359	AW975157 AI967991	Hs.26037 Hs.93574	ESTs homeo bax D3	3.3
30	426527	NM_001037		sodium channel, voltage-gated, type I, b	3.3
	454267	AA437199	Hs.656	cell division cycle 25C	3.3 3.3
	400302 434077	N48056 AF116659	Hs.1915 Hs.321151	folate hydrolase (prostate-specific memb Homo sapiens PRO1412 mRNA, complete cds	3.3
55	436602	AI793222	Hs.166817	ESTs	3.3
	449204	AB000099	Hs.23251	Down syndrome critical region gene 4	3.3 3.3
	417935 423310	R53697 AA325225	Hs.170044 Hs.124023		3.3
	436624		Hs.5241	fatty acid binding protein 1, liver	3.3
60	453406	Ai192987	Hs.61784	hypothetical protein FLJ14451	3.3 3.3
	420164	AW339037 AW779317	Hs.24908 Hs.258556	ESTs 5 ESTs	3.3
	447826 419875		Hs.93557	proenkephalin	3.3
	444612	AW138111	Hs.22902	ESTS	3.3 3.2
65	418504		Hs.85335 Hs.295014	Homo sapiens mRNA; cDNA DKFZp564D1462 (f 4 ESTs	3.2
	415242 418188				3.2
	430355	NM_00621		B phosphoinositide-3-kinase, catalytic, be	3.2 3.2
70	421640			gb:EST378726 MAGE resequences, MAGI Homo 5 Homo sapiens cDNA FLJ10229 fis, clone HE	3.2
70	432359 408806				3.2
	400409	AF153341	Hs.28395	4 Homo sapiens winged helix/forkhead trans	3.2
	44601		Hs.13531 Hs.78026		3.2 3.2
75	425499 403093		rt5./6020	LO13, FICANT SHIMA D SKIMA W CHAT	3.2
13	45297		Hs.91789	ESTs	3.2
	45418	6 BE141030		gb:MR0-HT0067-201099-002-h11 HT0067 Homo	3.2 3.2
	40148 40194				3.2
80	45745			gb:EST384766 MAGE resequences, MAGL Homo	3.2
	45410	0 Al693231	Hs.12604		3.2 3.2
	44844 42120				3.2
	42 120	· /4/20/011		-	

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	430142	NM_000437 AB040889	Hs.234392 Hs.281022	platelet-activating factor acetylhydrola	32
	433197 443509	AV645470	MS.20 1022	KIAA1456 protein	3.2 3.2
	440827	A1733110	Hs.128128	gb:AV645470 GLC Homo sapiens cDNA clone ESTs	3.2
5	432799	NM_016161	Hs.278960	alpha-1,4-N-acetylglucosaminyltransferas	3.2
,	409257	AW370362	10.21000	gb:RC1-BT0255-181099-012-d07 BT0255 Homo	3.2
	459235	BE246010	Hs.271468	Homo sapiens mRNA for FLI00038 protein,	3.2
	416789	AA223439	Hs.79933	cyclin (3.2
	429809	AL162010	Hs.223603	Homo sapiens mRNA; cDNA DKFZp761D09121 (3.2
10	420156	AW449258	Hs.6187	ESTs	3.2
	455577	BE006341		gb:RC2-BN0127-240300-011-b05 BN0127 Homo	3.2
	400617	AF151064	Hs.36069	hypothetical protein	3.2
	437129	AL049327	Hs.302057	Homo sapiens mRNA; cDNA DKFZp564E016 (fr	3.2
1.5	451820	AW058357	Hs.337353	EST8	3.2
15	457535	AA609685	Hs.278672	membrane component, chromosome 11, surfa	3.2
	419956	AL137939	Hs.40096	EST8	3.1
	456235	AA203637	14- 40704	gb:zx58b12.r1 Soares_fetal_fiver_spleen_	3.1
	423930	AA332697	Hs.42721	ESTs	3.1
20	403796	4414046	U- 757/6	aldohuda dahudunaaaaa 4 family manhay	3.1 3.1
20	414085	AA114016 AI793176	Hs.75746	aldehyde dehydrogenase 1 family, member ESTs	31
	445886	AI760159	Hs.145596 Hs.124833	ESTS	3.1
	414401 441573	BE563966	Hs.6529	ESTs, Wealdy similar to 178885 serine/th	3.1
	450725	R71389	Hs.175951	ESTs. Vicasiy sandar to 170000 serine iii	3.1
25	458805	AI282933	Hs.23294	hypothetical protein FLJ14393	3.1
	417868	AJ078534	Hs.122592	ESTs	3.1
	458391	AJ792628	Hs.133273	ESTs	3.1
	423346	AI267677	Hs.127416	synaptojanin 1	3.1
	454486	AW857077		gb:RC1-CT0302-140300-016-f04 CT0302 Homo	3.1
30	408341	AW182952	Hs.249957	ESTs	3.1
	410669	AW805749	Hs.318885	superoxide dismutase 2, mitochondrial	3.1
	404907				3.1
	434910	AI333863	Hs.215474	ESTs, Moderately similar to alternativel	3.1
~ ~	436990	AI149729	Hs.120557	ESTs	3.1
35	441921	A1733376	Hs.164478	hypothetical protein FLJ21939 similar to	3.1
	454673	AW812807		gb:RC3-ST0186-070100-016-c04 ST0186 Homo	3.1
	429470	AI878901	Hs.203862	guanine nucleotide binding protein (G pr	3.1
	404345	AA730407	Hs.159156	protocadherin 11	3.1
40	408217	AI433201	Hs.279860	tumor protein, translationally-controlle	3.1
40	417313	AA195602	Un 470007	gb:zr32f09.r1 Soares_NhHMPu_S1 Horno sapi	3.1 3.1
	427322	AK002017	Hs.176227 Hs.13056	hypothetical protein FLJ11155	3.1
	411003 425339	AA181018 AA936330	Hs.198113	hypothetical protein FLJ13920 ESTs	3.1
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (lg),	3.1
45	449078	AK001256	Hs.22975	KIAA1576 protein	3.1
15	429608	U49250	Hs.210862	T-box, brain, 1	3.1
	442308	AA989402	Hs.111	fibroblast growth factor 9 (glia-activat	3.1
	428465	AW970976	Hs.293653	ESTs	3.1
	411666	AF106564	Hs.71346	neurofilament 3 (150kD medium)	3.1
50	447965	AW292577	Hs.94445	ESTs	3.1
	413918	AW015898	Hs.71245	ESTs	3.1
	419682	H13139	Hs.92282	paired-like homeodomain transcription fa	3.1
	425810	AI923627	Hs.31903	ESTs	3.1
66	427865	AA416931	Hs.126065	ESTs	3.1
55	429060	AW139155	Hs.194995	hypothetical protein DKFZp434O0320	3.1
	430708	U78308	Hs.278485	olfactory receptor, family 1, subfamily	3.1
	448084	AI467800	Hs.271000	ESTs, Weakly similar to 138022 hypotheti	3.1
	454506	AW847346		gb:RC0-CT0205-240999-021-e01 CT0205 Homo	3.1
60	414629	AA345824	Hs.76688	carboxylesterase 1 (monocyte/macrophage	3.0
00	422963	M79141 BE241624	Hs.13234 Hs.82401	ESTs CD69 antigen (p60, early T-cell activati	3.0 3.0
	417696		Hs.225160	hypothetical protein FLJ13102	3.0
	448175 414686	BE296174 BE409757	Hs.23189	ESTs, Moderately similar to TBB2_HUMAN T	3.0
	458360	AI027207	Hs.132253	ESTs	3.0
65	451829	AW954081	Hs.247377	ESTs	3.0
Ų,	445179	AJ949743	Hs.224768		3.0
	433090	AI720050	Hs.145362		3.0
	432018	AA524447	Hs.152377		3.0
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	418808	AI821836	Hs.10359	ESTs	3.0
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	452893	H18017	Hs.22869	ESTs, Moderately similar to KIAA1395 pro	3.0
~~	423952	AW877787	Hs.136102	KIAA0853 protein	3.0
75	412000	AW576555	Hs.15780	ATP-binding cassette, sub-family A (ABC1	3.0
	405793				3.0
	410711	AB002316	Hs.65746	KIAA0318 protein	3.0
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TABLE 108:

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                                                                                           BE394588 AW024754 BE183166 BE183167
BE141030 BE141474 BE141467 BE141753 BE141024 BE141761 AW177583 AW177587 AW177582 AW177588 AW177588 AW177580 BE141600 BE1
                                 454065
                                                                                           BE141477 BE141520 BE141456 BE141492 BE141028 BE141775 BE141489 BE141751 AW177599 BE141750 AW177597 BE141512 BE141460
                                                           1049791_1
                                 454186
                                                                                            BE141749 AW177598
                                                                                           AW381980 BE152244 BE152235 BE152238 BE152232
AW857077 AW861268 AW847383 AW795787
AW847346 AW847395 AW847408 AW847385 AW847342 AW847396 AW847339 AW801718 AW801787
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                                                            1219857_1
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AW852286 AW851934 AW852096 AW852274
AW996689 AW996380 AW996453 BE085650 AW868687 BE085595
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455040
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                                                             1262318_1
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                                    455577
                                                             1333898_1
                                                                                             BE078070 BE061030 BE077927
                                                                                             BE067952 BE067945 BE067942 BE067943 BE067949 BE067954 BE067944 BE067953 BE067956 BE067946 BE155527 BE155503 BE155188 BE155126
                                   455617
                                                             1346117 1
                                                             1351148_1
                                   455697
                                                             1381569_1
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          70
                                                             168686_1
                                   456235
                                                                                              AW968614 AA243209 AA281411
                                                             184986_1
                                    456407
                                                                                               AW972675 AA541366 AA523039
                                                             339381_1
                                    457452
                                                                                               BE155356 BE153468 BE153461 BE155059 BE155210 BE155413 BE153577 BE153688 BE155063 BE155347 AI903640 BE155492
                                    459150
                                                             919196_1
           75
                                    TABLE 10C:
                                                                                Unique number corresponding to an Eos probeset Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Ounham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
                                    Pkey:
Ref:
                                                                                 Indicates ONA strand from which exons were predicted.
                                     Strand:
           80
                                                                                 Indicates nucleotide positions of predicted exons.
                                     Nt_position:
                                                                                                                             Nt_position
                                                                                                Strand
                                                                                                                              84912-85187
                                                              8118474
                                                                                                Plus
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                                      Minus
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                                                   31493-32842
60551-60802
198960-199619
                      9864757
8117489
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                                     Plus
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                      9212516
                                      Minus
           401485
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                                     Plus
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2982169
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41547-41757
                                     Plus
           401738
                                     Minus
10
           401780
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                                                   28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
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7523976
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120366-120845
           403323
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                                      Minus
                                                   26030-26173,27852-27997
           404769
                      8099713
                                     Minus
                                                   175801-176823
           404793
                      7232206
                                                   61087-61590
                                     Minus
           404828
                      6580415
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                                      Minus
          404907
404958
                      7331453
7407941
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                                                   102880-103828
25
                                     Minus
                                                   2731-4531
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                                                   11115-11552
                                      Minus
           405130
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                                                   150235-150449
                                     Plus
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                      8576241
                                      Plus
                                                   90303-90516
                      2642452
5649375
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216656-216848
           405354
                                     Plus
30
           405377
                                     Plus
           405629
                       4508116
                                                   101678-101866
                                     Minus
           405678
                       4079670
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                      1405887
           405793
                                     Minus
                                                   89197-89453
           405800
                      2791346
                                                   19271-19813
74553-75173
                                     Plus
35
           405867
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                                     Minus
           405911
                      6758795
                                     Plus
                                                   101008-101643
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                      8247789
                                                   135548-136177
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TABLE 11A: ABOUT 533 CNS-ENRICHED GENES SIGNIFICANTLY DOWN-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT CNS TISSUES

Table 11A lists about 533 CNS-enriched genes significantly down-regulated in glioblastoma compared to normal adult CNS tissues. These were selected from 59680 probesets on the Affymetrix/Eos Huo3 GeneChip array such that the ratio of "average" normal CNS to "average" glioblastoma was greater than or equal to 2. The "average" normal CNS level was set to the 75th percentile amongst various normal CNS issues. To enrich for CNS specific genes, the ratio of "average" CNS to "average" normal adult tissues was calculated to be greater than or equal to 2. The "average" CNS tevel was set to the 85th percentile amongst various non-CNS normal issues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and

the denominator before the ratios were evaluated.

Pkey: Unique Eos probeset identifier number

50 Examplar Accession number, Genbank accession number Unigene D: Unigene number

Unigene Title: Unigene gene title

R1: R2: Ratio of 75th percentile normal central nervous system tissue to 85th percentile tumor
R2: Ratio of 85th percentile central nervous system tissue to 85th percentile normal body tissue

55	Pkey	ExAcon	UnigeneID	Unigene Title	R1	R2
	417275	X63578	Hs.295449	parvalbumin	29.0	30.0
	430829	AW451999	Hs.194024	ESTs	25.7	6.2
	410657	AF063228	Hs.65248	dynein, cytoplasmic, intermediate polype	22.6	25.8
	419954	D14720	Hs.93883	myelin protein zero (Charcot-Marie-Tooth	21.2	30.3
60	416133	NM_001683	Hs.89512	ATPase, Ca++ transporting, plasma membra	15.5	16.8
	416018	AW138239	Hs.78977	proprotein convertase subtlisin/kexin t	15.2	18.0
	417167	AW206437	Hs.4290	ESTs	14.8	17.7
	433940	H05129	Hs.7459	cyclic AMP-regulated phosphoprotein, 21	13.4	18.1
	413324	V00571	Hs.75294	corticotropin releasing hormone	13.1	18.0
65	439830	AA846666	Hs.151489	ESTs, Weakly similar to XE7_HUMAN PROTEI	12.6	16.5
	408068	AW148652	Hs.167398	ESTs	12.6	16.9
	429096	AB011106	Hs.196012	KIAA0534 protein	12.2	21.1
	412638	AA910199	Hs.203838	ESTs	12.2	16.0
	442593	R39804	Hs.31961	ESTs	10.8	15.0
70	446353	AI290919	Hs.153661	ESTs	10.4	13.2
. •	426365	AA376667	Hs.10283	RNA binding motif protein 8B	10.0	5.9
	414937	R38698	Hs.12382	ESTs	10.0	10.8
	419643	F06066	Hs.91791	chromosome 11 open reading frame 25	9.5	10.9
	412454	RS5745	Hs.167330	ESTs	9.5	14.1
75	439366	AF100143	Hs.6540	fibroblast growth factor 13	9.4	12.3
• •	441790	AW294909	Hs.132208	ESTs	9.2	3.2
	448117	H49129	Hs.172982	ESTs	9.1	12.8
	433558	AA833757	Hs.201769	ESTs, Weakly similar to T24435 hypotheti	9.0	14.7
	412453	R20205	Hs.167330	ESTs	9.0	13.7
80	408920	AL120071	Hs.48998	fibronectin teucine rich transmembrane p	8.9	17.3
••	409031	AA376836	Hs.76728	ESTs	8.7	8.6
	446544	A1631932	Hs.7047	ESTs, Weakly similar to Unknown (H.sapie	8.2	20.0
	439480	AL038511	Hs.125316	ESTs, Weakly similar to S33990 finger or	8.2	8.3

					8.0	8.9
	410200		Hs.101915 S	stargardt disease 3 (autosomal dominant)	7.9	9.6
	408428	NM_014787 AI885608		onaJ (Hsp40) homolog, subfamily 8, membe ESTs	7.9	11.3
	437073 408434	AW195317		hypothetical protein FLJ22344	7.9	16.4
5	440209	H05049	Hs.22269 (neurexin 3	7.8 7.8	34.3 9.0
	408119	W26213	Hs.101672	ESTs, Weakly similar to T00331 hypotheti	7.0 7.7	5.0 5.0
	429611	AI889077 R25234		Homo sapiens BAC clone CTB-60N22 from 7q contactin 1	7.7	9.9
	423440 445148	AI214510		ESTs	7.6	9.1
l0	416294	D86980	Hs.79170	KIAA0227 protein	7.6 7.6	7.6 10.3
	424087	N69333		contactin 1	7.5 7.5	9.3
	437479	R61866 AA744550		ESTs ESTs	7.1	2.8
	430573 448958	AB020651		KIAA0844 protein	7.1	10.4
15	419474	AW968619	Hs.155849	ESTs	7.1 7.0	3.0 6.9
	423605	AF047826	Hs.129887	cadherin 19, type 2	7.0	9.2
	433098	AW190593 AJ436187	Hs.151143 Hs.296261	ESTs guarrine nucleotide binding protein (G pr	6.9	3.1
	449511 428414	AL049980	Hs. 184216	DKFZP564C152 protein	6.8	5.0
20	443155	R54485	Hs.23772	ESTs	6.8 6.8	3.5 8.1
	450561	R49674	Hs.25909	ESTs	6.8	2.0
	433068	NM_006456	Hs.288215 Hs.209569	sialyttransferase ESTs	6.6	10.5
	423589 415681	AA328082 A1379882	Hs.72630	ESTs	6.5	9.0
25	413510	F13044		gb:HSC3HH101 normalized infant brain cDN	6.4 6.4	7.1 9.5
	427992	Y15014	Hs. 181353	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	6.4	5.7
	450642	R39773	Hs.7130	copine IV KIAA0231 protein	6.4	8.2
	429322 447482	D86984 AB033059	Hs.199243 Hs.18705	KIAA1233 protein	6.4	2.3
30	446129	AW244073	Hs.145946	ESTs	6.3	8.3
50	421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mime	6.3 6.2	2.1 10.3
	434273	AA913143	Hs.26303	ESTs	6.2	3.5
	408480	A1350337	Hs.164568 Hs.209890	fibroblast growth factor 7 (keratinocyte EST	6.2	12.4
35	451301 438356	A1769514 AA805530	Hs.48527	ESTs	6.2	8.1
33	426388	AW081394	Hs.97103	ESTs	6.2	8.6
	452502	A1904296	•	gb:PM-BT046-220199-286_1 BT046 Homo sapi	6.1 6.1	2.8 6.3
	408165	AL137573	Hs.43143	Homo sapiens mRNA; cDNA DKFZp564A2463 (f	6.1	6.3
40	442979	AW440782 NM_001248	Hs.174743 Hs.47042	ESTs ectonucleoside triphosphate diphosphohyd	6.0	3.8
40	408713 430004	U27768	Hs.227571	regulator of G-protein signalling 4	5.9	21.4
	425087	R62424	Hs.126059	ESTs	5.9	8.1 3.1
	441695	T12411	Hs.183745	hypothetical protein FLJ 13456	5.9 5.8	12.5
45	417175	R44558	Hs.94002	ESTs gb:Homo sapiens mRNA; cDNA DKFZp547J184	5.8	2.2
45	437483 436427	AL390174 Al344378	Hs.143399	ESTs	5.8	13.8
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	5.7	4.4
	408478	NM_000806	Hs.45740	gamma-aminobutyric acid (GABA) A recepto	5.7 5.7	12.5 6.8
50	442676	AI733585	Hs.130897	ESTs	5.7	6.4
50	446443	AV659082 AW192083	Hs.134228 Hs.290855	ESTs ESTs	5.6	15.6
	459080 431984	AL080239	Hs.272284		5.6	8.2
	428356	AL046991	Hs.10338	ESTs	5.6 5.4	6.2 4.9
E E	417877	AI025829	Hs.86320	ESTs neurofilament, heavy polypeptide (200kD)	5.3	13.1
55	429290 408556	AF203032 U49516	Hs.198760 Hs.46362	5-hydroxytryptamine (serotonin) receptor	5.3	6.6
	431930		Hs.272211		5.2	6.0
	438285	AA782845	Hs.22790	ESTs	5.2 5.2	7.3 2.7
<i>c</i> n	439901		Hs.124169		5.2	8.1
60	449222	4151495097			5.1	2.5
	436953			Homo sapiens cDNA FLJ13097 fis, clone NT	5.1	3.0
	436773			PC4 and SFRS1 interacting protein 1	5.1 5.1	7.3 12.9
	409263			ESTs	5.1	3.4
65	453830			ESTs phosphatidylinositol binding clathrin as	5.0	4.8
	441535 416496			regulator of G-protein signalling 7	5.0	20.1
	417284		Hs.10724	2 Horno sapiens cDNA FLJ12965 fis, clone NT	5.0	3.9 6.1
	44860	5 AL109678			5.0 4.9	6.7
70	44224				4.9	5.2
	42797: 41604			4 Homo sapiens cDNA FLJ12048 fis, clone HE	4.9	2.8
	44492		- ::		4.8	3.7
	40893	6 AL138043	Hs.29354	9 ESTs	4.8	6.6 3.1
75	41494	3 D80647	Hs.12419		4.8 4.8	23
	42925		Hs.91848 5 Hs.41185		4.8	9.1
	40790 41657				4.7	2.2
	42048				4.7	2.8
80	40479	13		M. O. Hall annual and annual and M.	4.6 4.6	2.2 7.4
	43089		Hs.24812 75 Hs.56022		4.6	5.4
	43857 44458			ESTs	4.6	6.0
	*****			1.00	1	

	414272	AI651603	Hs.46988	ESTs	4.5	2.2
	414699	AI815523	Hs.76930	synuclein, alpha (non A4 component of am	4.5	30.9
	423449	Al497900	Hs.33067	ESTs	4.5	20.8
_	433521	T66087	Hs.112482	Homo sapiens unknown mRNA sequence	4.4	2.0
5	429876	AB028977	Hs.225974	KIAA1054 protein	4.4	19.2
	429726	AW628326 A8035356	Hs.27151	ESTs	4.4	10.2 9.4
	449093 415716	N59294	Hs.22998 Hs.179662	neurexin 1 nucleosome assembly protein 1-6ke 1	4.4 4.4	9.4 15.1
	419656	AB002314	Hs.92025	KIAA0316 gene product	4.4	8.2
10	425864	U56420	Hs.159903	offactory receptor, family 5, subfamily	4.4	2.4
	435078	AW518888	Hs.40937	ESTs	4.4	5.7
	432712	AB016247	Hs.288031	sterol-C5-desaturase (fungal ERG3, delta	4.3	5.9
	426867	AA460967	Hs.22668	ESTs	4.3	6.0
15	412112	BE180342	11- 49494	gb:RC3-HT0622-130400-012-a07 HT0622 Homo	4.3	3.2
13	410171	H07892	Hs.12431 Hs.227591	ESTs Markhy similar to 19012024 Law via	4.3 4.2	5.3 5.0
	442339 421249	BE299668 AA285362	115.22/331	ESTs, Weakly similar to 1901303A Leu zip gb:HTH277 HTCDL1 Homo sapiens cDNA 5/3'	4.2	3.5
	422528	AB011182	Hs.118087	KIAA0510 protein	4.2	3.9
	434460	AA478486	Hs.3852	KIAA0368 protein	4.1	8.3
20	410362	H04811	Hs.93164	proprotein convertase subtilisin/kexin t	4.1	7.0
	449754	H00820	Hs.30977	ESTs, Weakly similar to B34087 hypotheti	4,1	3.9
	408496	A1683802	Hs.136182	ESTs	4.1	4.7
	434101 430212	AA625205 AA469153	Hs.259599	KIAA1622 protein gb:nc67f04.s1 NCI_CGAP_Pr1 Homo sapiens	4.1 4.0	6.3 2.5
25	453165	S74727	Hs.32042	aspartoacytase (aminoacytase 2, Canavan	4.0	7.4
23	456407	AW968614	13.02072	gb:EST380690 MAGE resequences, MAGJ Horno	4.0	5.1
	441869	NM_003947	Hs.8004	huntingtin-associated protein interactin	4.0	32.3
	429628	H09604	Hs.13268	ESTs	4.0	4.5
20	410087	F12079	Hs.332579	ESTs	4.0	6.9
30	419910	AA662913	Hs.190173	ESTs, Weakly similar to A46010 X-linked	4.0	2.6
	441005	Z41305	Hs.303172	Homo sapiens mRNA; cDNA DKFZp547G133 (fr	3.9	21.7
	412677 453341	AW029608 AI758912	Hs.17384 Hs.296341	ESTs adenytyl cyclase-associated protein 2	3.9 3.9	2.2 7.2
	416854	H40164	Hs.80296	Purkinje cell protein 4	3.9	2.2
35	414666	NM_004466	Hs.76828	glypican 5	3.8	6.2
	418217	AI910647	Hs.13442	ESTs	3.8	3.2
	421855	F06504	Hs.27384	ESTs, Moderately similar to ALU4_HUMAN A	3.8	2.2
	414764	AW013887	Hs.72047	ESTs	3.8	10.7
40	433629	R13140	Hs.13359	ESTs	3.7 3.7	2.7 2.1
40	424738 407706	A/963740 AA191085	Hs.46826 Hs.26612	ESTs ESTs, Moderately similar to S23650 retro	3.7	5.3
	437268	AI754847	Hs.227571	regulator of G-protein signalling 4	3.7	53.7
	423135	N67655	Hs.26411	ESTs	3.7	21.7
	446818	A1342668	Hs.279765	ESTs	3.7	2.6
45	427562	R56424	Hs.26534	ESTs	3.6	3.6
	439274	AF086092	Hs.48372	ESTs	3.6	34.5
	452381	H23329	Hs.290880	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.6 3.6	6.0 5.1
	422897 429656	AA679784 X05608	Hs.4290 Hs.211584	ESTs neurofilament, light polypeptide (68kD)	3.6	24.6
50	417154	AI674701	Hs.21388	ESTs	3.6	5.8
	447176	Z42549	Hs.160893	ESTs	3.6	6.4
	405977				3.6	3.9
	423568	NM_005256	Hs.129818	growth arrest-specific 2	3.6	2.5
55	441235	A1884586	Hs.135570	Homo sapiens cDNA: FLJ21268 fis, clone C	3.6	5.4
))	426775 414831	AA384564 M31158	Hs.108829 Hs.77439	ESTs protein kinase, cAMP-dependent, regulato	3.6 3.6	3,4 2.8
	425153	AW023193	Hs.27046	ESTs	3.6	4.9
	446495	D60923	Hs.153460	ESTs	3.5	9.8
	445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	3.5	16.6
60	416421	AA134006	Hs.79306	eukaryotic translation initiation factor	3.5	5.0
	418207	C14685	Hs.34772	ESTs	3.5	16.0
	425383	D83407	Hs.156007 Hs.23926	Down syndrome critical region gene 1-lik triadin	· 3.5 3.5	6.2 2.5
	417027 408367	AA192306 AK001178	Hs.44424	homolog of rat orphan transporter v7-3	3.5	5.3
65	408776	AA057365	Hs.63356	ESTs, Wealdy similar to 138022 hypotheti	3.5	5.5
•••	453220	AB033089	Hs.32452	Homo saplens mRNA for KIAA1263 protein,	3.5	23.6
	419347	C15944	Hs.90005	superiorcervical ganglia, neural specifi	3.5	42.3
	433803	AI823593	Hs.27688	ESTs	3.4	3.6
70	450715	AI266484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	3.4	4.1
70	415076 423826	NM_000857 U20325	Hs.77890 Hs.1707	guanylate cyclase 1, soluble, beta 3 cocaine- and amphetamine-regulated trans	3.4 3.4	9.8 4.7
	427173	BE255017	Hs.97540	ESTs	3.4	2.4
	446092	N33522	Hs.145894		3.4	3.5
	416868	A1656856	Hs.292597	ESTs	3.4	4.5
75	458234	BE551408	Hs.127196		3.4	4.5
	434053	AW445136	Hs.134945		3.4	3.9
	428536	AJ143139 AJ267589	Hs.2288 Hs.302689	visinin-like 1	3.3 3.3	42.3 14.4
	410366 425785	Al267589 T27017	Hs.159528		3.3 3.3	4.6
80	434998	AW975157	Hs.26037	ESTs	3.3	4.7
	456359	AI967991	Hs.93574	homeo box D3	3.3	4.4
	426527	NM_001037			3.3	5.2
	400302	N48056	Hs.1915	tolate hydrolase (prostate-specific memb	3.3	9.0

	419875			proenkephalin	3.3 3.3	3.6 3.0
	444612			ESTs ESTs	3.2	2.2
	415242 421640	R45986 AW966652	Hs.295014	gb:EST378726 MAGE resequences, MAGI Homo	3.2	3.8
5	408806	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone C	3.2	2.4
_	446015	T30968	Hs.13531	hypothetical protein FLJ10971	3.2 3.2	3.2 2.2
	425495	AA358454	Hs.78026	ESTs, Weakly similar to similar to ankyr	3.2	2.9
	403092 452971	AI873878	Hs.91789	ESTs	3.2	4.5
10	454100	AI693231	Hs.126043	chromosome 21 open reading frame 51	3.2	2.7
	448440	AA173467	Hs.62402	p21/Cdc42/Rac1-activated kinase 1 (yeas)	3.2 3.2	28 27
	421200	AA284811	Hs.264433 Hs.128128	ESTs ESTs	3.2	21
	440827 429809	AI733110 AL162010	Hs.223603	Homo sapiens mRNA; cONA DKFZp761D09121 (3.2	4.3
15	420156	AW449258	Hs.6187	ESTs	3.2	19.0
	457535	AA609685	Hs.278672	membrane component, chromosome 11, surfa	3.2 3.1	2.0 8.7
	419956	AL137939	Hs.40096 Hs.42721	ESTs ESTs	3.1	2.7
	423930 417868	AA332697 A1078534	Hs.122592	ESTs	3.1	12.6
20	423346	AJ267677	Hs.127416	synaptojanin 1	3.1	12.0
	441921	A1733376	Hs.164478	hypothetical protein FLJ21939 similar to	3.1 3.1	4.3 5.3
	429470	AI878901	Hs.203862 Hs.279860	guanine nucleotide binding protein (G pr tumor protein, translationally-controlle	3.1	7.1
	408217 427322	AI433201 AK002017	Hs.176227	hypothetical protein FLJ11155	3.1	6.3
25	449078	AK001256	Hs.22975	KIAA1576 protein	3.1	30.1
	429608	U49250	Hs.210862	T-box, brain, 1	3,1 3.1	2.2 3.0
	442308	AA989402	Hs.111	fibroblast growth factor 9 (glia-activat neurofilament 3 (150kD medium)	3.1	10.9
	411666	AF 106564 AA416931	Hs.71346 Hs.126065	ESTs	3.1	7.5
30	427865 430708	U78308	Hs.278485	offactory receptor, family 1, subfamily	3.1	3.4
50	451829	AW964081	Hs.247377	ESTs	3.0	6.2 2.4
	405911			COT	3.0 3.0	6.2
	418808	AI821836	Hs.10359 Hs.22869	ESTs ESTs, Moderately similar to KIAA1395 pro	3.0	5.1
35	452893 423952	H18017 AW877787	Hs.136102	KIAA0853 protein	3.0	2.1
,,,	423532	AW576555	Hs.15780	ATP-binding cassette, sub-family A (ABC1	3.0	2.1
	405793				3.0 3.0	2.7 14.3
	410711	AB002316	Hs.65746	KIAA0318 protein	3.0	2.1
40	427071	AA397958	Hs.192719 Hs.33187	ESTs KIAA0748 gene product	3.0	14.5
40	453534 413903	NM_014796 AA496493	Hs.23136	ESTs	3.0	2.2
	426866	U02330	Hs.172816		3.0	11.3
	434945	AB033065	Hs.4280	KIAA1239 protein	3.0 2.9	3.5 4.9
45	412639	AW961284	Hs. 296235	ESTs KIAA0820 protein	2.9	33.1
45	453590 414502	AF150278 AL133721	Hs.33578 Hs.224680		2.9	2.3
	434367	AB020700	Hs.3830	KIAA0893 protein	2.9	23.1
	425121	AI797511	Hs.154679		2.9 2.9	8.1 20.8
50	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1	2.9	3.2
50	401213 401028	AW673312	Hs.50848	hypothetical protein FLJ20331	2.9	3.4
	415191	AA190381	Hs.120810		2.9	3.0
	449275	AW450848	Hs.205457		2.9 2.9	5.6 35.0
55	419863	AW952691	Hs.93485	Homo sapiens mRNA; cDNA DKFZp761D191 (fr ESTs	2.9	2.0
55	411421 430865	BE272110 AI073424	Hs.21177 Hs.5232	HSPC125 protein	2.9	11.4
	437486	AW952089	Hs.5636	RAB6A, member RAS oncogene family	2.9	2.2
	442357	AI458586	Hs.13570	5 ESTs	2.9 2.9	6.0 2.2
60	408274		U- CC000	gb:yg12g11.r1 Soares infant brain 1NIB H	2.8	5.0
60	444185	AW298350	Hs.66020 Hs.22999	COT-	2.8	5.1
	420173 428358		Hs.10191		2.8	7.0
	447252		Hs.12449	Homo sapiens transmembrane protein HTMP1	2.8	4.4 10.6
	440260		Hs.7130	copine IV	2.8 2.8	8.4
65	417084		Hs.33067 Hs.22479		2.8	2.8
	438257 441934		Hs.7344	ESTS	2.8	6.2
	447885		Hs.30317		2.8	3.5
	423552		Hs.12978		2.8 2.8	3.4 14.4
70	450940		Hs.14320		2.8 2.8	21.7
	410011 445887		Hs.57856 Hs.14559		2.8	5.1
	425494		Hs.78026		2.8	2.4
	43820		Hs.2258	B ESTs	2.8	11.9
75	43619	9 R38946	Hs.1279		2.8 2.8	6.0 2.4
	43482		Hs.2226 Hs.1269		2.8 2.8	3.4
	41546 41807				2.8	4.5
	43214			22 ESTs, Weakly similar to T34549 probable	2.8	9.5
80	43037	1 D87466	Hs.2401		2.8 2.7	7.0 2.5
	43735		Hs.3316 Hs.7093		2.7	3.6
	41583 43867				2.7	2.5
	70001					

	419558	AW953679		gb:EST365749 MAGE resequences, MAGC Homo	2.7	3.1
	446318	AI949389	Hs.18067	ESTs	27	4.1
	445183	AB007877	Hs.12385	KIAA0417 gene product	2.7	5.3
_	457012	R41480	Hs.127630	ESTs	2.7	19.0
5	431988	AC002302	Hs.77202	protein kinase C, beta 1	2.7 2.7	7.2
	430223 447932	NM_002514 AA837474	Hs.235935 Hs.20021	nephroblastoma overexpressed gene vesicle-associated membrane protein 1 (s	27	2.8 3.8
	450214	BE439763	Hs.227571	regulator of G-protein signalling 4	27	6.9
	434731	AA648049	Hs.121518	ESTs	2.7	5.0
10	428839	A1767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	2.7	5.2
	407709	AA456135	Hs.23023	ESTs	2.7	2.5
	422420	U03398	Hs.1524	tumor necrosis factor (ligand) superfami	2.7	3.3
	443305	AJ050693	Hs.133318	ESTs	2.7	5.9
15	435648	H24347	Hs.27524	ESTs	2.7 2.7	15.0
15	41B407	AL044818 AW975687	Hs.84928 Hs.292979	nuclear transcription factor Y, beta	27	2.7 6.0
	436771 428689	NM_014351	Hs.189810	ESTs suffortranterase family 4A, member 1	2.7	4.8
	440503	NM_006539	Hs.7235	calcium channel, voltage-dependent, gamm	2.7	4.4
	441006	AW605267	Hs.7627	CGI-60 protein	2.7	3.1
20	410330	AW023630	Hs.46786	ESTs	2.6	29.5
	434398	AA121098	Hs.3838	serum-inducible kinase	2.6	2.6
	438831	BE263273	Hs.6439	synapsin II	26	7.8
	419066	Z98492	Hs.6975	PRO1073 protein	26	3.4
25	412643	AW971239	Hs.293982	ESTs	26	2.2
25	430456	AA314998	Hs.241503	hypothetical protein	2.6 2.6	17.9 2.9
	416498 401421	U33632	Hs.79351	potassium channel, subfamily K, member 1	2.6	2.0
	419530	X98330	Hs.90821	ryanodine receptor 2 (cardiac)	2.6	4.2
	441817	AW969706	Hs.293332	ESTs	26	3.8
30	439203	AA448930	Hs.8453	KIAA1587 protein	2.6	4.2
•	426054	U12431	Hs.166109	ELAV (embryonic lethal, abnormal vision,	2.6	5.1
	444583	AW994403	Hs.100861	hypothetical protein FLJ14600	2.6	3.7
	417919	A1928203	Hs.86379	ESTs	2.6	3.0
25	434293	NM_004445	Hs.3796	EphB6	2.6	3.2
35	431716	D89053	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	2.6 2.6	6.4 2.2
	443037 440736	AW500305 D56919	Hs.299166 Hs.265848	syntaxin 7 myomegalin	2.6	7.1
	404648	D30313	115.203040	myomegan	26	3.0
	429995	AA463571		gb:zx72e09.r1 Soares_total_fetus_Nb2HF8_	2.6	3.5
40	436508	AW604381	Hs.121121	ESTs, Weakly similar to S00755 pleckstri	2.6	3.9
	441190	H09073	Hs.25046	ESTs	2.6	3.1
	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	2.6	2.9
	442731	AI868167	Hs.131044	ESTs	2.6	4.1
45	416836	D54745	Hs.80247	cholecystokinin	2.6	14.9
45	449071	NM_005872	Hs.22960	breast carcinoma amplified sequence 2	2.5	2.4
	436321	AA709133	Hs.180144	ESTs	2.5 2.5	2.8 3.6
	439693 443212	AI741B16 AW269515	Hs.125897 Hs.102500	ESTs hypothetical protein FLJ20481	2.5	2.8
	423981	AL122104	Hs.136664	Homo sapiens mRNA, cDNA DKFZp434A1627 (f	2.5	3.8
50	407868	NM_000950	Hs.40637	profine-rich Gla (G-carboxyglutamic acid	2.5	3.1
	443992	AW022228	Hs.322922	ESTs	2.5	27.9
	444124	R43097	Hs.6818	ESTs	2.5	5.3
	411379	AI816344	Hs.12554	ESTs, Weakly similar to NPL4_HUMAN NUCLE	2.5	38.0
55	440474	AI207936	Hs.7195	gamma-aminobutyric acid (GABA) A recepto	2.5	3.8
55	446277	AI284218	Hs.159204	ESTs	25	2.2
	410111	AI620206 AB011131	Hs.189647	ESTs	2.5 2.5	3.5 4.8
	445162 410718	A1920783	Hs.12376 Hs.191435	piccolo (presynaptic cytomatrix protein) ESTs	2.5	4.5
	417201	T60432	Hs.269084	ESTs, Moderately similar to AF097994 1 L	2.5	2.9
60	420274	AW968000	Hs.143389	ESTs. Weakly similar to T14318 ubiquitin	2.5	2.8
	433496	AF064254	Hs.49765	VLCS-H1 protein	2.5	4.7
	437331	AL353933	Hs.21710	hypothetical protein DKFZp761G0313	2.5	3.3
	437368	AI471969	Hs.182606	ESTs	2.5	3.0
<i>C</i>	441985	BE047625	Hs.169815	ESTs	2.5	3.6
65	410025	BE220489	Hs.113592	ESTs, Moderately similar to I54374 gene	2.5 2.5	9.2
	414680	AA743331	Hs.272572	hemoglobin, alpha 2 ESTs	2.5	3.6 23.9
	429956 429028	AI374651 AA443439	Hs.22542 Hs.48797	ESTS	25	2.8
	438109	AJ076621	Hs.71367	ESTs, Moderately similar to ALU7_HUMAN A	2.5	3.1
70	439780	AL109688		db:Homo sapiens mRNA full length insert	2.5	2.3
	440888	N45600	Hs.326880		2.5	3.9
	445246	AJ217713	Hs.147586	ESTs	2.5	2.6
	440152	A8002376	Hs.7006	KIAA0378 protein	2.4	23.6
75	432740	AF061034	Hs.278898	tumor necrosis factor alpha-inducible ce	2.4	21
75	415122	D60708	Hs.22245	ESTS	2.4 2.4	3.9 9.8
	432298	AL118812	Hs.274293		2.4 2.4	9.8
	437948 421360	AA772920 AA297012	Hs.303527 Hs.103839		2.4	2.8
	427115	AW972853	Hs.112237		2.4	2.2
80	452074	BE299035	Hs.27747	G protein-coupled receptor 37 (endotheli	2.4	10.0
	436639	D14838	Hs.111	fibroblast growth factor 9 (glia-actival	2.4	3.5
	434520	AA205273	Hs.177011		2.4	3.1
	411529	AA430348	Hs.317596	Homo sapiens cDNA FLJ12927 fis, clone NT	. 2.4	3.0

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	442272	AA988302		ESTs	2.4	2.1 2.7
	422927	AW247388		calcium binding protein 1 (calbrain)	24 24	2.7
	444647	H14718		Human clone 23589 mRNA sequence	2.4	15.0
5	415827	H17462 AA017432		ESTs ESTs, Weakly similar to Z202_HUMAN ZINC	2.4	3.9
,	451397 445200	AA084460		somatostatin	2.4	3.7
	451062	AL110125	Hs.25910	Homo sapiens mRNA; cDNA DKFZp564C1416 (f	2.4	24
	420328	Y19062	Hs.96870	staufen (Drosophila, RNA-binding protein	2.4	4.3
	432122	AA526514		gb:ni60f02.s1 NCI_CGAP_Ov2 Homo sapiens	2.4 2.4	4.3 3.5
10	444125	AJ124882		ESTs	2.4	10.8
	430538	AB032435	Hs.242821 Hs.3052	differentiation-associated Na-dependent early growth response 4	2.4	2.4
	457519 409371	X69438 R51736	Hs.12381	ESTs	2.4	21
	456303	AA224872	Hs.115088	ESTs	2.4	3.2
15	440105	AA694010	Hs.6932	Homo sapiens clone 23809 mRNA sequence	2.4	23.4
	400979			·	2.4	4.1
	435296	R49685	Hs.24980	ESTS	2.4 2.4	6.5 18.5
	408950	AA707814	Hs.14945	long fatty acyl-CoA synthetase 2 gene	2.4	2.2
20	452032	BE244005	Hs.27610	retinoic acid- and interferon-inducible cytochrome P450 retinoid metabolizing pr	2.4	2.7
20	432098	AF252297 AW015458	Hs.91546 Hs.297017	ESTs	2.4	2.5
	408974 412177	Z23091	Hs.73734	glycoprotein V (platelet)	2.4	2.8
	413153	N94205	15.10.04	gb:za27a08.r1 Soares fetal liver spieen	2.4	2.5
	417583	AA658782	Hs.191284	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.4	2.6
25	452034	F12234	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	2.3	3.0
	424940	AA985308	Hs.194327	ESTs	2.3 2.3	6.3 4.1
	431706	AJ816086	Hs.296341	adenylyl cyclase-associated protein 2	23	2.9
	419125	AA642452	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro ATPase, aminophospholipid transporter-li	2.3	8.7
20	423641	AL137256	Hs.130489	ESTs, Weakly similar to TIM_HUMAN PROBAB	2.3	3.2
30	436407	T88803 AL109781	Hs.271507 Hs.21754	Homo sapiens mRNA full length insert cDN	2.3	5.2
	448681 415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito	2.3	54.7
	410765	AI694972	Hs.66180	nucleosome assembly protein 1-like 2	2.3	9.1
	422386	AF105374	Hs.115830	heparan sutfate (glucosamine) 3-O-sutfol	2.3	5.0
35	414828	AA156651		gb:zl05h05.r1 Soares_pregnant_uterus_NbH	2.3	2.4
	445556	AI910241	Hs.12887	actin-related protein 3-beta	2.3 2.3	8.5 26.3
	426968	U07616	Hs.173034	amphiphysin (Stiff-Mann syndrome with br	2.3	2.5
	444562	AA186715	Hs.336429	RIKEN cDNA 9130422N19 gene	2.3	7.6
40	423420	AI571364	Hs.128382	Homo sapiens mRNA; cDNA DKFZp76111224 (f ESTs	2.3	26.3
40	439450	R51613 AW802282	Hs.125304 Hs.22265	ругичаte dehydrogenase phosphatase	2.3	2.2
	427127 447179	AW015633	Hs.157299	ESTs	2.3	3.8
	414711	AJ310440	Hs.288735	Homo sapiens cDNA FLJ13522 fis, clone PL	2.3	2.3
	433449	AW772282		gb:hn71b05.x1 NCI_CGAP_Kid11 Homo sapien	2.3	3.8
45	414320	U13616	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	2.3	2.5 7.8
	416778	M16505	Hs.79876	steroid sulfatase (microsomal), arylsulf	2.3 2.3	7.0 4.1
	425130	AA448208	Hs.99163	ESTs 40	2.3	2.5
	456664	AW963354	Hs.334409	metallothionein 1G ESTs	23	4.2
50	438283	AI458931 AW007066	Hs.37282 Hs.18949	ESTS, Weakly similar to CA2B_HUMAN COLLA	2.3	3.0
20	417455 412100	AW892731	rts. 10545	gb:CM0-NN0005-100300-279-c02 NN0005 Homo	2.3	3.7
	448981	AI968719	Hs.195387		2.3	3.2
	416101	R24854	Hs.268806		2.3	6.5
	439731	Al953135	Hs.45140	hypothetical protein FLJ14084	2.3	17.8
55	415734	NM_014747		KIAA0237 gene product	2.3 2.3	40.1 2.9
	424596	AB020639	Hs.151017		2.3	2.4
	420230	AL034344	Hs.284186	forkhead box C1 hypothetical protein DKFZp761D221	2.3	5.7
	451559 404835	AL119980	Hs.20935	hypothetical protest and approvident	2.3	2.1
60	456765	A1497900	Hs.33067	ESTs	2.3	4.1
00	455517	AW984068		gb:RC0-HN0006-160300-011-e06 HN0006 Homo	2.3	2.4
	408206		Hs.43670	kinesin family member 3A	2.2	18.5
	411770	NM_01427		heat shock protein (hsp110 family)	2.2	3.9 2.6
15	430105		Hs.2540	cholinergic receptor, nicotinic, atpha p	2.2 2.2	4.9
65	458694		Hs.13298	ESTs 3-hydroxy-3-methylglutaryl-Coenzyme A sy	2.2	4.4
	415091		Hs.77910 Hs.15396		2.2	2.4
	439642				2.2	4.9
	450138 454222			ESTs, Weakly similar to A46010 X-linked	2.2	3.7
70	405326		113.7555		2.2	2.7
. •	431342				2.2	5.2
	453101	AW952778			2.2	3.3 2.8
	408897		Hs.28370		2.2 2.2	4.6
75	451398		Hs.14447		2.2	10.4
75	438208				2.2	6.1
	408449		8 Hs.16616 Hs.71592		2.2	3.1
	414130 445010		Hs.12246		2.2	3.9
	42437				2.2	2.3
80	42464				2.2	11.7
	40972	9 D51315	Hs.10628		2.2	4.9 19.9
	43280	9 AA565509	Hs.13170	3 ESTs	2.2 2.2	10.4
	42289	0 Z43784	Hs.75890	ankyrin 3, node of Ranvier (ankyrin G)	2.2	10.4

	428532	AF157326	Hs.184786	TBP-Interacting protein	2.2	6.5
	413074	AJ871368	Hs.8417	hypothetical protein OKFZp761M0423	22	3.4
	414442	AA156238	Hs.32501	ESTs	2.2	3.2
•	452768	AW069459	Hs.61539	ESTs	2.2	2.0
5	450440	AB024334	Hs.25001	tyrosine 3-monooxygenase/typtophan 5-mo	2.2 2.2	3.2 2.3
	426281 428411	AK000987 AW291464	Hs.169111 Hs.10338	oxidation resistance 1 ESTs	22	2.3 2.3
	413787	AI352558	Hs.75544	tyrosine 3-monooxygenase/tryptophan 5-mo	22	3.1
	451734	NM_006176	Hs.26944	neurogramin (protein kinase C substrate,	2.2	8.5
10	439108	AW163034	Hs.6467	synaptogyrin 3	2.2	7.9
	405385				2.2	2.4
	447285	AJ371849	Hs.200696	ATPase, Class VI, type 11C	2.2 2.2	2.2 3.1
	452667 422234	T87219 AF119818	Hs.13219 Hs.113287	ESTs discs, large (Drosophila) homolog-associ	2.1	8.3
15	410339	AI916499	Hs.298258	ESTs	2.1	3.2
	413231	D87451	Hs.75244	BCL2-like 2	2.1	4.5
	447104	R19085	Hs.210706	Homo sapiens cDNA FLJ13182 fis, clone NT	2.1	2.2
	451952	AL120173	Hs.301663	ESTS	2.1 2.1	36.5
20	415841 441086	Z45637 Al928489	Hs.7093 Hs.213490	ESTs ESTs, Wealthy similar to N33_HUMAN N33 PR	2.1	2.4 2.2
20	450407	NM_000810	Hs.24969	gamma-aminobutyric acid (GABA) A recepto	2.1	6.6
	427627	R87582	Hs.179915	guanine nucleotide binding protein (G pr	2.1	5.3
	449712	R56545	Hs.6100	EST ₈	2.1	4.5
25	409660	AW452065	Hs.258905	ESTs .	2.1	21
25	430434	AL049548	Hs.241420	Homo sapiens mRNA for KIAA1756 protein,	2.1 2.1	5.4 3.0
	434138 448610	AA625804 NM_006157	Hs.21602	gb:zu86h01.s1 Soares_testis_NHT Homo sap nel (chicken)-like 1	2.1	4.8
	418948	AI217097	113.21002	gb:qd43h07.x1 Soares_fetal_heart_NbHH19W	21	2.9
	414876	AW950925	Hs.924	crystallin, mu	2.1	3.4
30	440426	Al159800	Hs.7181	Homo sapiens cDNA FLJ13663 fis, clone PL	2.1	3.7
	451249	AA016227	Hs.27280	ESTs	2.1	4.1
	451475	T19093	Hs.26450 Hs.21896	KIAA0725 protein	21 21	2.1 29.7
	448743 430814	AB032962 U89336	Hs.247993	KIAA1136 protein NG5 protein	2.1	2.7
35	426990	AL044315	Hs.173094	Horno sapiens mRNA for KIAA1750 protein,	2.1	2.3
	426642	AW068223	Hs.171581	ubiquitin C-terminal hydrolase UCH37	2.1	4.5
	427335	AA448542	Hs.251677	G antigen 7B	2.1	2.2
	459089	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp564O1763 (f	2.1 2.1	2.3 5.9
40	435832 446383	AA425688 T05816	Hs.41641 Hs.92511	Bruno (Drosophila) -like 4, RNA binding ESTs	2.1	2.9
70	412768	AW996044	Hs.26239	Human DNA sequence from clone RP11-43882	21	2.1
	453976	BE463830	Hs.163714	ESTs	2.1	4.2
	415111	R39039	Hs.328455	EST	2.1	3.3
45	452238	F01811	Hs.187931	ESTs	2.1	4.9
45	445279	R41900	Hs.22245	ESTs	2.1 2.1	9.8 3.1
	448799 418338	AI937094 NM_002522	Hs.179080 Hs.84154	ESTs neuronal pentraxin I	21	8.3
	445725	AK000956	Hs.13209	hypothetical protein FLJ10094	2.1	5.4
	443537	D13305	Hs.203	cholecystokinin B receptor	2.1	4.1
50	454066	X00356	Hs.37058	calcitonin/calcitonin-related polypeptid	2.1	6.4
	429954	AI918130	Hs.21374	ESTs	2.1 2.1	7.2 3.9
	415292 423563	H29016 R34734	Hs.200576 Hs.75209	ESTs protein kinase (cAMP-dependent, catalyti	2.1	3.5
	423303 424906	AI566086	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3	2.1	4.7
55	459309	AA040620	Hs.5672	hypothetical protein AF140225	. 2.1	2.2
	439340	AB032436	Hs.6535	brain-specific Na-dependent inorganic ph	2.1	4.7
	402598	BE314624	Hs.3128	polymerase (RNA) II (DNA directed) polyp	2.1	5.4
	435406 448792	F26698 R42550	Hs.4884 Hs.12826	calcium/calmodulin-dependent protein kin ESTs	2.1 2.1	6.6 4.1
60	449500	AW956345	Hs.12026	ESTs	21	2.4
•	441134	W29092	Hs.7678	cellular retinoic acid-binding protein 1	2.1	5.8
	433361	AW469373	Hs.300141	ribosomat protein L39	2.1	2.7
	452946	X95425	Hs.31092	EphA5	2.1	5.0
65	426167 453666	AF039023 AW015681	Hs.167496 Hs.135229		2.0 2.0	2.2 3.1
05	424632	AB014523	Hs.151406		2.0	3.5
	448589	AF017090	Hs.21554	KIAA1107 protein	2.0	4.1
	430416	AC005531	Hs.57806	Homo sapiens PAC clone RP4-701016 from 7	2.0	2.3
70	445627	AW818475	Hs.7363	ESTs	2.0	2.1
70	417092	H97508	Hs.181165		2.0 2.0	2.5 4.7
	453653 435850	AW505554 AF250847	Hs.144559 Hs.283514		2.0	3.7
	435086	AW975243	Hs.122596		2.0	2.1
	423191	D61506	Hs.8417	hypothetical protein DKFZp761M0423	2.0	2.1
75	411562	AL050201	Hs.70769	hypothetical protein DKFZp586E1923	2.0	2.8
	431645	AF078849	Hs.266483		2.0	2.5 3.6
	429834	AI929645 BE540565	Hs.225936 Hs.159460		2.0 2.0	3.0 17.5
	439607 408033	AW138045	Hs.242256		2.0	4.0
80	430317	AB020645	Hs.239189		2.0	2.7
	419631	AW188117	Hs.303154	popeye protein 3	2.0	2.6
	432660	AI288430	Hs.64004	ESTs	2.0	2.3 15.9
	454048	H05626	Hs.6921	ESTs	2.0	13.3

				DKFZP586B0923 protein		2.0 2.0	3.1 2.9
		AL119114 Al267700	Hs.77196 Hs.317584	spectrin, alpha, non-erythrocytic 1 (alp ESTs		20	4.8
	420276	AA290938	Hs.190561	ESTs, Highly similar to SORL_HUMAN SOR	τι	2.0	5.1 15.9
5	424983	A1742434	Hs.169911	ESTs Homo sapiens cDNA FLJ13155 fis, clone NT		2.0 2.0	2.7
	446296 450006	AA985662 AI241555	Hs.63131 Hs.60171	ESTs		2.0	3.5
10	TABLE 118 Pkey:	: Uniqu	e Eos probese	d identifier number			
10	CAT number	er: Gene	cluster number	f			
	Accession:	Genb	ank accession	numbers			
	Pkey	CAT Number	Acces				
15	408274 412100	104999_1 1277224_1		15 Z43964 AA053547 92731 H08502 Z45826			
	412112	1277883_1			0218 BE180226 BE1804	13 BE180416	5 AW901899 BE180228 AW901897 BE180224 1 BE180341 AW901894 BE180217 BE180227 AW901891
			AW9	01898 BE180223 BE180219 BE180346 BE16 0345 AW893614 AW893615 H85799 H83501	0343 BE180220	23 01.10022	100
20	413153	1350849_1	N942	05 BE067565 BE067556			
	413510	1374377_1		44 T77009 BE145525 BE145493	•		
	414828 418948	149563_1 180608_1	A121	i6651 AA156622 R14472 7097 AW886090 W38035 W38792 AA232835	AW936043		
	419558	185904_1	AVAZO	53679 AW953680 AA244436 H82527 AA361	046 AA244483 H82526		
25	421249	200649_1 204833_1	AA2i	35362 AW752386 AW847156 AA285373 AW6 66652 AW966653 AA294989 AA385977	113313 A41013330		
	421640 429995	311738_1	AA4	53571 AI277645 AL118763			
	430212	314437_1		59153 A1718503 AA469225 26514 AW973343 AA554293			
30	432122 433449	341756_1 366532_1	AW	772282 AA592974			
	434138	380572_1		25804 AW418787 AW074833 AI675642 AI39	3368		
	437483 439780	43756_1 47673_1		90174 AW898817 09688 R23665 R26578			
	452502	919733_1	AI90	04296 BE007223 R30687			
35	455517 456407	1321782_1 184986_1		984068 AW984072 AW984077 968614 AA243209 AA281411			
•							
	TABLE 11 Pkey:		one onwhet co	presponding to an Eos probeset			A STATE OF THE PAIR
40	Ref:	Con		The 7 digit numbers in this column are Gent	oank Identifier (GI) numbe	ers. "Dunhan	n, et al.º refers to the publication entitled "The DNA
	Strand:	seq	uence of hum	en chromosome 22" Dunham, et al. (1999) Na and from which exons were predicted.	<u>nule</u> 402.405-455.		
	Nt_positi	on: Indi	icates nucleoti	de positions of predicted exons.			
45	Pkey	Ref	Strand	Nt_position			
73	400979	8072554	Plus	160842-161028			
	401213	9858408 7452889	Plus Minus	98243-98380,98489-98619 142291-142461			
	401421 403092	8954241	Plus	174720-175016,175104-175406,175508-	175813		
50	404648	9796894	Minus	115334-116020			
	404793 404835	7232206 6970743	Minus Plus	61087-61590 85462-85684,88139-88287,90338-91018	,94827-94990		
	405326	4375975	Plus	10633-10709,30805-30893,38078-38253	,55112-55327,57718-571	818,66696-66	841
55	405385 405793	6552772 1405887	Plus Minus	48332-48454 89197-89453			
55	405911	6758795	Plus	101008-101643			
	405977	8247789	Minus	135548-136177			
	<u></u>				CTOMA COMPARED TO	O NORMAL (FNTRAL NERVOUS SYSTEM
60	TABLE	12A: ABOUT 6	78 GENES UP-	P-REGULATED IN LOWER GRADE GLIOBLE adulated in lower grade glioblastoma (LGG) of	ompared to normal centra	al nervous sy	stem (CNS). These were selected from 59580 probesets on n or equal to 2.5. The "average" LGG level was set to the 85°
	the Affy	metrix/Eos Hu0	3 GeneChip a	rray such that the ratio of average LGG to a	to the BAR named	ile amoonst v	prious CNS tissues. In order to remove gene-specific
	percent	ile amongst vari	ious LGG tum on enecific by	ors. The "average" normal CNS ussue level w oridization, the 10° percentile value amongst t	rarious non-malignant list	sues was sub	stracted from both the numerator and the denominator before
65	the ratio	o was evaluated	J.				
	Pkey:	U	nique Eos pro	beset identifier number ssion number, Genbank accession number			
	ExAccr Unigen	eID: U	inigene numbe	er			
70	Unigen	e Title: U	Inigene gene t	itle R GRADE GLIOBLASTOMA to normal CNS			
70	_R1:			_		RI	
	Pkey	ExAcon AL035668	Unigene Hs.7385			20.3	
	412420 42480		Hs.1532	03 MyoD family inhibitor		19.5	
75	45339	2 U23752	Hs.3296	 SRY (sex determining region Y)-box 11 Target Exon 		18.5 16.9	
	40260 44419		Hs.105			15.0	
	40963	8 AW45042	0 Hs.213	S ESTs		14.0 14.0	
80	44373 45675			792 delta (Drosophila)-like 3		13.6	
00	44734	2 Al199268	Hs.193	22 Homo sapiens, Similar to RIKEN cDNA	2010	12.2 10.3	
	43300 42701					9.5	
	42101	- 70700173		• •			

	425187	AW014486	Hs.22509	ESTs	9.0
	440210	AW674562	Hs.125296	ESTs	8.8
	448769 437034	N66037 AA742643	Hs.38173	gb:ny91c01.s1 NCI_CGAP_GCB1 Homo sapiens	8.4 8.2
5	449539	W80363	Hs.58446	ESTs	8.1
	417061	AI675944	Hs.188691	Homo sapiens cONA FLI12033 fis, clone HE	8.0
	435020 414217	AW505076 Al309298	Hs.301855 Hs.279898	DiGeorge syndrome critical region gene 8 Homo sapiens cDNA: FLJ23165 fis, clone L.	7.8 7.7
	449300	A1656959	Hs.346514	ESTs	7.6
10	449969	AW295142	Hs.180187	Homo sapiens cDNA FLJ14337 fis, clone PL	7.5
	452372	A1885742	Hs.228474	ESTs	7.2 7.2
	410102 417308	AW248508 H60720	Hs.279727 Hs.81892	ESTs; homologue of PEM-3 [Ciona savignyl KIAA0101 gene product	7.2
	447004	AW296968	Hs.157539	ESTs	7.1
15	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	7.1
	424635	AA420687	Hs.115455	Homo sapiens cDNA FLJ14259 fis, done PL Target Exon	7.1 7.1
	406478 428728	NM_016625	Hs.191381	hypothetical protein	6.9
••	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	6.9
20	428037	N47474	Hs.89230	potassium intermediate/small conductance	6.7
	423343 418097	AA324643 R45137	Hs.246106 Hs.21868	ESTs ESTs	6.7 6.7
	431553	X78075	Hs.2799	cartilage linking protein 1	6.6
26	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	6.6
25	425397 419169	J04088 AW851980	Hs.156346 Hs.262346	topoisomerase (DNA) II alpha (170kD) ESTs, Wealdy similar to S72482 hypotheti	6.4 6.4
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	6.4
	445908	R13580	Hs.13436	Homo sapiens clone 24425 mRNA sequence	6.3
30	402855	F11690		NM_001839*:Horno sapiens calponin 3, acid gb:HSC300041 normatized infant brain cDN	6.2 6.2
30	424009 400419	AF084545		Target	6.2
	446584	U53445	Hs.15432	downregulated in ovarian cancer 1	6.0
	414020	NM_002984	Hs.75703	small inducible cytokine A4 (hornologous	6.0
35	426140 427144	AF131798 X95097	Hs.343768 Hs.2126	Homo sapiens clone 25119 mRNA sequence vasoactive intestinal peptide receptor 2	5.9 5.9
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	5.8
	405238			Target Exon	5.7
	421977	W94197	Hs.110165	ribosomal protein L26 homolog	5.7 5.6
40	405348 428795	R45503	Hs.97469	C7001664:gi[12698061 dbj[BAB21849.1] (AB ESTs, Highly similar to A39769 N-acetyll	5.4
•••	422672	X12784	Hs.119129	collagen, type IV, atpha 1	5.3
	403349	NM_001406		ephrin-83	5.3
	453941 429139	U39817 F09092	Hs.36820 Hs.66087	Bloom syndrome ESTs	5.2 5.2
45	454860	AW835767	15.0007	gb:QV4-LT0016-240200-110-b08 LT0016 Homo	5.2
	452279	AA286844	Hs.61260	hypothetical protein FLJ13164	5.1
	418030	BE207573 M64590	Hs.83321 Hs.27	neuromedin 8 glycine dehydrogenase (decarboxylating;	5.1 5.1
	429469 450639	AI703186	Hs.277174	ESTs	5.1
50	412811	H06382		ESTs	5.1
	442832	AW206560	Hs.253569	ESTs	5.1 5.1
	436608 408161	AA628980 AW952912	Hs.300383	down syndrome critical region protein DS hypothetical protein MGC3032	5.1
	443744	A1084326	Hs.271548	ESTs, Weakly similar to 178885 serine/th	5.1
55	447497	AW167254	Hs.205722	ESTs	5.0 5.0
	450811 433244	A1739486 AB040943	Hs.245497 Hs.271285	ESTs KIAA1510 protein	4.9
	438458	AW975186	10.21.200	gb:EST387294 MAGE resequences, MAGN Homo	4.9
60	438456	AA913381	Hs.20594	ESTs	4.9
UU	411048 456304	AK001742 AI820973	Hs.67991	hypothetical protein DKFZp434G0522 gb:nc21c02.y5 NCI_CGAP_Pr1 Homo sapiens	4.9 4.9
	442547	AA306997	Hs.217484	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.9
	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	4.8
65	402274 420092	AA814043	Hs.88045	C19000498°;gi 4567179 gb AAD23607.1 AC00 ESTs	4.8 4.8
05	436282	R91913	Hs.272104		4.8
	430809	A1791150	Hs.262009	ESTs, Moderately similar to 138022 hypot	4.8
	455104	BE064863		gb:RC1-BT0313-110300-015-f06 BT0313 Homo	4.8 4.8
70	403961 424954	NM_000546	Hs.1846	Target Exon turnor protein p53 (Li-Fraumeni syndrome)	4.8
. •	414825	X06370	Hs.77432	epidermal growth factor receptor (avian	4.8
	447891	R41754	Hs.6496	ESTs	4.7
	423529 422737	T87318 M26939	Hs.120411 Hs.119571		4.7 4.7
75	428722	U76456	Hs.190787		4.6
-	437698	R61837	Hs.7990	ESTs, Moderately similar to 184505 calci	4.6
	403481	AW513691	Hs.270149	Target Exon ESTs, Weakly similar to 2109260A B cell	4.6 4.6
	426075 422170	A1791949	Hs.112432		4.6
80	416379	N38857	Hs.203933	ESTs	4.6
	406481	BE311901	Hs.28935	Target Exon gb:601142614F1 NIH_MGC_14 Homo sapiens c	4.5 4.5
	456052 423178	AI033140	Hs.124983		4.5
				•	

	444070	hm	Un 71122 -	raveliain 1	4,5
			He 44653 1	neuroligin 1 Homo sapiens cDNA: FLJ22669 fis, clone H	4.5
	432625		Hs.94830 (ESTs, Moderately similar to T03094 A-kin	4.5 4.5
_	452994	AW962597	Hs.31305	KIAA1547 protein	4.4
5	449961	AW265634	Hs.133100	ESTs NM_014226*:Homo sapiens renal tumor anti	4,4
	401454 406395			Target Exon	4.4
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	4.4
	453792	AL134539	He 254129	KIAA1678	4.4 4.4
10	415131	D61119		gb:HUM158C11B Clontech human fetal brain	4.4
	437695	AA769202 AW136820		ESTs ESTs	4.4
	422081 437748	AF234882		suppression of tumorigenicity 7	4.3
	433323	AA805132	Hs.159142	ESTs	4.3 4.3
15	420352	BE258835	11. 40004	gb:601117374F1 NIH_MGC_16 Homo sapiens c Homo sapiens clone 24421 mRNA sequence	4.3
	444218 441035	AF070641 Al694309	Hs.10684 Hs.126458	ESTs	4.3
	443836	BE221613	Hs.140553	ESTs	4.3
	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeal (LRR) protein	4.3 4.3
20	450166	AA429504	41- 407000	ESTs ESTs, Weakly similar to I38022 hypotheti	4.2
	429149	AW193360 R92347	Hs.197962 Hs.34574	ESTs, Wealdy Similar to ALU1_HUMAN ALU S	4.2
	422798 451254	AI571016	Hs.172967	ESTs	4.2
	409189	AA125984		gb:zn27h06.r1 Stratagene neuroepithelium	4.2 4.2
25	445118	AI208762	Hs.345572	ESTs	4.2
	444326	AI939357 C14904	Hs.270710 Hs.45184	ESTs Homo sapiens cDNA FLJ12284 fis, clone MA	4.2
	456060 404120	C14304	113.43104	C5000537":gi[3298595]gb[AAC41376.1] (AF0	4.2
	436899	AA764852	Hs.291567	ESTs	4.1 4.1
30	407624	AW157431	Hs.248941	ESTs	4.1
	453361	AA035197	Hs.107375 Hs.145020	ESTs ESTs, Weakly similar to KIAA1205 protein	4.1
	447439 438372	AA313565 Al140189	Hs.123191	ESTs	4.1
	438624	AA889055	Hs.123468	ESTs	4.1 4.1
35	422493	AW474183	Hs.250173	hypothetical protein FLJ13158	4.1
	406872	AI760903	Hs.37251	gb:wi09h08.x1 NCI_CGAP_CLL1 Homo sapiens ESTs	4.1
	425295 425849	AA431366 AJ000512	Hs.296323	serum/alucocorticoid regulated kinase	4.1
	434206	AW136973	Hs.180479	ESTs, Weakly similar to S69890 mitogen i	4.0
40	420602	AF060877	Hs.99236	regulator of G-protein signalling 20	4.0 4.0
	400645	4 4 20 5 2 4 2	Un 222005	Target Exon ESTs, Weakly similar to TRHY_HUMAN TRICH	4.0
	456306 419326	AA225313 W94915	Hs.222886 Hs.42419	ESTs. Weakly similar to the true to the tr	4.0
	414948	C15240	Hs.182155		4.0
45	423198	M81933	Hs.1634	cell division cycle 25A	4.0 4.0
	411537	BE073250	11- 400200	gb:MR0-BT0551-060300-102-e05 BT0551 Homo Homo sapiens clone 23556 mRNA sequence	3.9
	421637 439231	AF035290 AW581935	Hs.106300 Hs.141480		3.9
	429433	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	3.9
50	424186	AI536021	Hs.288706	Homo sapiens cDNA FLJ10281 fis, clone HE	3.9 3.9
	449932		Hs.263024		3.9
	434072		Hs.283059 Hs.164007		3.9
	434784 425146		13.10-1007	gb:EST366697 MAGE resequences, MAGC Horno	3.9
55	428538		Hs.98643	ESTs	3.9 3.9
	443318		Hs.133141		3.9
	416857 411688		Hs.292453	gb:EST365510 MAGE resequences, MAGB Homo	3.9
	447343		Hs.236894	ESTs, Highty simitar to S02392 alpha-2-m	3.9
60	425905		Hs.31858	novel C3HC4 type Zinc finger (ring finge	3.8 3.8
	403696		11. 40434	C4001100°:gij5852342 gb AAD54015.1 (AF0	3.8
	415884		Hs.13471	ESTs gb:RC3-CT0254-031099-012-c05 CT0254 Homo	3.8
	432646 447057		Hs.15769		3.8
65	400814			Target Exon	3.8 3.8
	441329		Hs.46821		3.8 3.8
	416664		Hs.20289 Hs.17029		3.8
	426044 455648			gb:RC4-BT0311-241199-012-c08 BT0311 Homo	3.8
70	41904		Hs.89568	ets variant gene 1	3.8
	44507	5 Al651827	Hs.34476	SOT WESTS	3.8 3.8
	45721				3.8
	42000 42806			33 ESTs	3.7
75	41642			7 Rac/Cdc42 guarnine exchange factor (GEF)	3.7
	45303	8 AW29241	5 Hs.2050	9 HBV pX associated protein-8	3.7 3.7
	40458	4	0 U-4E22	Target Exon 90 ESTs, Highly similar to JC2463 vasoactiv	3.7
	44714 45343				3.7
80	42964	3 AA455889	Hs.1672	79 FYVE-finger-containing Rab5 effector pro	3.7
	45807	2 AI890347		23 Homo sapiens cDNA; FLJ22785 fis, clone K	3.7 3.7
	45966		Hs.2928	ESTs solute carrier family 7 (cationic amino	3.7
	43218	38 AI362952	HS.2320	autote Carres (anny r Josephan Carres	

	430744	AA485229	Hs.105649	ESTs	3.7
	454392	BE260893	Hs.236131	homeodomain-interacting protein kinase 2	3.7
	454457 435095	AW753456 AAD21160	Hs.4750	gb:QV2-CT0261-261099-011-d11 CT0261 Homo	3.7 3.7
5	438206	AA780385	Hs.187885	hypothetical protein DKFZp564K0822 ESTs	3.7
•	418967	NM_001725	Hs.89535	bactericidal/permeability-increasing pro	3.7
	427809	M26380	Hs.180878	lipoprotein lipase	3.7
	427722	AK000123	Hs.180479	hypothetical protein FU20116	3.7 3.7
10	413986 438898	Z43567 AI819863	Hs.106243	gb:HSC1FC021 normalized infant brain cDN ESTs	3.7
10	418483	W26076	Hs.221847	ESTs	3.7
	415849	R20529	Hs.6806	ESTs	3.6
	438380	T06430	Hs.6194	chondroitin sulfate proteoglycan BEHAB/b	3.6
15	440296 438025	D30829 AW501360	Hs.180610 Hs.258910	splicing factor proline/glutamine rich (ESTs	3.6 3.6
15	458970	AW246119	Hs.25300	phosphatidylinositol 4-kinase type ()	3.6
	448002	Y15227	Hs.20149	deleted in lymphocytic leukemia, 1	3.6
	432058	AW665996	Hs.130729	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.6
20	409557 418049	BE182896 AA211467	Hs.211193 Hs.190488	ESTs Homo sapiens, Similar to nuclear localiz	3.6 3.6
20	425331	AW962128	113.130100	gb:EST374201 MAGE resequences, MAGG Horno	3.6
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	3.6
	404185			Target Exon	3.6
25	427517	AA644142	Hs.7107	ESTs, Wealthy similar to ALU7_HUMAN ALU S	3.6 3.6
25	421094 440388	AW978202 Al693520	Hs.289064 Hs.223000	hypothetical protein FLJ22251 ESTs	3.6
	415934	NM_000928	Hs.992	phospholipase A2, group IB (pancreas)	3.6
	408292	AW178363		gb:RC3-HT0105-010999-002-H06 HT0105 Homo	3.6
20	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	3.6 3.6
30	451826	AA020741 AL035460	Hs.171611 Hs.177536	ESTs metallocarboxypeptidase CPX-1	3.6
	427375 419485	AA489023	Hs.99807	ESTs, Weakly similar to unnamed protein	3.6
	416370	N90470	Hs.203697	ESTs, Wealthy similar to 138022 hypotheti	3.6
25	418400	BE243026	Hs.301989	KIAA0246 protein	3.6
35	435674	AA725002	Hs.272018	low molecular mass ubiquinone-binding pr gb:Human nebulin mRNA, partial cds	3.5 3.5
	407013 403108	U35637		ENSP00000241415":Hypothetical 67.7 kDa p	3.5
	422564	AJ148006	Hs.222120	ESTs	3.5
40	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	3.5
40	436338	W92147	Hs.118394	ESTs	3.5 3.5
	447458 457364	AI741082 AW971037	Hs.158961	ESTs gb:EST383123 MAGE resequences, MAGK Horno	3.5
	458814	AI498957	Hs.170861	ESTs, Weakly similar to Z195_HUMAN ZINC	3.5
4.5	441701	AW339828	Hs.127497	ESTs	3.5
45	405558	A A 456403	U= 0074	Target Exon	3.5 3.5
	452682 434589	AA456193 AF147363	Hs.9071	progesterone membrane binding protein gb:Homo sapiens full length insert cDNA	3.5
	443282	T47764	Hs.132917	ESTs	3.5
50	405183			NM_016358*:Homo sapiens iroquois homeobo	3.5 3.5
50	410064 425234	X53416 AW152225	Hs.195464 Hs.165909	filamin A, alpha (actin-binding protein- ESTs, Weakly similar to 138022 hypotheti	3.5
	404272	Attibetes	113.103303	Target Exon	3.5
	428808	AA436007	Hs.188780	ESTs	3.5
55	447444	AK000318	Hs.18616	hypothetical protein FLJ20311	3.5 3.4
55	450475 454451	AW805634 AW846706	Hs.205015	ESTs ab:QV3-CT0192-211099-008-g02 CT0192 Homo	3.4
	400379	NM_018432		Homo sapiens ovarian cancer related prot	3.4
	440948	AW188311	Hs.128619		3.4
60	449611	AI970394	Hs.197075	= -	3.4 3.4
60	445666 445828	R59960 F05802	Hs.282386 Hs.81907	ESTs ESTs	3.4
	437528	N59646	Hs.169745		3.4
	442927	AI024347	Hs.131519		3.4
15	451130	AJ762250	Hs.345554		3.4
65	454765	AW819629 Y09306	Hs.30148	gb:RC5-ST0293-140200-014-H05 ST0293 Homo homeodomain-interacting protein kinase 3	3.4 3.4
	459200 433791	AA719352	Hs.112718		3.4
	444911	U06117	Hs.250	xanthene dehydrogenase	3.4
	439753	BE262233	Hs.7423	hypothetical protein from EUROIMAGE 2168	3.4
70	440933	AI208217	Hs.142879		3.4 3.4
	447726 403849	AL137638	Hs.19368	matrilin 2 Target Exon	3.4
	422418	AK001383	Hs.116385		3.3
25	439533	W76021		gb:zd64c04.r1 Soares_fetal_heart_NbHH19W	3.3
75	416422	H60457		ESTs, Moderately similar to ZN91_HUMAN Z	3.3 3.3
	441668 432890	AI611973 NM_014442	Hs.136313 Hs.279751		3.3 3.3
	432890	AW895309	113.213131	gb:QV4-NN0038-300300-155-e07 NN0038 Homo	3.3
00	417130	AW276858	Hs.81256	S100 calcium-binding protein A4 (calcium	3.3
80	447854	AW138454	Hs.11594	ESTs	3.3
	448048 404632	BE281291	Hs.170408	SESTs, Moderately similar to A47582 B-cel NM_022490:Homo sapiens hypothetical prot	3.3 3.3
	411565	AW851728		gb:MR2-CT0222-011199-007-d06 CT0222 Homo	3.3

	436267 426625	AW450938 T78300		ESTs serologically defined colon cancer antig	3.3 3.3
	401272			C9000559*:gij12314195jembjCAB99338.11 (A	3.3 3.3
5	433128 401702	AB021923		EST-YD1 protein NM_001171*:Homo sapiens ATP-binding cass	3.3
•	454363	AW816274	Hs.250154	hypothetical protein FLJ12973	3.3 3.3
	440332 454177	AI218517 AW807321		ESTs gb:MR4-ST0062-240300-003-g05 ST0062 Hamo	3.3
	423784	AK000039	Hs.132826	Homo sapiens cDNA FLJ14913 fis, clone PL	3.3
10	440688	AW404591		ESTs, Weakly similar to Z192_HUMAN ZINC N-ethylmaleimide-sensitive factor attach	3.3 3.3
	410267 455778	AW978005 BE088746	Hs.12600	gb:CM2-BT0693-210300-123-d09 BT0693 Homo	3.3
	430183	BE010038		gb:PM3-BN0176-100400-001-g04 BN0176 Homo	3.2
15	451597	AW295250 AI826288	Hs.207536 Hs.171637	ESTs hypothetical protein MGC2628	3.2 3.2
15	451446 421353	AW292857	Hs.255130	ESTs	3.2
	442710	AI015631	Hs.23210	ESTs	3.2 3.2
	420560	AW207748	Hs.59115 Hs.82101	ESTs pteckstrin homology-like domain, family	3.2
20	417404 437834	NM_007350 AA769294	Hs.283854	gb:nz36g03.s1 NCI_CGAP_GCB1 Homo sapiens	3.2
	430694	AA810624	Hs.30936	ESTs, Weakly similar to H2BH_HUMAN HISTO	3.2 3.2
	412021	AW885592 AI056847	Hs.20654	gb:RC4-OT0071-090300-011-g11 OT0071 Homo ESTs	3.2
	443431 445774	AI254165	Hs.339968	ESTs	3.2
25	413335	A1613318	Hs.48442	ESTs	3.2 3.2
	450692 411671	H50603 BE049094	Hs.94037	hypothetical protein FLJ23053 ESTs	3.2
	404592	DC0-303+		NM_022739*:Homo sapiens E3 ubiquitin lig	3.2
20	402747		11-040443	Target Exon	3.2 3.2
30	428600 420300	AW863261 AA258245	Hs.242413 Hs.127573	hypothetical protein DKFZp434K1421 Homo sapiens FKSG41 (FKSG41) mRNA, compl	3.2
	445347	AF035318	Hs.12533	Homo sapiens clone 23705 mRNA sequence	3.2
	458438	AI141520	Hs.151464 Hs.129220	ESTs, Weakly similar to ALUC_HUMAN !!!! ESTs	3.2 3.2
35	442314 436291	AI311854 BE568452	Hs.344037	protein regulator of cytokinesis 1	3.2
55	413249	AF167160	Hs.75251	DEAD/H (Asp-Glu-Ala-Asp/His) box binding	3.2
	448789	BE539108	Hs.22051	hypothetical protein MGC15548 Target Exon	3.2 3.2
	403291 436210	A1825420	Hs.197824	ESTs	3.2
40	418079	R40058	Hs.6911	ESTs	3.2 3.2
	413951	AW051200 AA700705	Hs.75640 Hs.13852	natriuretic peptide precursor A ESTs	3.2
	435828 437722	AW292947	Hs.122872	ESTs, Weakly similar to JU0033 hypotheti	3.2
A.E	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	3.2 3.1
45	405046 444315	R07860	Hs.20039	C3000978;gij9280045 dbj BAB01579.1 (AB0 ESTs	3.1
	453096	AW294631	Hs.11325	ESTs	3.1
	433835	A1806185		gb:wf26a10.x1 Soares_NFL_T_GBC_S1 Homo s	3.1 3.1
50	430608 453324	R45584 W26592	Hs.23025 Hs.232089	ESTs, Weakly similar to ALU5_HUMAN ALU S ESTs	3.1
50	414884	R54418	Hs.183745	hypothetical protein FLJ13456	3.1
	446862	AV660697	Hs.282700		3.1 3.1
	427241 416486	AA399988 H81336	Hs.112087 Hs.37560	ESTs	3.1
55	429940	W25215		gb:zb87a09.r1 Soares_senescent_fibrobias	3.1 3.1
	430535 439544	AW968485 W26354	Hs.28891	gb:EST380561 MAGE resequences, MAGJ Homo hypothetical protein FLJ11360; artemis p	3.1
	437083	AW082597	Hs.244862	ESTs	3.1
60	435677	AA694142	Hs.293726		3.1 3.1
60	458810 443484	BE407125 AI091458	Hs.231510 Hs.134559		3.1
	427581	NM_014788		KIAA0129 gene product	3.1
	444016	AA448154	: 11- 127227	gb:zw82h09.r1 Soares_testis_NHT Homo sap axin 2 (conductin, axil)	3.1 3.1
65	423337 403288	NM_004655	5 Hs.127337	C1001737*:gi[7511201 pir[]T27904 hypothe	3.1
•	450125	AA005418	Hs.158186		3.1 3.1
	438138	R98299 AI208737	Hs.177502 Hs.122810		3.1
	436222 443433		Hs.301667	7 ESTs	3.1
70	443725	AW245680		growth arrest and DNA-damage-inducible,	3.1 3.1
	432044 405760			gb:EST384819 MAGE resequences, MAGL Homo Target Exon	3.1
	423789		Hs.13285	1 hypothetical protein FLJ11222	3.1
75	411605	AW006831			3.1 3.1
75	417893 449246		Hs.19000 Hs.23363		3.1
	429528	AI985303	Hs.99361	ESTs	3.1
	456645		Hs.11010		3.1 3.1
80	412490 421679		Hs.28885 Hs.20393	I '	3.1
	434503	T96231	Hs.17762	ESTs	3.1
	450756 415293		Hs.14406 Hs.10654		3.1 3.0
	410293	143402	113.1000		

	403212			NM 019595:Homo sapiens intersectin 2 (IT	3.0
	422757	AI909935	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	3.0
	427624	AA406245	Hs.24895	ESTs	3.0
_	449256	AA059050	Hs.59847	ESTs	3.0
5	411543 409112	AW851248 BE243971	Hs.50649	gb:IL3-CT0220-160200-066-F01 CT0220 Homo	3.0 3.0
	414403	AW969551	Hs.76064	quinone oxidoreductase homolog ribosomal protein L279	3.0
	427418	AA402587	Hs.325520	LAT1-3TM protein	3.0
10	455481	AW948317		gb:RCO-MT0015-280300-021-a09 MT0015 Homo	3.0
10	444396 407235	T65213 D20569	Hs.4257 Hs.169407	ESTs SAC2 (suppressor of actin mutations 2, y	. 3.0 3.0
	431431	AL096711	Hs.252953	Human DNA sequence from clone RP3-403A15	3.0
	451391	AA017410	Hs.40568	EST\$	3.0
15	430251	AA609246	Hs.181451	ESTs •	3.0
13	420658 442786	AW965215 H50733	Hs.130707 Hs.256261	ESTs Moderately similar to ALU8_HUMAN A	3.0 3.0
	440897	AW104275	Hs. 148348	ESTs	3.0
	444609	AW571659	Hs.278081	ESTs	3.0
20	433062	AK001757	Hs.281348	hypothetical protein FLJ 10895	3.0
20	408523 44 3 477	AW833259 R32325	Hs.314287 Hs.221794	ESTs ESTs	3.0 3.0
	423869	BE409301	Hs.134012	C1q-related factor	3.0
	405488			ENSP00000220888*:ZINC FINGER TRANSCRIPTI	3.0
25	414988	C17535	11- 203044	gb:C17535 Human placenta cDNA (TFujiwara	3.0
25	440471 416355	AA886146 H49875	Hs.307944 Hs.268906	ESTs ESTs	3.0 3.0
	408926	AF217525	Hs.49002	Down syndrome cell adhesion molecule	3.0
	424028	AF055084	Hs.153692	Horno sapiens cDNA FLJ14354 fis, clone Y7	2.9
20	438201	AA780243	Hs.54647	ESTs	2.9
30	413851 402229	AW897510 BE262804	Hs.137387	ESTs mitochondrial ribosomal protein S2	2.9 2.9
	444145	BE153823	Hs.282385	ESTs, Weakly similar to 2004399A chromos	2.9
	423770	AW976766	Hs.132776	Homo sapiens cDNA FLJ10077 fis, clone HE	2.9
25	439627	BE621702	Hs.29076	hypothetical protein FLJ21841	2.9
35	414232	W86946	Hs.238246	hypothetical protein FLJ22479 ENSP0000209376*:PRED65 protein (Fragmen	2.9 2.9
	400533 440483	AI200836	Hs.150386	ESTs	2.9
	443502	AI074528	Hs.133949	ESTs	2.9
40	449667	AB023227	Hs.23860	KIAA1010 protein	2.9
40	446809	AW590171	Hs.101413	ESTs	2.9 2.9
	408788 413627	AL134947 BE182082	Hs.213956 Hs.246973	Homo sapiens BAC clone RP11-102O5 from Y ESTs	2.9
	449655	AI021987	Hs.59970	ESTs	2.9
4.5	407378	AA299264	Hs.57776	ESTs, Moderately similar to 138022 hypot	2.9
45	400090	*********		Eos Control	2.9 2.9
	454968 423352	AW849045 AA324808	Hs.193576	gb:IL3-CT0214-150300-085-H06 CT0214 Homo ESTs	2.9
	426197	AA004410	Hs. 100009	acyl-Coenzyme A oxidase 1, palmitoyl	2.9
~^	452102	U04343	Hs.27954	CD86 antigen (CD28 antigen ligand 2, B7-	2.9
50	415346	Z43108	11- 400000	gb:HSC13E071 normalized infant brain cDN	2.9 2.9
	436726 442513	AA324975 AF150207	Hs.198689 Hs.207949	ESTs, Wealdy similar to T00079 hypotheti ESTs	2.9
	425012	177666	Hs.92414	Homo sapiens cDNA: FLJ22030 fis, clone H	2.9
	402322			Target Exon	2.9
55	427235	AJ126288	Hs.192232	ESTs	2.9 2.9
	456412 431196	AW749617 AW974436	Hs.280776 Hs.154929	tankyrase, TRF1-interacting ankyrin-rela ESTs	2.9
	439379	AA835002	Hs.125611	ESTs	2.9
.	423757	AL049337	Hs.132571	Homo sapiens mRNA; cDNA DKFZp564P016 (fr	2.9
60	446134	AW161234 AI052789	Hs.13993 ·	TBP-like 1 FSTs	2.9 2.9
	435645 449385	AJ052789 AJ650471	Hs.133263 Hs.347290	ESTs	2.9
	444161	N52543	Hs.142940	ESTs	2.9
	406635	U07162		gb:Human clone LNA11 autoantibody lg hea	2.9
65	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	2.9
	458760 427245	AI498631 AA421022	Hs.111334 Hs.97739	ferritin, light polypeptide ESTs	2.9 2.9
	400658	7441022	113.37100	ENSP00000237081*:KIAA1217 PROTEIN (FRAGM	2.9
	430701	A1760833	Hs.293971	ESTs	2.9
70	435294	T84084	Hs.196008	Homo sapiens cDNA FLJ11723 fis, clone HE	2.9
	429927 446160	NM_001115 AW392197	Hs.2522 Hs.218003	adenylate cyclase 8 (brain) ESTs	2.9 2.9
	420674	NM_000055	Hs.1327	butyrytcholinesterase	2.9
~~	424330	AW073953	Hs.333396	Homo sapiens cDNA FLJ13596 fis, clone PL	2.9
75	418915	AJ474778	Hs.118977		2.9
	425922	AL 157466 AW958148	Hs.162751 Hs.129454	Homo sapiens mRNA; cDNA DKFZp761E2423 (f ESTs	2.9
	447512 449990	AW950140 AJ279010	Hs.48821	ESTS	2.5
	423779	AW071837	Hs.57971	ESTs	2.8
80	427395	AW298741	Hs.97861	ESTs, Moderately similar to 138022 hypot	2.8
	416188	BE157260	Hs.79070 Hs.2057	v-myc avian myelocytomatosis viral oncog uridine monophosphate synthetase (orotat	2.8 2.8
	426746 400362	J03626 AF068294	Hs.2057 Hs.272414		2.8

					2.0
				IRAS-like suppressor	2.8 2.8
		AW297465	Hs.267150	(IAA1409 prolein 25001632*:gi 10645308 gb AAG21430.1 AC00	2.8
	403903	Al151091		ESTs	2.8
5	444491 455899	BE155112	113.270717	gb:PM1-HT0350-151299-003-a03 HT0350 Homo	2.8
,	457292	AI921270	Hs.281462	hypothetical protein FLJ14251	2.8
	428305	AA446628		cartilage linking protein 1	2.8 2.8
	435375	AJ733610		ESTs	2.8
10	409078	AW327515		ESTs hypothetical protein MGC15729	2.8
10	436109	AA922153		ESTs	2.8
	444656 426384	AJ277924 AJ472078	Hs.303662	hypothetical protein FLJ13189 (FLJ13189)	2.8
	424200	AA337221	. 10.00000	gb:EST41944 Endometrial tumor Homo sapie	2.8
	438243	AI581311		ESTs	2.8
15	434012	AA621425	Hs.186256	ESTs	2.8 2.8
	402711			Target Exon	2.8
	442955	AI683534	Hs.131583	ESTs ESTs, Weakly similar to A46010 X-linked	2.8
	418319	AW611703 BE220137	Hs.190173 Hs.124323	ESTs	2.8
20	438934 438689	AW129261	Hs.181672	ESTs	2.8
20	420083	AA478847	Hs.42484	hypothetical protein FLJ10618	2.8
	400315	U46120	Hs.193392	Human expressed unknown mRNA	2.8 2.8
	433563	A1732637	Hs.277901	ESTs	2.8
0.5	458093	AI207788	Hs.343628	siatytransferase 4B (beta-galactosidase gb:zf72c03.s1 Soares_pineal_gland_N3HPG	2.8
25	409157	AA064631	Hs.207077	ESTs	2.8
	450597	AI701635 AW601773	Hs.270259	ESTs	2.8
	425300 458617	Z25900	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (fr	2.8
	418312	AW972468	Hs.170307	Ral guanine nucleotide exchange factor R	2.8
30	430335	D80007	Hs.239499	KIAA0185 protein	2.8 2.8
	454581	AW809189		gb:MR4-ST0118-261099-012-e10 ST0118 Homo	2.8
	419735	AW750056	Hs.169577 Hs.190668	Homo sapiens cDNA FLJ14743 fis, clone NT ESTs	2.8
	436265	AA731331 AF086294	Hs.125844	ESTs	2.8
35	439481 441964	AA972619	Hs.20506	ESTs, Weakly similar to 138022 hypotheti	2.8
23	422648	D86983	Hs.118893	Melanoma associated gene	2.8
	430503	AA533574	Hs.152274	ESTs	2.8 2.8
	403942			Target Exon	2.8
40	420565	A1806770	Hs.30258	ESTs ESTs, Weakly similar to ALUB_HUMAN !!!!	2.8
40	439069	H63144	Hs.184178 Hs.87469	putative acid-sensing ion channel	2.8
	436480 408137	AJ271643 Al694131	Hs.29002	KIAA1706 protein	2.8
	451692	AL137422	Hs.26849	Homo sapiens mRNA; cDNA DKFZp761A1623 (f	2.8
	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi	2.8
45	452526	W38537	Hs.280740	hypothetical protein MGC3040	2.8 2.8
	414300	A1304870	Hs. 188680	ESTs	2.8
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	2,7
	437933	A1276132	Hs.146155	ESTs Target Exon	2.7
50	405941 443210	AJ692649	Hs.9451	hypothetical protein MGC13168	2.7
50	450651	W79000	Hs.44545	ESTs, Weakly similar to B34087 hypotheti	2.7
	426765	AA743603	Hs.172108	nucleoporin 88kD	2.7 2.7
	418886	AA993982	Hs.130858		2.7
E E	429483	AA974832	Hs.128708		2.7
55	430426	AA478807	Hs.125173 Hs.271737		2.7
	439019 400924		115.271757	Target Exon	2.7
	458070		Hs.209406	ESTs. Wealdy similar to 138600 zinc fing	2.7
	427299		Hs.214263	ESTs, Moderately similar to ALU1_HUMAN A	2.7
60	442621		Hs.130553	B ESTs, Weakly similar to ALUA_HUMAN !!!!	2.7 2.7
	437643			gb:Homo sapiens mRNA full length insert Homo sapiens cDNA: FLJ22373 fis, clone H	2.7
	426925		6 Hs.315689 Hs.293420		2.7
	443392 429972		Hs.23451		2.7
65	438875			9 ESTs	2.7
05	422551			gb:EST379359 MAGE resequences, MAGJ Horno	2.7
	446139		Hs.39749	ESTs	2.7 2.7
	429115				2.7
70	428612				2.7
70	439947			estrotactin 1 ESTs, Moderately similar to ALU1_HUMAN A	2.7
	439699 438339		Hs.18756 Hs.24316	8 ESTs	2.7
	456680				2.7
	412074		Hs.73139	ADP-ribosyltransferase 1	2.7
75	41222	5 AW90204	2	gb:QV0-NN1022-170400-193-c02 NN1022 Homo	2.7 2.7
	43880	1 AA825971			2.7
	44289		Hs.13188		2.7
	43296		Hs.27986	NM_001334*:Homo sapiens cathepsin O (CTS	2.7
80	40379 40033		Hs.24800		2.7
00	41546		Hs.2602	74 ESTs	2.7
	42871		6 Hs.53120	5 ESTs	2.7 2.7
	45775		Hs.1639	44 ESTs	2.1

	424480	AA341442	Hs.205299	ESTs	2.7
	444822	BE164351	Hs.292767	hypothetical protein FLJ 23109	2.7
	432651	AW973744	Hs.293100	ESTs	2.7
5	439823	AW665287	Hs.124514	ESTs	2.7 2.7
,	457021 440026	AW968934 AA861299	Hs.173108 Hs.160371	Homo sapiens cDNA: FLJ21897 fis, clone H ESTs	27
	446960	AW294936	Hs.156762	ESTs	2.7
	435046	AA662772	Hs.174330	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.7
	431999	AL133573	Hs.272312	Homo sapiens mRNA; cDNA DKFZp434J2235 (f	2.7
10	458527	AI950256	Hs.224875	ESTs	2.7
	445899	AI263736	Hs.145626	ESTS ENCONOMINATED MARRIED A PRODUCTION OF THE	2.7 2.7
	404254 402344			ENSP0000082468*:DJ45P21.3 (butyrophilin Target Exon	2.7
	426503	AA380153		gb:EST93093 Skin tumor I Homo sapiens cD	2.7
15	446420	AW015693	Hs.135614	ESTs	2.7
	426914	AA393328	Hs.194303	ESTs	2.7
	407903	AI287341	Hs.154029	bHLH factor Hes4	2.7 2.7
	433009 403431	AA761668		gb:nz24c08.s1 NCI_CGAP_GCB1 Homo sapiens Target Exon	2.7
20	403290			C100010111:gij4758212fref[NP_004411.1] d	2.7
	435143	R12375	Hs.194600	ESTs	2.7
	416569	H64891		gb:yr68h03.r1 Soares fetal liver splaen	2.7
	428690	AI948490	Hs.98765	ESTs	2.7
25	425128	BE561929	Hs.154718	tumor protein OS2-like 2 ESTs	2.7 2.7
23	443361 404053	AI792628	Hs.133273	Target Exon	2.7
	435113	AA665469	Hs.117136	ESTs	2.6
	405717			CX000838:gi[10092633[ref]NP_055314.1] pu	2.6
20	413098	BE065279		gb:RC1-BT0314-030500-016-b09 BT0314 Homo	2.6
30	444884	AI201094	Hs.148540	ESTs	2.6 2.6
	419015 423234	179262 AA323534	Hs.14463 Hs.296162	ESTs AD037 protein	2.6
	406871	AA993857	Hs. 180842	ribosomal protein L13	2.6
	428670	AA431682	Hs.134832	ESTs	2.6
35	408371	AF161545	Hs.44439	hypothetical protein	2.6
	413929	BE501689	Hs.75617	collagen, type IV, alpha 2	2.6
	408369	R38438	Hs.182575	solute carrier family 15 (H??? transport	2.6 2.6
	419817 415788	AA743434 AW628686	Hs.193778 Hs.78851	ESTs KIAA0217 protein	2.6
40	427388	BE379610	Hs.177592	ribosomal protein, large, P1	2.6
. •	451018	AW965599	Hs.247324	mitochendrial ribosomal protein S14	2.6
	405863			Target Exon	2.6
	454037	AW998716		gb:PM4-BN0067-250300-002-111 BN0067 Homo	26
45	430147	R60704	Hs.234434	hairy/enhancer-of-split related with YRP	2.6 2.6
43	425480 407182	AB023198 AA312551	Hs.158135 Hs.230157	KIAA0981 protein ESTs	2.6
	439538	AA837323	Hs.56407	ESTs	2.6
	449249	T52285	Hs.193115	Homo sapiens mRNA for KIAA1764 protein,	2.6
	429569	AA454993	Hs.138343	ESTs, Weakly similar to 178885 serine/th	2.6
50	402936			ENSP00000217246*:DJ803K15.1 (novel prote	2.6 2.6
	420670 455409	AW973577 AW936832		ESTs gb:PM2-DT0023-050400-003-h03 DT0023 Homo	2.6
	413151	H47969	Hs.141971	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.6
	422484	AA568770	Hs.123158	Homo sapiens cDNA FLJ12830 fis, clone NT	2.6
55	400780			NM_007325":Homo sapiens glutamate recept	2.6
	429258	AA448765		gb:zx10e09.r1 Soares_total_fetus_Nb2HF8_	2.6 2.6
	448970 402615	AW138582		gb:UI-H-BI1-acw-a-06-0-UI.s1 NCI_CGAP_Su C1003844*:gij6912550/ref NP_036483.1 ol	2.6
	417099	BE537357	Hs.306995	hypothetical protein MGC5457	2.6
60	428397	AA428040		gb:zw50e02.r1 Soares_total_fetus_Nb2HF8_	2.6
	449164	AI632772	Hs.264165	ESTs	2.6
	412584	X54870	Hs.74085	DNA segment on chromosome 12 (unique) 24	2.6 2.6
	443635	A1080230	Hs.134214	ESTs Targel Exon	2.6
65	402981 433258	A1806626	Hs.207300		2.6
05	428917	AA437337	Hs. 16689	ESTs	2.6
	418557	8E140602	Hs.246645	ESTs	2.6
	445211	BE045601	Hs.118248		2.6
70	404423	A17C7007	Un 44444	C8000067*:gi 10432400jemb CAC10290.1 (A ESTs	2.6 2.6
70	435953 435937	A1767087 AA830893	Hs.114142 Hs.119769		26
	439220	AW295340	Hs.130417		2.6
	419597	W73692		gb:zd50c01.s1 Soares_fetal_heart_NbHH19W	2.6
76	436852	AI814817	Hs.269099		2.6
75	430569		Hs.178098		2.6 2.6
	443845		Hs.148485 Hs.238246		2.6 2.6
	414223 443770		10.430240	gb:MR3-ST0218-191199-012-a10 ST0218 Homo	2.6
	450443		Hs.120744		2.6
80	435523	T62849	Hs.11090	membrane-spanning 4-domains, subfamily A	2.6
	400492		Un 3444F	C10001573°:gi[7302749]gb[AAF57827.1] (AE	2.6 2.6
	450202 416845	AW969756 H95279	Hs.34145 Hs.293788	ESTs, Wealdy similar to 849647 GTP-bindi gb:yu20h02.s1 Soares (etal liver spteen	2.6
	710043	1133213	. 10.2501 00	gary a series and a series and a series appropria	

		******	U= 150120 1	FOT-	2.6
	446423 447587			ESTs ESTs	2.6
	437014	AA808757		ESTs, Weakly similar to S59501 interfero	2.6
_	426411	AK000708		hypothetical protein FLJ20701	2.6 2.6
5	432668	AA558601		ESTs ESTs	2.6
	436682 426894	AI590055 AI204209		ESTs	2.6
	402605	7425 1200		Target Exon	2.6
• •	457554	AA570111		ESTs, Wealtly similar to ALUE_HUMAN !!!!	2.6 2.6
10	438166	N30158	Hs.122645 Hs.8904	ESTs Ig superfamily protein	2.6
	443021 427005	AA368546 AA394228		ESTs	2.6
	437085	AA743935	Hs 202329	ESTs	2.6
	408603	R25283		Homo sapiens mRNA; cDNA DKFZp564H1916 (f	2.6 2.5
15	431019	NM_005249	Hs.2714	forthead box G18 hypothetical protein FLJ21369	2.5
	437287 458552	AA748180 AW136139	Hs.159346 Hs.245856	ESTs	2.5
	436350	AA713661	Hs.121091	ESTs	2.5
	421988	AW450481	Hs.161333	ESTs	2.5 2.5
20	416704	H77795	Hs.39785	ESTs	2.5 2.5
	447830 413278	R98920 BE563085	Hs.164314 Hs.833	ESTs interferon-stimulated protein, 15 kDa	2.5
	406789	AI041403	12.000	ribosomal protein L29	2.5
	433683	AI817723	Hs.22678	hypothetical protein FLJ21832	2.5 2.5
25	433523	H29882	11 444526	ESTs	2.5 2.5
	452296	T65535 AA436884	Hs.111539 Hs.48926	ESTs ESTs	2.5
	428878 442476	AF069475	(13.40320	gb:AF069475 Homo sapiens astrocytoma lib	2.5
	452785	AL359942	Hs.296434	erythroid differentiation and denucleati	2.5
30	444422	A1768623	Hs.108264	ESTs	2.5 2.5
	420579	AA278449 H66470	Hs.137429 Hs.16004	ESTs ESTs	2.5
	416505 402595	1100470	NS. 10004	C10015781:gi 6759903 gb AAF28099.1 (AF1	2.5
	447930	R44574	Hs.107510	ESTs	2.5
35	459527	AW977556	Hs.291735	ESTs, Weakly similar to 178885 serine/th	2.5 2.5
	458421	A1279978	Hs.22547 Hs.293441	ESTs immunoglobulin heavy constant mu	2.5
	427527 436035	AI809057 AA703679	Hs.106999	ESTs, Weakly similar to SYT5_HUMAN SYNAP	2.5
	453362	H14988	Hs.107375	ESTs	2.5
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	433325	AW206986	Hs.143905	ESTs Homo sapiens cDNA: FLJ23028 fis, clone L	2.5
	415983 431198	A1436798 AL047634	Hs.117078 Hs.231913	ESTs	2.5
	430530	AA480870	Hs.47660	ESTs	2.5
45	455276	8E176479		gb:RC3-HT0585-160300-022-b09 HT0585 Homo	2.5 2.5
	416665	H72974		gb:yu28a10.s1 Soares fetal liver spleen	2.5 2.5
	422352 427613	AA766296 AW273851	Hs.99200 Hs.98025	ESTs ESTs	2.5
	453685	AL110309	115.30025	gb:DKFZp564L0278_r1 564 (synonym: hfbr2)	2.5
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	436361	AA825814	Hs.149065	ESTs CYBNI analysis	2.5 2.5
	427709	AJ631811 AF224266	Hs.180403 Hs.272373	STRIN protein interleukin 20	2.5
	432036 422752	BE247253	Hs.21263	suppressor of potassium transport defect	2.5
55	413786	AW613780	Hs.13500	ESTs	2.5
	439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	2.5 2.5
	451533	NM_004657 D59968	Hs.26530 Hs.45184	serum deprivation response (phosphatidyl Homo sapiens cDNA FLJ12284 fis, clone MA	2.5
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60	458891	Al659166	Hs.207144		2.5
	427140	AA398487	Hs.97642	ESTs	2.5 2.5
	405239		Hs.184339	oxidative 3 alpha hydroxysteroid dehydro KIAA0175 gene product	2.5
	428450 443753		Hs.134749		2.5
65	432888		1,0,,,,,,,,	gb:yd81a08.s1 Soares fetal liver spleen	2.5
	445065		Hs.302024		2.5 2.5
	431202		Hs.188822		2.5
	445658 435330		Hs.172660 Hs.173174		2.5
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	456232	AL040357		gb:DKFZp434O0713_r1 434 (synonym: htes3)	2.5 2.5
	421955		Hs.12157		2.5
	420796 425429		Hs.99931 Hs.15721		2.5
75	425428 437627				2.5
	408574	AA328046	Hs.46405	polymerase (RNA) II (DNA directed) polyp	25
	418733	3 AA227714			2.5 2.5
	440473				2.5
80	422106 411480		Hs.11173 2	gb:IL3-CT0214-231299-053-A09 CT0214 Homo	2.5
55	436391			4 ESTs	2.5
	42494	7 R77952		ESTs, Weakly similar to alternatively sp	2.5 2.5
	45083	1 R37974	Hs.25255	ESTs	25

	447527 424686	AJ702896 AA345504	Hs.42091	ESTs gb:EST51529 Gall bladder (I Homo sapiens	2.5 2.5
5	453385 TABLE 128	AW296101	Hs.252806	ESTs	2.5
•	Pkey: CAT numb Accession:	Uniqu er: Gene	e Eos probes cluster numb ank accession		
10	Pkey 408292	CAT Number 1050507_1	Accession AW178363	AW846011 AW845964 AW845988 AW845977 A	W846002
	409157 409189	110363_1 110687_1	AA064631 /	14722000 Aa064793 14127189 Aa065075 Aa070377 aa100017 aa0	79891 AA113255 AA075168 AA082764 AA083380 NB4829 AA084752 AA076512 AA085119
15	411480	1247089_1	AW848022	AW848704 AW848168 AW848959 AW848476 A	\W848699 AW848700 AW848761
	411537 411543	1248899_1 1249127_1	AW851248	3E073378 BE073379 AW850533 AW850529 AW851425 AW850805 AW851021 AW850905	
	411565 411671	1249756_1 125369_1		AW851607 AW851621 AW851702 AW851647 A 4A700765 H86770 AA094646 R02483 C03868 N	
20	411688	1254076_1	AW953440	T08189 AW857085	
	412021 412135	1272156_1 1279148_1		AW885594 AW885579 AW885651 AW895290 AW895307 AW895397 AW895378 A	\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\
25	412225 412811	1284108_1 132943_1	AW902042	N77591 IOS7730 AA352014 R13591 AA121201 D604201	BE263253 BE047862 Z41952 AI424991 AI693507 AI863108 AA599060 AI091148 AA598689
23	413098	1349115_1	R39887 AA BE065279	813482 AW016452 H06383 R41807 Al364268 A Beo65306 Beo65164 Beo65389	A620528 AI241940 AW089149 AW090733 AW088875 Z38240 AA121202 R17734
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	415346 416422	1534581_1 1593811_1		5295 R 1 3085 8709 H 7 3528 H 5 4 3 3 5 R 8 7 1 5 4	
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40	424200	236595_1		AA336756 AW966196	
	424686 424947	242486_1 245247_1		AA345251 AW963243 L348809 AW959960 AW959962 AI565552 AW07	70702 AA973910 R85973
	425146	247244_1		AW954629 AA351258 R25935	
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	428397	290994_1	AA428040	AW889864 AA836434	
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50	430183	31412_2	BE010038	AA676833 Al311783 T86895 W68032 BE06439	33 BE064394 BE157228 BE183282 AI936370 AA552514 T67280 AA039909
50	430535 432044	319643_1 340773_1		5 AW968670 AA480922 BE350425 7 AA524829 AW972733	
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•	438243	453072_1	AI581311	AA781682 AA781678	
	438458 439533	457837_1 47349_1		5 AA807807 D29548 F088052 W72465	
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65	443770 444016	579849_1 58899_1		4 AW815926 AI085174 5 AV647571	
	448970	791254_1	AW13858	2 A1638298 A1631640 A1963868 A1611082	
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75	454581 454765	1225710_1 1233905_1		9 AW809219 AW813574 9 AW854320	
	454860	1237732_1	AW83576	7 AW835537 BE160187	
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                                                Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunharn, et al." refers to the publication entitled "The DNA
                Pkey:
Ref:
                                                sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
15
                                                Indicates DNA strand from which exons were predicted.
                 Strand:
                                                Indicates nucleotide positions of predicted exons.
                 Nt_position:
                                                                               Nt_position
                Pkey
400492
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                                                                                      20805-20960
                         406395
                                          9256242
                                                                 Minus
                                                                                       68314-68523,68853-68950
                                          9857502
                                                                  Plus
                        406478
                                                                                      91439-91579
                                             9864741
                        406481
        80
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TABLE 13A: 964 GENES UP-REGULATED IN LOWER GRADE GLIOBLASTOMA COMPARED TO NORMAL ADULT TISSUES
Table 13A lists about 678 genes up-regulated in lower grade glioblastoma (LGG) compared to normal normal adult tissues. These were selected from 59680 probesets on the
Table 13A lists about 678 genes up-regulated in lower grade glioblastoma (LGG) compared to normal normal adult tissues. These were selected from 59680 probesets on the
Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" LGG to "average" normal tissues was greater than or equal to 3.0. The "average" LGG tevel was set to the 85th

ζ.

percentile amongst various LGG tumors. The "average" normal tissue level was set to the 85th percentile amongst various non-mafignant adult tissues. In order to remove gene-specific background levets of non-specific hybridization, the 10th percentile vatue amongst the various non-mafignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number

ExAccn: Exemptar Accession number, Genbank accession number
UniquenelD: Unique number

Unique Title: Unique gene title

R1: Ratio of LOWER GRADE GLIOBLASTOMA to NORMAL ADULT TISSUES

5

10	Pkey	ExAcon	UnigeneID	Unigene Title	R1 ·
	427343	AI880044	Hs.176977	protein kinase C binding protein 2	67.6
	409389	AB007979	Hs.301281	Homo sapiens mRNA, chromosome 1 specific	58.2
	418375	NM_003081	Hs.84389	synaptosomal-associated protein, 25kD	53.8 50.6
15	431917	D16181	Hs.2868	peripheral myelin protein 2	50.6 48.3
15	428321	A1699994	Hs.2868	peripheral myelin protein 2 myelin-associated oligodendrocyte basic	44.3
	426325 435147	D28114 AL133731	Hs.169309 Hs.4774	Homo sapiens mRNA; cDNA DKFZp761C1712 (f	44.2
	456759	BE259150	Hs.127792	detta (Drosophila)-like 3	43.8
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	40.8
20	429007	D80642		gb:HUM092E098 Human fetal brain (TFujiwa	40.1
	417183	R52089	Hs.172717	ESTS	38.8
	430838	N46664	Hs.169395	hypothetical protein FLJ 12015	36.8
	413472	8E242870	Hs.75379	solute carrier family 1 (glial high affi	34.9
25	425088	AA663372	Hs.169395	hypothetical protein FLJ12015	34.4 34.2
25	429276	AF056085 Z48051	Hs.198612 Hs.141308	G protein-coupled receptor 51	33.9
	424140 450133	AW969769	Hs.105201	myelin oligodendrocyte głycoprotein ESTs	33.8
	423849	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f	32.8
	413333	M74028	Hs.75297	fibroblast growth factor 1 (acidic)	32.8
30	449494	AW237014	Hs.315369	Homo sapiens cDNA: FLJ23075 fis, clone L	31.3
	402604			Target Exon	30.3
	412733	AA984472	Hs.74554	KIAA0080 protein	28.8
	416829	AB013805	Hs.80220	catenin (cadherin-associated protein), d	28.2
25	439239	AI031540	Hs.235331	ESTs	27.9 27.1
35	444378	R41339 F05538	Hs.47860	neurotrophic tyrosine kinase, receptor, ESTs	· 26.2
	439415 425048	H05468	Hs.4273 Hs.164502	ESTs	25.5
	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	25.3
	425057	AA826434	Hs.1619	achaete-scute complex (Drosophila) homol	24.0
40	425799	T08133	Hs.182906	Homo sapiens mRNA for KIAA1872 protein,	23.5
	447359	NM_012093	Hs.18268	adenylata kinase 5	23.5
	425842	AI587490	Hs.159623	NK-2 (Drosophila) homolog B	23.2
	423853	AB011537	Hs.133466	slit (Drusophila) homolog 1	23.2
15	435708	AI362949	Hs.75169	ESTs	22.9 21.6
45	437268	A1754847	Hs.227571	regulator of G-protein signalling 4 dystrobrevin, elpha	21.1
	409395 441285	U46745 NM_002374	Hs.336678 Hs.167	microtubule-associated protein 2	20.4
	422656	AI870435	Hs.1569	LIM homeobox protein 2	20.0
	425523	AB007948	Hs.158244	KIAA0479 protein	19.7
50	437204	AL110216	Hs.22826	ESTs, Weakly similar to ISS214 salivary	19.5
	416370	N90470	Hs.203697	ESTs, Weakly similar to 138022 hypotheti	19.4
	441497	R51064	Hs.23172	ESTs	19.3
	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	19.1 18.9
55	408604 413597	D51408 AW302885	Hs.21925 Hs.117183	ESTs ESTs	18.8
33	422980	N46569	Hs.76722	CCAAT/enhancer binding protein (C/EBP),	18.8
	428392	H10233	Hs.2265	secretory granule, neuroendocrine protei	18.6
	429466	M85835	Hs.12827	ESTs	18.2
	448302	AI480208	Hs.182906	Homo sapiens mRNA for KIAA1872 protein,	18.2
60	439199	R40373	Hs.26299	ESTs	17.4
	448743	AB032962	Hs.21896	KIAA1136 protein	17.4
	418338	NM_002522	Hs.84154	neuronal pentraxin I	17.3 17.2
	444513	AL120214 AK001468	Hs.7117 Hs.62180	glutamate receptor, ionotropic, AMPA 1 anillin (Drosophila Scraps homolog), act	17.1
65	444783 447004	AW296968	Hs.157539		16.8
05	425984	AW836277	Hs.165636		16.5
	448672	AI955511	Hs.225106	2.72	16.1
	452372	AJ885742	Hs.228474		15.8
	424120	T80579	Hs.290270	ESTs .	15.7
70	424581	M62062	Hs.150917	catenin (cadherin-associated protein), a	15.6
	424790	AL119344	Hs.13326	ESTs, Wealdy similar to 2004399A chromos	15.4
	426269	H15302	Hs.168950		15.2 15.2
	446692	Z44514 A1370936	Hs.34074	Homo sapiens mRNA for KIAA1763 protein, dipentidylpentidase VI	14.9
75	453642 429037	A1370936 X81895	Hs.194765		14.7
, ,	441440	AI807981	Hs.30495	ESTs	14.6
	429927	NM_001115		adenylate cyclase 8 (brain)	14.6
	415849	R20529	Hs.6806	ESTs	14.4
	418110	R43523	Hs.217754		14.2
80	434277	X77748	Hs.3786	glutamate receptor, metabotropic 3	14.0
	409638	AW450420	Hs.21335	ESTs	14.0
	441350	AB020690	Hs.7782	paraneoplastic antigen MA2 KIAA0237 gene product	13.9 13.7
	415734	NM_014747	Hs.78748	• •	10.7
				216	

					13.6
		AI221919	h Hs.322469 t	ypothetical protein FLJ10582 ranscriptional activator of the c-fos p	13.4
			ns.322403 l Hs.14945 l	ong fatty acyl-CoA synthetase 2 gene	13.3
			He 254179 1	(IAA167B	13.3 13.3
5			Hs.184261 1	ESTs, Weakly similar to T26686 hypotheti chondroitin sulfate proteoglycan BEHAB/b	13.2
	438380		Hs.6194 (Hs.78913 (chemokine (C-X3-C) receptor 1	13.2
	415910 412266			ESTs	13.2 13.1
	436878	BE465204		ESTs	13.1
10	428536		Hs.2288	visinin-like 1 UDP glycosyltransferase 8 (UDP-galactose	13.1
	425649 428982	U30930 NM_005097	Hs.158540 Hs.194704	leucine-rich, glioma inactivated 1	13.0
	437948	AA772920		ESTs	13.0 12.9
	444124	R43097	Hs.6818	ESTs Homo sapiens cDNA FLJ13458 fis, clone PL	12.7
15	428342	AI739168 X14767	Hs.89768	gamma-aminobutyric acid (GABA) A recepto	12.7
	419249 412959	D87458	Hs.75090	KIAA0282 nrotein	12.6
	419863	AW952691	Hs.93485	Homo sapiens mRNA; cDNA DKFZp761D191 (fr	12.6 12.6
20	431467	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (f forkhead box G18	12.4
20	431019	NM_005249 AF155140	Hs.2714 Hs.98738	gonadotropin-regulated testicular RNA he	12.4
	420547 430091		Hs.233023	KIAA1132 protein	12.4
	448595	AB014544	Hs.21572	KIAA0644 gene product	12.2 12.2
26	447342	Al199268	Hs.19322 Hs.146343	Homo sapiens, Similar to RIKEN cDNA 2010 ESTs	12.0
25	409049 421264	AI423132 AL039123	Hs.103042	microtubule-associated protein 1B	11.9
	451952	AL120173	Hs.301663	ESTs	11.9 11.8
	411305	BE241596	Hs.69547	myelin basic protein	11.6
20	433551	AI985544	Hs.12450 Hs.77202	protocadherin 9 protein kinase C, beta 1	11.6
30	431988 415170	AC002302 R44386	Hs.164578	FSTs	11.5
	408562	Al436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	11.4 11.4
	435501	AW051819	Hs.129908	KIAA0591 protein	11.1
25	429656	X05608	Hs.211584 Hs.23539	neurofilament, light polypeptide (68kD) ESTs	11.1
35	423419 424432	R55336 AB037821	Hs.146858	protocadherin 10	10.9
	433896	AW294729	Hs.274461	ESTs	10.9 10.9
	415293	R49462	Hs.106541	ESTs	10.9
40	447101	N72185 AA694010	Hs.44189 Hs.6932	ESTs Homo sapiens clone 23809 mRNA sequence	10.9
40	440105 438054	AA776626	Hs.169309	ESTs	10.8
	433597	AA708205	Hs.100343	ESTs	10.7 10.6
	421659	NM_014459		protocadherin 17	10.6
45	445102	AW204610 NM_001851	Hs.22270 Hs.154850	ESTs collagen, type IX, alpha 1	10.6
43	425154 451625	R56793	Hs.106576	alanine-olyoxylate aminotransferase 2-li	10.6
	435191	R15912	Hs.4817	Homo sapiens clone 24461 mRNA sequence	10.6 10.5
	450154	R15891	Hs.281587		10.4
50	407886 420345	AW969688 AW295230	Hs.100826 Hs.25231	ESTs	10.4
30	428728				10.3 10.3
	424997	AL138167	Hs.96920	ESTs	10.2
	440184		Hs.7022 Hs.89584	dedicator of cyto-kinesis 3 insulinoma-associated 1	10.2
55	419078 445495		Hs.38489	ESTs, Wealdy similar to 138022 hypotheti	10.1
	416857		Hs.29245	B ESTs	10.0 10.0
	445041		Hs.28298		9.8
	419271 446711		Hs.23853 Hs.12450		9.8
60	426847		Hs.29862		. 9.7 9.7
•	427304	AA761526	Hs.16385	3 ESTs	9.7
	418097		Hs.21868 Hs.34651		9.7
	449300 41998		Hs.5856	ESTs, Highly similar to bA393J16.3 [H.sa	9.7
65	44378		Hs.19012	5 basic-helix-loop-helix-PAS protein	9.5 9.5
	41548	6 H12214	Hs.13284		9.5
	45322			aryl-hydrocarbon receptor nuclear transl	9.4
	43820 42402				9.4
70	41968	3 AA248897	Hs.4878	ESTs	9.4 9.2
_	41417	5 Al308876			9.2
	40029 40894			DALL DALL DECAMAGES IF	9.2
	45404		Hs.6921	FSTs	9.2
75	45402	7 R40192	Hs.2152		9.1 9.0
	44101				9.0
	42518 44558		6 Hs.2250 Hs.2687		8.9
<u>.</u> -	45394	41 U39817	Hs.3682	0 Bloom syndrome	8.9 8.8
80	4224	11 AW74944			8.8
	4473 4244		Hs.1726 Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	8.7
	4489		Hs.2254		8.7
				_	

	448986	H42169	Hs.347310	hypothetical protein FLJ14627	8.6
	423135	N67655	Hs.26411	ESTs	8.5
	418030	BE207573	Hs.83321	neuromedin 8	8.4
5	448769	N66037	Hs.38173	ESTs	8.4
,	407748 400293	AL079409 N51002	Hs.38176 Hs.306480	KIAA0606 protein; SCN Circadian Oscillat Homo sapiens mRNA; cDNA DKFZp761E2112 (f	8.3 8.3
	415279	F04237	Hs.1447	glial fibrillary acidic protein	8.2
	451516	AI800515	Hs.12024	ESTs	8.2
10	419629	AB020695	Hs.91662	KIAA0888 protein gb:ny91c01.s1 NCI_CGAP_GC81 Homo sapiens	8.2
10	437034 456965	AA742643 AW131888	Hs.172792	ESTs, Weakly similar to hypothetical pro	8.2 8.1
	417417	F05745	Hs.89512	ATPase, Ca transporting, plasma membrane	8.1
	452279	AA286844	Hs.61260	hypothetical protein FLJ13164	8.1
15	422864	AA318323 W38537	Hs.12827 Hs.280740	gb:EST20390 Retina II Homo sapiens cDNA hypothetical protein MGC3040	8.1 8.0
13	452526 435793	AB037734	Hs.4993	KIAA1313 protein	7.9
	415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito	7.9
	407168	R45175	Hs.117183	ESTs	7.9
20	447414	D82343 AI015631	Hs.74376 Hs.23210	neuroblastoma (nerve tissue) protein ESTs	7.8 7.8
20	442710 416836	D64745	Hs.80247	cholecystokinin	7.8
	419721	NM_001650	Hs.288650	aquaporin 4	7.7
	438080	AA777381	Hs.291530	ESTs, Weakly similar to ALUC_HUMAN !!!!	7.7
25	436109 428845	AA922153 AL157579	Hs.132760 Hs.153610	hypothetical protein MGC15729 KIAA0751 gene product	7.7 7.7
23	448321	NM_005883	Hs.20912	adenomatous polyposis coli like	7.7
	410305	AF030409	Hs.62185	solute carrier family 9 (sodium/hydrogen	7.6
	443392	AI055821	Hs.293420	ESTs .	7.6
30	429038 418738	AL023513 AW388633	Hs.194766 Hs.6682	seizure related gene 6 (mouse)-lika solute carrier family 7, (cationic amino	7.5 7.5
50	423361	AW170055	Hs.47628	ESTs	7.5 7.5
	447198	D61523	Hs.283435	ESTs	7.5
	448555	AI536697	Hs.159863	ESTs	7.5
35	458332 407034	A1000341 U84540	Hs.220491	ESTs gb:Human dystrobrevin isoform DTN-3 (DTN	7.4 7.4
22	425354	U62027	Hs.155935	complement component 3a receptor 1	7.4
	426814	AF036943	Hs.172619	myelin transcription factor 1-like	7.4
	448507	AL133109	Hs.21333	Homo sapiens mRNA; cDNA DKFZp566N1047 (f	7,4
40	439845 449078	AL355743 AK001256	Hs.56663 Hs.22975	Homo sapiens EST from clone 41214, full KIAA1576 protein	7.4 7.3
40	410102	AW248508	Hs.279727		7.2
	425741	AF052152	Hs.159412	Homo sapiens clone 24528 mRNA sequence	7.2
	440210	AW674562	Hs.125296	ESTs	7.2
45	415651 428409	AI207162 AW117207	Hs.3815 Hs.98523	stathmin-like-protein RB3 ESTs	7.2 7.1
15	413409	AJ638418	Hs.1440	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	7.1
	443992	AW022228	Hs.322922	ESTs	7.1
	455601	AI368680	Hs.816	SRY (sex determining region Y)-box 2	7.1
50	427540 439979	R12014 AW600291	Hs.20976 Hs.6823	ESTs hypothetical protein FLJ10430	7.0 7.0
-	424893	AW295112	Hs.153648	Homo sapiens cDNA FLJ13303 fis, clone OV	7.0
	452355	N54926	Hs.29202	G protein-coupled receptor 34	7.0
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	7.0 7.0
55	440152 454293	AB002376 H49739	Hs.7006 Hs.134013	KIAA0378 protein ESTs, Moderately similar to HK61_HUMAN H	7.0
	425782	U66468	Hs.159525	cell growth regulatory with EF-hand doma	7.0
	416805	F13271	Hs.79981	Human clone 23560 mRNA sequence	7.0
	419991	AJ000098 AW956360	Hs.94210 Hs.4748	eyes absent (Drosophila) homotog 1 adenylate cyclase activating polypeptide	7.0 6.9
60	424343 408369	R38438	Hs.182575	solute carrier family 15 (H??? transport	6.9
	449605	AW138581	Hs.198416	ESTs	6.9
	444396	T65213	Hs.4257	ESTs	6.9
	444165 414245	AL137443 BE148072	Hs.10441 Hs.75850	hypothetical protein FLJ11236 WAS protein family, member 1	6.9 6.9
65	412155	R38167	Hs.12449	Homo sapiens transmembrane protein HTMP1	6.9
	424624	AB032947	Hs.151301	Ca2+dependent activator protein for secr	6.9
	448681	AL109781	Hs.21754	Homo sapiens mRNA full length insert cDN	6.9
	411379 446782	AJ816344 AJ653048	Hs.12554 Hs.144006	ESTs, Weakly similar to NPL4_HUMAN NUCLE ESTs	6.9 6.8
70	426919	AL041228		ELAV (embryonic lethal, abnormal vision,	6.8
	423346	AI267677	Hs.127416	synaptojanin 1	6.8
	436643	AA757626	Hs.10941 Hs.77631	ESTs, Wealtly similar to IPP1_HUMAN PROTE glycine cleavage system protein H (amino	6.8 6.8
	414922 410037	D00723 AB020725	Hs.58009	KIAA0918 protein	6.8
75	442613	A1004002	Hs.130522	Ky channel-interacting protein 1	6.8
	413589	AW452631	Hs.313803	ESTs, Highly similar to AF157833 1 noncl	6.8
	422175	N79885 AW117261	Hs.6382 Hs.125914	ESTs, Highly similar to T00391 hypotheti ESTs	6.8 6.7
	421141 452786	R61362	Hs.106642	ESTs, Wealthy similar to T09052 hypotheti	6.7 6.7
80	441916	AA993571	Hs.129075	ESTs	6.7
	448533	AL119710	Hs.21365	nucleosome assembly protein 1-like 3	6.7
	428037 423343	N47474 AA324643	Hs.89230 Hs.246106	potassium intermediate/small conductance ESTs	6.7 6.7
	7230-3	, , , , , , , , , , ,			•

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				n of a sal markida	6.7
				adenylate cyclase activating polypeptide alycoprotein M6A	6.7
				ESTs	6.7
	424922			hypothetical protein MGC10825	6.7 6.6
5	449328	AI962493		ESTS	6.6
	431553	X78075 AW449258		cartilage linking protein 1 ESTs	6.6
	420156 431117	AF003522		delta (Drosophila)-like 1	6.6
	422960	AW890487	Hs.63984	cadherin 13, H-cadherin (heart)	6.6 6.5
10	429239	AA448419		ESTs ESTs	6.5
	453924 433929	R49295 Al375499	Hs.24886 Hs.27379	ESTS	6.5
	426529	AF090100	Hs.170241	Homo sapiens clone IMAGE 23915	6.5 6.4
	414683	S78296	Hs.76888	hypothetical protein MGC12702	6.4
15	409746	NM_004794	Hs.56294 Hs.262346	RAB33A, member RAS oncogene family ESTs, Weakly similar to S72482 hypotheti	6.4
	419169 453590	AW851980 AF150278	Hs.33578	KIAA0820 protein	6.4
	422263	AA307639	Hs.129908	KIAA0591 protein	6.4 6.4
20	421688	AK000307	Hs.106825	hypothetical protein FLJ20300 gb:yh88b01.s1 Soares placenta Nb2HP Homo	6.3
20	447197	R36075 F07396	Hs.46627	ESTs	6.3
	425588 410366	AI267589	Hs.302689	hypothetical protein	6.3
	419498	AL036591	Hs.20887	hypothetical protein FLJ10392	6.3 6.3
05	446997	AA383439	Hs.16758	Spir-1 protein potassium intermediate/small conductance	6.3
25	427958 445908	AA418000 R13580	Hs.98280 Hs.13436	Homo sapiens clone 24425 mRNA sequence	6.3
	412068	S72043	Hs.73133	metallothionein 3 (growth inhibitory fac	6.3 6.3
	452834	A1638627	Hs.105685	KIAA1688 protein	6.3
20	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor. diacylgtycerol kinase, zeta (104kD)	6.2
30	418512 410099	AW498974 AA081630		KIAA0036 gene product	6.2
	452744	AJ267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	6.2 6.2
	427897	NM_017413	Hs.303084	apelin; peptide ligand for APJ receptor Rac/Cdc42 guanine exchange factor (GEF)	6.2
25	416427	BE244050	Hs.79307 Hs.48372	ESTs	6.2
35	439274 431552	AF086092 A1815863	Hs.259873	axonal transport of synaptic vesicles	6.2
	439607	BE540565	Hs.159460	ESTs	6.2 6.2
	408950	AA707814	Hs.14945	long fatty acyl-CoA synthetase 2 gene KIAA0027 protein	6.2
40	412709	AL022327 AF218942	Hs.74518 Hs.24889	formin 2	6.1
40	435624 425977	R15138	Hs.165570		6.1 6.1
	420077	AW512260	Hs.87767	ESTs	6.1
	457005	AJ007421	Hs.172597		6.1
45	440471 423770	AA886146 AW976766	Hs.307944 Hs.132776		6.1
40	438624	AA889055	Hs.123468	ESTs	6,1 6.1
	452752	AW044058	Hs.33578	KIAA0820 protein	6.1
	438208	AL041224	Hs.65379 Hs.79000	ESTs growth associated protein 43	6.1
50	416072 407808	AL110370 AA663559	Hs.279789		6.1
50	433701	AW445023	Hs.15155	ESTs	6.1 6.1
	419704		Hs.45057	ESTs 8 tryptophan rich basic protein	6.1
	429250 433244		Hs.198309 Hs.271289		6.0
55	422544		Hs.11814) KIAA0716 gene product	6.0 6.0
	420133			3 ESTs 5 ESTs Months similar to 2109260A R cell	6.0
	440491		Hs.13055 Hs.10326		6.0
	422728 415257		Hs.27513	ESTs	5.9
60	417160	N76497	Hs.1787	amtentiniri orotein 1 (Pelizaeus-Merzbac	5.9 5.9
	430188				5.9
	437377 430471			hypothetical protein FLJ 10142	5.9
	43352		110.2 110.	ESTs	5.9 5.9
65	40892	6 AF217529			5.9
	42731				5.9
	42614 40989			gb:EST368183 MAGE resequences, MAGD Homo	5.8
	45951		Hs.2468	SR EST	5.8 5.8
70	44291	0 Al365130			5.8
	41473				5.8
	42433 40314		, 15.1010	NM 002706*:Homo sapiens protein phosphat	5.8
	42011	1 AA25565		gb:zs21h11.r1 NCI_CGAP_GCB1 Homo sapiens	5.8 5.8
75	45081	13 A1739625	5 Hs.2033	76 ESTs Target Exon	5.8
	40214 43479		3 Hs.1324		5.8
	42242			173 hypothetical protein FLJ22672	5.8
	4457	45 AB00792	4 Hs.1324	IS KIAA0455 gene product	5.8 5.8
80					5.7
	4514 4411			intermediate filament protein syncoitin	5.7
	4245				5.7

	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEUS_HUMAN LEUKE	5.7
	405238			Target Exon	5.7
	432890	NM_014442	Hs.279751	siatic acid binding lg-like lectin 8	5.7 5.7
5	440492 413492	R39127 D87470	Hs.21433 Hs.75400	hypothetical protein OKFZp547J036 KIAA0280 protein	5.7
,	427624	AA406245	Hs.24895	ESTs	5.7
	418079	R40058	Hs.6911	ESTs	5.6
	424458	M29273	Hs.1780	myelin associated glycoprotein	5.6 5.6
10	448299 429698	AA497044 AI685086	Hs.20887 Hs.26339	hypothetical protein FLJ10392 ESTs, Wealdy similar to S21348 probable	5.6
10	430228	AW950939	Hs.6382	ESTs, Highly similar to T00391 hypotheti	5.6
	445255	NM_014841	Hs.12477	synaptosomal-associated protein, 91 kDa	5.6
	436887	AW953157	Hs.193235	hypothetical protein DKFZp547D155	5.6 5.6
15	452898 435538	AA814497 AB011540	Hs.78792 Hs.4930	ESTs low density incorrotein receptor-related	5.6
13	436035	AA703679	Hs.106999	ESTs, Wealdy similar to SYT5_HUMAN SYNAP	5.5
	412190	R16180	Hs.274461	ESTs	5.5
	459278	AW294659	Hs.34054	Homo sapiens cDNA: FLJ22488 fis, clone H	5.5 5.5
20	416490 423449	AF090116 AI497900	Hs.79348 Hs.33067	regulator of G-protein signalling 7 ESTs	5.5 5.5
20	440866	AI703103	Hs.271360	hypothetical protein MGC16275	5.5
	432154	Al701523	Hs.112577	EST8	5.4
	423476	AL035633	Hs.185701	Human DNA sequence from clone RP5-1046G1 Homo segriens mRNA full length insert cDN	5.4 5.4
25	428588 447773	F12101 AJ423930	Hs.36790	ESTs, Wealdy similar to putative p150 (H	5.4
	436936	AL134451	Hs.197478	ESTs	5.4
	427250	R35941	Hs.25418	ESTs	5.4
	427302	AA400540 AF034799	Hs.135282 Hs.30881	Horno sapiens cDNA FLJ11554 fis, clone HE protein tyrosine phosphatase, receptor t	5.4 5.4
30	452856 428795	R45503	Hs.97469	ESTs, Highly similar to A39769 N-acetyll	5.4
50	407385	AA610150	Hs.272072	ESTs, Weakly similar to 138022 hypotheti	5.4
	405348			C7001664:gi[12698061 dbj[BAB21849.1] (AB	5.4
	438330	AW450572	Hs.257316	ESTS	5.3 5.3
35	426503 448148	AA380153 NM_016578	Hs.20509	gb:EST93093 Skin tumor I Homo sapiens cD HBV pX associated protein-8	5.3
55	410386	W26187	Hs.3327	Homo sapiens cDNA: FLJ22219 fis, clone H	5.3
	445225	AI216555	Hs.202398	ESTs	5.3
	428784	Y12851	Hs.193470	purinergic receptor P2X, ligand-gated io	5.3 5.3
40	418759 402605	AA227879	Hs.187621	ESTs Target Exon	5.3
40	412046	Y07847	Hs.73088	RAS-related on chromsome 22	5.3
	423869	BE409301	Hs.134012	C1q-related factor	5.2
	430130	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (5.2 5.2
45	453096 450475	AW294631 AW805634	Hs.11325 Hs.205015	ESTs ESTs	5.2
73	429139	F09092	Hs.66087	ESTs	5.2
	451783	R42554	Hs.210862	T-box, brain, 1	5.2
	436568	H12049	Hs.91564	ESTs	5.2 5.2
50	424330 408453	AW073953 Al369838	Hs.333396 Hs.45127	Homo sapiens cDNA FLI13596 fis, clone PL chondroitin sulfate proteoglycan 5 (neur	5.2
50	447499	AW262580	Hs.147674	protocadherin beta 16	5.2
	402855			NM_001839°:Homo sapiens calponin 3, acid	5.2
	420805	L10333	Hs.99947	reticulon 1	5.2 5.2
55	426457 417355	AW894667 D13168	Hs.169965 Hs.82002	chimerin (chimaerin) 1 endothelin receptor type 8	5.1
75	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	5.1
	450639	AI703186	Hs.277174	ESTs	5.1
	412811	H06382		ESTs Homo sapiens ovarian cancer related prot	5.1 5.1
60	400379 441869	NM_018432 NM_003947	Hs.8004	huntingtin-essociated protein interactin	5.1
	442832	AW206560	Hs.253569	ESTs	5.1
	422709	AA315331	Hs.153485	ESTs	5.1
	411555	AF113537	Hs.70669 Hs.89566	HMP19 protein ets variant gene 1	5.1 5.0
65	419043 430979	T19167 Al479755	Hs.129010		5.0
•	451320	AW118072		diacytglycerol kinase, zeta (104kD)	5.0
	423678	AW963357	Hs.7847	ESTs	5.0
	429918	AW873986	Hs.119383 Hs.296434		5.0 5.0
70	452785 453128	AL359942 AW026516	Hs.31791	acytohosphatase 2, muscle type	5.0
	428001	H97428	Hs.219907	ESTs, Moderately similar to Transforming	5.0
	430183	BE010038		gb:PM3-BN0176-100400-001-g04 BN0176 Homo	5.0
	449969 430108	AW295142 AW163034	Hs.180187 Hs.6467	Homo sapiens cDNA FLJ14337 fis, clone PL synaptogyrin 3	5.0 5.0
75	439108 426271	AF026547	Hs.169047		5.0
	451752	AB032997	Hs.26966	KIAA1171 protein	5.0
	420578	AA813546	Hs.99034	GTP-binding protein Rho7	4.9
	427315	AA179949 AW504300	Hs.175563 Hs.295605		4.9 4.9
80	428186 445133	AW157646	Hs.198689		4.9
~ •	410359	R38524	Hs.106313	ESTs	4.9
	427144		Hs.2126	vasoactive intestinal peptide receptor 2	4.9 4.9
	448548	R13209	Hs.21413	solute carrier family 12, (potassium-chl	7.3

	ACTECS	AA331517	Hs.286055 d	chimerin (chimaerin) 2	4.9
	457561 409100		Hs.42245	ESTs, Moderately similar to 138022 hypot	4.9
	437117	AL049256	Hs.122593 I	ESTs	4.9
_	415101		Hs.144534	ESTS	4.9 4.9
5	438458	AW975186		gb:EST387294 MAGE resequences, MAGN Homo brain-specific angiogenesis inhibitor 3	4.9
	442026 438283	AI243749 AI458931		ESTs	4.9
	449714	AB033015		KIAA1189 protein	4.9
	420871	AA702972	Hs.65300	ESTS	4.9
10	425256	BE297611		collapsin response mediator protein 1	4.9 4.9
	424001	W67883		paternally expressed 10 hypothetical protein FLJ23033	4.8
	419103 446727	Z40229 AB011095		KIAA0523 protein	4.8
	408670	AF160967	Hs.46784	potassium large conductance calcium-acti	4.8
15	428189	AA424030	Hs.46627	ESTs	4.8
	420092	AA814043	Hs.88045	ESTs	4.8 4.8
	410631	AA086469	Hs.47171	ESTs	4.8
	449277	AA001064 R91913	Hs.43670 Hs.272104	ESTs ESTs, Moderately similar to ALU1_HUMAN A	4.8
20	436282 414706	AW340125	Hs.76989	KIAA0097 gene product	4.8
20	438703	AI803373	Hs.31599	ESTs	4.8
	439340	AB032436	Hs.6535	brain-specific Na-dependent inorganic ph	4.8 4.7
	445890	AF055019	Hs.21906	Homo sapiens clone 24670 mRNA sequence hypothetical protein FLJ23112	4.7
25	436734	A1937612 A1241733	Hs.273758 Hs.43871	ESTs	4.7
23	408177 445740	T78281	Hs.13226	Homo sapiens clone 25181 mRNA sequence	4.7
	459527	AW977556	Hs.291735	ESTs, Wealdy similar to 178885 serine/th	4.7
	445523	Z30118	Hs.293788	ESTs, Moderately similar to unnamed prot	4.7 4.7
20	409172	Z99399	Hs.122593	ESTs suppression of tumorigenicity 7	4.7
30	437748	AF234882 AF035290	Hs.5814 Hs.106300	Homo sapiens clone 23556 mRNA sequence	4.7
	421637 448044	AI458682	115.100000	ab:tk13e01.x1 NCI_CGAP_Lu24 Homo sapiens	4.7
	459311	R40192	Hs.21527	Human DNA sequence from clone GS1-115M3	4.7
~-	447891	R41754	Hs.6496	ESTs	4.7 4.7
35	426968	U07616	Hs.173034	amphiphysin (Stifl-Mann syndrome with br NM_002688*:Homo sapiens peanut (Drosophi	4.7
	404819 409125	R17268	Hs.343567	axonal transport of synaptic vesicles	4.7
	437762	T78028	Hs.154679	synaptotagmin I	4.7
	441668	AI611973	Hs.136313	ESTs	4.7
40	444190	AIB78918	Hs.10526	cysteine and glycine-rich protein 2	4.6 4.6
	429269	AA449013	Hs.99203	ESTs gb:nz24c08.s1 NCt_CGAP_GCB1 Homo sapiens	4.6
	433009	AA761668 D44643	Hs.14144	secreted modular calcium-binding protein	4.6
	416586 427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	4.6
45	426925	NM_001196	Hs.315689	Homo sapiens cDNA: FLJ22373 fis, clone H	4.6
	410264	AK001853	Hs.61508	Homo sapiens cDNA FLJ10991 fis, clone PL	4.6 4.6
	437698	R61837	Hs.7990	ESTs, Moderately similar to 184505 calci alanine-glyoxylate aminotransferase 2-li	4.6
	445813 424264	Z42023 D80400	Hs.106576 Hs.239388	Human DNA sequence from clone RP1-304B14	4.6
50	448765	R15337	Hs.21958	Homo sapiens mRNA; cDNA DKFZp547D086 (fr	4.6
-	419723	AL120193	Hs.339810	longevity assurance (LAG1, S. cerevisiae	4.6 4.6
	424282	R76421	Hs.135694	ESTs	4.6
	429401	AW296102	Hs.99272	ESTs, Weakly similar to S32567 A4 protei qb:EST90805 Synovial sarcoma Homo sapien	4.5
55	426413 407896	AA377823 D76435	Hs.41154	Zic family member 1 (odd-paired Drosophi	4.5
55	413248	T64858	Hs.21433	hypothetical protein DKFZp547J036	4.5
	443731	AI083928	Hs.145418		4.5
	449539		Hs.58446	ESTs	4.5 4.5
60	420362		Hs.97206 Hs.220587	huntingtin interacting protein 1 ESTs, Moderately similar to ALUS_HUMAN A	4.5
ŲΨ	443301 423178	AI733614 AI033140	Hs.124983		4.5
	437933		Hs.14615	S ESTs	4.5
	446544	AI531932	Hs.7047	ESTs, Weakly similar to Unknown [H.sapie	4.5 4.5
~~	411642				4.5
65	428282		Hs.44653		4.5
	411498 408622				4.5
	436637		Hs.26766	ESTs	4.5
	438456		Hs.20594	ESTs	4.5 4.4
70	400533		11- 75040	ENSP00000209376*:PRED65 protein (Fragmen	4.4
	413951) Hs.75640 Hs.5422	natriuretic peptide precursor A glycoprotein M6B	4.4
	417632 425138		Hs.16746	- At	4,4
	45721				4.4
75	41381	2 AW188687	Hs.44748	ESTs	4.4 4.4
	44845				4.4
	43228				4.4
	45876 40581	-	118,11130	NM_002578:Homo sapiens p21 (CDKN1A)-acti	4.4
80	44787		Hs.16425	52 ESTs	4.4
	43134	2 AW97101	B Hs.21659	ESTs	4.4 4.4
	40857		Hs.1951		4.4
	44572	9 H21066	Hs.1322		

	422253	W81526	Hs.118329	ESTs, Moderately similar to GAD_HUMAN GA	4.4
	419088	AI538323	Hs.52620	integrin, beta 8	4.4
	428305	AA446628	Hs.2799	cartilage linking protein 1	4.4
5	410768 428722	AF038185 U76456	Hs.66187 Hs.190787	Homo sapiens clone 23700 mRNA sequence tissue inhibitor of metalloproteinase 4	4.4 4.4
•	451621	AI879148	Hs.26770	fatty acid binding protein 7, brain	4.4
	424240	AB023185	Hs.143535	calcium/catmodulin-dependent protein kin	4.3
	433932 439935	AW954599	Hs.169330	neuronal protein	4.3 4.3
10	436039	S75105 AW023323	Hs.8358 Hs.121070	glutamate receptor, ionotropic, kainate ESTs	4.3
	416220	N49776	Hs.170994	hypothetical protein MGC10946	4.3
	409953	AA332277	Hs.57691	cadherin 18, type 2	4.3
	456497 420352	AW967956 BE258835	Hs.123648	ESTs, Weakly similar to AF108460 1 ubinu gb:601117374F1 NIH_MGC_16 Homo sapiens c	4.3 4.3
15	454032	W31790	Hs.194293	ESTs, Weakly similar to 154374 gene NF2	4.3
	421790	AW896201	Hs.22654	sodium channel, voltage-gated, type I, a	4.3
	444218	AF070641	Hs.10684 Hs.146274	Homo sapiens clone 24421 mRNA sequence ESTs	4.3 4.3
	436391 452106	AJ227892 AJ141031	Hs.21342	ESTS ESTS	4.3
20	422465	AF073710	Hs.117149	regulator of G-protein signalling 9	4.3
	439285	AL133916		hypothetical protein FLJ20093	4.3
	404541 424572	M19650		NM_030795:Homo sepiens stathmin-like 4 (2,3-cyclic nucleotide 3' phosphodieste	4.3 4.3
	449048	Z45051	Hs.22920	similar to \$68401 (cattle) glucose induc	4.3
25	409182	AA064970	Hs.122593	ESTs	4.3
	444600 408838	R41398 Al669535	Hs.6996 Hs.40369	ESTs ESTs	4.3 4.3
	410592	R94088	Hs.43569	ESTs	4.3
••	440168	AA868507	Hs.126141	ESTs	4.2
30	445078	AI869975	Hs.4775	junctophilin 3	4.2 4.2
	428670 411666	AA431682 AF106564	Hs.134832 Hs.71346	ESTs neurofilament 3 (150kD medium)	4.2
	412505	AA974491	Hs.21734	ESTs	4.2
26	418506	AA084248	Hs.85339	G protein-coupled receptor 39	4.2
35	441707	R42637 AI672096	Hs.21963 Hs.9012	hypothetical protein DKFZp76180514 ESTs, Weakly similar to S26650 DNA-bindi	4.2 4.2
	449433 441523	AW514263	Hs.301771	ESTs, Weakly similar to ALUF_HUMAN !!!!	4.2
	448243	AW369771	Hs.52620	integrin, beta 8	4.2
40	429149	AW193360	Hs.197962	ESTs, Weakly similar to 138022 hypotheti	4.2 4.2
40	430676 404584	AF084866		gb:Homo saplens envelope protein RIC-3 (Target Exon	4.2
	422798	R92347	Hs.34574	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.2
	451254	AI571016	Hs.172967	ESTs	4.2
45	428585	AB007863	Hs.185140	KIAA0403 protein Horno sapiens mRNA; cDNA DKFZp434N079 (fr	4.2 4.2
43	439231 425287	AW581935 R88249	Hs.141480 Hs.155524	peanut (Drosophila)-like 2	4.2
	425790	AW136286	Hs.288446	ESTs	4.2
	450407	NM_000810	Hs.24969	gamma-aminobutyric acid (GABA) A recepto	4.2 4.2
50	425241 445292	AA324624 AV653264	Hs.155247 Hs.13982	aldolase C, fructose-bisphosphate Homo sapiens cDNA FLJ14666 fis, clone NT	4.1
50	400777	A4003204	713.10006	NM_007325*:Homo sapiens glutamate recept	4.1
	422170	AI791949	Hs.112432	anti-Mullerian hormone	4.1
	410765 425402	AI694972	Hs.66180 Hs.24970	nucleosome assembly protein 1-like 2 ESTs, Weakly similar to B34323 GTP-bindi	4.1 4.1
55	438461	Al215881 AW075485	Hs.286049	phosphoserine aminotransferase	4.1
	421268	AI126821	Hs.30514	ESTS	4.1
	416439	AA180363	Hs.118769 Hs.227699	ESTs ESTs, Weakly similar to T2D3_HUMAN TRANS	4.1 4.1
	419687 435040	A1638859 A1932350	Hs. 152825	ESTs	4.1
60	439774	AL360257	Hs.213493	Homo sapiens mRNA full length insert cDN	4.1
	458435	AI418718	Hs.144121	ESTs, Weakly similar to T46916 hypotheti Homo sapiens mRNA; cDNA DKFZp547N093 (fr	4.1 4.1
	410320 436899	AA084071 AA764852	Hs.93816 Hs.291567	ESTs	4.1
	454171	AW854832	10.251001	gb:QV2-CT0261-201099-011-05 CT0261 Homo	4.1
65	453118	AW195849	Hs.252757	ESTs	4.1
	428771	AB028992 AW298350	Hs.193143 Hs.66020	KIAA1069 protein ESTs	4.1 4.1
	444185 422374	AW732869	Hs.1519	protein kinase, cAMP-dependent, regulato	4.1
	430147	R60704	Hs.234434		4.1
70	456060	C14904	Hs.45184	Homo sapiens cDNA FLJ12284 fis, clone MA	4.1 4.1
	433819 415827	AW511097 H17462	Hs.112765 Hs.23079	ESTs ESTs	4.1
	437397	AA349847	Hs.4221	hypothetical protein DKFZp761H039	4.1
75	441390	A1692560	Hs.131175		4.1
75	440483	A1200836	Hs.150386 Hs.196008		4.0 4.0
	435294 447397		Hs.18442	E-1 enzyme	4.0
	425390	AI092634	Hs.156114	protein lyrosine phosphatase, non-recept	4.0
80	432022		Hs.272348		4.0 4.0
OV	420602 408081		Hs.99236 Hs.167409	regulator of G-protein signaffing 20 ESTs	4.0
	453313		Hs.153748	hypothetical protein FLJ22490	4.0
	436511	AA721252	Hs.291502		4.0
				000	

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					4.0
	4405.1			trophin-1 interacting protein 1; activi	4.0
				ynuclein, beta ESTs	4.0
		A1469935	Hs.22792 8	STs	4.0
5		Al339732		G-rich RNA sequence binding factor 1	4.0 4.0
	440553		Hs.344043 Hs.208339	Homo sapiens cDNA FLJ14459 fis, clone HE Homo sapiens mRNA; cDNA DXFZp762G113 (fr	4.0
	437449 445888		Hs.13415	Homo sapiens clone 24571 mRNA sequence	4.0
	439450		Hs.125304	ESTs	4.0 4.0
10	453792	AL134539		KIAA1678	4.0
	459080	AW192083	Hs.290855 Hs.6421	ESTs hypothetical protein DKFZp761N09121	4.0
	438810 446233	AW897846 AI282028		ESTs	4.0
	412754	AW160375	Hs.74565	amyloid beta (A4) precursor-like protein	4.0
15	412326	R07566		small inducible cytokine A3 (homologous	4.0 4.0
	434859	BE255080		collapsin response mediator protein-5; C ESTs	4.0
	423279 416340	AW959861 N31772	Hs.290943 Hs.79226	fasciculation and elongation protein zet	3.9
	410126	BE169274	1.0	KIAA0036 gene product	3.9 3.9
20	431173	AW971198	Hs.294068	ESTs	3.9
	446936	H10207	Hs.47314 Hs.119062	ESTs ESTs	3.9
	424899 419038	AL119387 AW134924	Hs.190325	ESTs	3.9
	450530	NM_006668	Hs.25121	cytochrome P450, subfamily 46 (cholester	3.9 3.9
25	438142	T90309	Hs.269651	ESTs	3.9
	412659	AW753865	Hs.74376	offactomedin related ER localized protei ESTs	3.9
	412788 410909	AA120960 AW898161	Hs.198416 Hs.53112	ESTs, Moderately similar to ALU8_HUMAN A	3.9
	429433	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	3.9 3.9
30	432809	AA565509	Hs.131703	ESTS	3.9 3.9
	424186	AI536021	Hs.288706	Homo sapiens cDNA FLJ10281 fis, clone HE KIAA0981 protein	3.9
	425480	AB023198 AI675444	Hs.158135 Hs.263024	ESTs	3.9
	449932 434072	H70854	Hs.283059	Homo sapiens PRO1082 mRNA, complete cds	3.9
35	450590	AI701507	Hs.273740	ESTs	3.9 3.9
	419586	AI088485	Hs.144759	ESTs, Wealdy similar to 138022 hypotheti	3.9
	414040	N58513 AJ271643	Hs.32171 Hs.87469	ESTs putative acid-sensing ion channel	3.9
	436480 443210	AJ692649	Hs.9451	hypothetical protein MGC13168	3.9
40	448448	NM_014954	Hs.21239	KIAA0985 protein	3.9 3.9
	447067	R42098	Hs.21964	ESTs ELAV (embryonic lethal, abnormal vision,	3.9
	413199	M62843 AL031658	Hs.75236	Human DNA sequence from clone RP1-310013	3.9
	429421 415796	R87548	Hs.78854	ATPase, Na? transporting, beta 2 polypep	3.8
45	417333	AL157545	Hs.173179		3.8 3.8
	418771	AA807881	Hs.25329	ESTs	3.8
	417565	A1203405 AL035668	Hs.47831 Hs.73853	ESTs bone morphogenetic protein 2	3.8
	412420 450202	AW969756	Hs.34145	ESTs, Weakly similar to B49647 GTP-bindi	3.8
50	435312	AJ243396	Hs.4865	voltage-gated sodium channel beta-3 subu	3.8 3.8
	435832	AA425688	Hs.41641	Bruno (Drosophila) -like 4, RNA binding putative ankyrin-repeat containing prote	3.8
	435854	AJ278120 AI821122	Hs.4996	gb:ns91g10.y5 NCI_CGAP_Pr3 Homo sapiens	3.8
	459079 425905		Hs.318584	novel C3HC4 type Zinc finger (ring finge	3.8
55	421977		Hs.110169		3.8 3.8
	437756		Hs.197096	6 ESTs C4001100°:gij5852342 gb AAD54015.1 (AF0	3.8
	403696 453033		Hs.31463		3.8
	455055			1 ESTs	3.8 3.8
60	415884		Hs.13471	ESTs gb:RC3-CT0254-031099-012-c05 CT0254 Homo	3.8
	432646				3.8
	451059 447057		Hs.26715 Hs.15769	· 211 · · ·	3.8
	418915		Hs.11897		3.8
65	441111	AI806867	Hs.12659	4 ESTs	3.8 3.8
	447818		Hs.21906		3.8
	45718		Hs.11856 Hs.84244		3.8
	41835 41071			*	3.8
70	42887		Hs.4892	5 ESTs	3.8 3.8
_	43894	4 AA302517			3.8
	42089				3.8
	41832 42720		Hs.9242	3 KIAA1566 protein	3.7
75	44531		3 Hs.1251	3 Homo sapiens done 23687 mRNA sequence	3.7 3.7
. •	42884	1 AI418430			3.7
	41482		Hs.7742 8 Hs.1331		3.7
	44331 40772			31 ESTs	3.7
80	42964	43 AA45588	9 Hs.1572	79 FYVE-finger-containing Rab5 effector pro	3.7 3.7
	44412	27 N63620	Hs.1328		3.7
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	4580	12 70030341	113.2/16		

	459660	M79082		ESTs	3.7
	432188	AI362952	Hs.2928	solute carrier family 7 (cationic amino	3.7
	437627 408508	AW469925 AI806109	Hs.257837 Hs.135736	ESTs KIAA1580 protein	3.7 3.7
5	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	3.7
_	410623	AW958932	Hs.293833	ESTs	3.7
	430744	AA485229	Hs.105649	ESTs	3.7
	454392 453739	8E260893 AL120266	Hs.236131	homeodomain-interacting protein kinase 2 ESTs	3.7 3.7
10	407198	H91679		gb:yv04a07.s1 Soares fetal liver spleen	3.7
	405239	U89281		oxidative 3 alpha hydroxysteroid dehydro	3.7
	433615	AA732982	Hs.269607	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7 3.7
	424800 451027	AL035588 AW519204	Hs.153203 Hs.40808	MyoD family inhibitor ESTs	3.7 3.7
15	415131	D61119		gb:HUM158C11B Clontech human fetal brain	3.7
	443454	AI057494	Hs.133421	ESTs	3.7
	423779 452092	AW071837 BE245374	Hs.57971 Hs.27842	ESTs hypothetical protein FLJ11210	3.7 3.7
	435910	AI084152	Hs.21782	ESTs, Weakly similar to ALU7_HUMAN ALU S	3.6
20	447028	AI973128	Hs.167257	brain link protein-1	3.6
	452997	N64777	Hs.44656	ESTs .	3.6
	408601 407332	U47928 AI801565	Hs.86122 Hs.200113	protein A Homo sapiens cONA FLJ11379 fis, clone HE	3.6 3.6
	455646	BE064420	13.200110	gb:RC4-BT0311-241199-012-c08 BT0311 Homo	3.6
25	433657	AJ244368	Hs.8124	PH domain containing protein in retina 1	3,6
	421679	Al475110 AA324885	Hs.203933 Hs.22777	ESTs carbonic anhydrase XI	3.6 3.6
	448985 41470 9	AA324663 AA704703	Hs.77031	Sp2 transcription factor	3.6
	411775	H08342		gb:yl87b09.r1 Soares infant brain 1NIB H	3.6
30	439099	AB037800	Hs.6462	protein kinase C and casein kinase subst	3.6
	436315 423611	BE390513 AB011163	Hs.27935 Hs.129908	hypothetical protein MGC4837 KIAA0591 protein	3.6 3.6
	453169	AB037815	Hs.32156	KIAA1394 protein	3.6
20	436954	AA740151	Hs.130425	ESTs	3.6
35	439249	AF086060 AW665996	Hs.170053	G-protein coupled receptor 88	3.6 3.6
	432058 419390	AVV003990 AI701162	Hs.130729 Hs.90207	ESTs, Wealty similar to ALU1_HUMAN ALU S hypothetical protein MGC11138	3.6
	428483	AI908539	Hs.184592	KIAA0344 gene product	3.6
40	409557	BE182896	Hs.211193	ESTs	3.6
40	418049	AA211467 AL117428	Hs.190488	Homo sapiens, Similar to nuclear localiz DKFZP434A236 protein	3.6 3.6
	443774 425331	AW962128	Hs.9740	gb:EST374201 MAGE resequences, MAGG Horno	3.6
	445105	AF238869	Hs.283955	Homo sapiens clone GLSH-2 similar to gli	3.6
45	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	3.6
43	446420 428138	AW015693 AA773842	Hs.135614 Hs.293799	ESTs ESTs	3.6 3.6
	404185	74173072	115.230733	Target Exon	3.6
	427517	AA644142	Hs.7107	ESTs, Wealdy similar to ALU7_HUMAN ALU S	3.6
50	443150	AI034467	Hs.34650	ESTs gb:EST366342 MAGE resequences, MAGC Homo	3.6 3.6
50	408065 435092	AW954272 AL137310	Hs.4749	Homo sapiens mRNA; cDNA DKFZp761E13121 (3.6
	418064	BE387287	Hs.83384	S100 calcium-binding protein, beta (neur	3.6
	433560	Al925195	Hs.130891	hypothetical protein MGC4400	3.6
55	432882 412350	NM_013257 AI659306	Hs.279696 Hs.73826	serum/glucocorticoid regulated kinase-li protein tyrosine phosphatase, non-recept	3.6 3.6
55	439753	8E262233	Hs.7423	hypothetical protein from EUROIMAGE 2168	3.6
	451734	NM_006176	Hs.26944	neurogranin (protein kinase C substrate,	3.6
	437056	AJ147061	11- 22450	gb:ok33a11.s1 Soares_NSF_F8_9W_OT_PA_P_S ESTs	3.6 3.6
60	438328 451489	AI492261 NM_005503	Hs.32450 Hs.26468	amyloid beta (A4) precursor protein-bind	3.6
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	441834 421183	AL138034 AL135740	Hs.7979 Hs.102447	KIAA0738 gene product TSC-22-like	3.5 3.5
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	419929	U90268	Hs.11217 Hs.93810	cerebral cavernous mattermations 1	3.5
70	407792	AI077715	Hs.39384	putative secreted figand homologous to f	3.5
	422564	AI148006	Hs.222120		3.5
	433323 435743	AA805132 T66861	Hs.159142 Hs.12962	ESTs ESTs	3.5 3.5
	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	3.5
75	403341			Target Exon	3.5
	443761	AI525743	Hs.345187	ESTs KJAA0202 protein	3.5 3.5
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00	445424	AB028945	Hs.12696	cortactin SH3 domain-binding protein	3.5
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	430456 419647	AA314998 AA348947	Hs.241503 Hs.91816	hypothetical protein hypothetical protein	3.5 3.5
	412707	AW206373	Hs.16443	Homo sapiens cDNA: FLJ21721 fis, clone C	3.5
			-		

					3.5
				nypothetical protein DKFZp547F072 ESTs	3.5
	451066 425234		Hs.165909	FSTs. Weakly similar to I38022 hypotheti	3.5
_	420071	,	Hs 94806	ATP-binding cassette, sub-family A (ABC1	3.5 3.5
5	432625 442118	AI243596 AA976718		ESTs, Moderately similar to T03094 A-kin ESTs	3.5
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	434542	AA769310	Hs.61260	hypothetical protein FLJ13164	3.4 3.4
	419235	AW470411	Hs.288433	neurotrimin guanine nucleotide binding protein (G pr	3.4
15	440700 417084	AW952281 H08370	Hs.296184 Hs.33067	ESTs	3.4
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	439920	H05430	Hs.288433	neurotrimin	3.4 3.4
	453710	AL119136 BE276738	Hs.236131 Hs.74578	homeodomain-interacting protein kinase 2 DEAD/H (Asp-Gtu-Ala-Asp/His) box polypep	3.4
20	412783 435977	AL138079	Hs.5012	brain-specific membrane-anchored protein	3.4
	431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	3,4 3,4
	449611	AI970394	Hs.197075	ESTs Homo sapiens mRNA; cDNA DKFZp586P1124 (f	3.4
	448543 430968	AW897741 AW972830	Hs.21380	gb:EST384925 MAGE resequences, MAGL Homo	3.4
25	413530	AA130158	Hs.19977	ESTs, Moderately similar to ALU8_HUMAN A	3.4 3.4
	412043	BE156622	Hs.333371	Homo sapiens clone TA40 untranslated mRN	3.4
	445666 412820	R59960 BE001236	Hs.282386	ESTs gb:CM3-BN0075-240200-101-d11 BN0075 Homo	3,4
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	419852 448750	U95020	Hs.21903	calcium channel, voltage-dependent, beta	3.4
~-	435741	A1240668	Hs.113099	ESTs	3.4 3.4
35	445828	F05802	Hs.81907 Hs.90005	ESTs superiorcervical ganglia, neural specifi	3.4
	419347 431733	C15944 AW298410	Hs.21475	ESTs	3.4
	415949	H10562	Hs.21691	ESTs	3.4 3.4
40	400205		11- 1C074E	NM_006265*:Homo sapiens RAD21 (S. pombe) crumbs (Drosophila) homolog 1	3.4
40	437528 442593	N59646 R39804	Hs.169745 Hs.31961	ESTs	3.4
	442927	AI024347	Hs.131519	ESTs	3.4
	429528	A1985303	Hs.99361	ESTs	3.4 3.4
45	450756	A1733488 A1198874	Hs.144062 Hs.28847	ESTs AD026 protein	3.4
43	437387 430347	NM_002039		GRB2-associated binding protein 1	3.4
	404283			ENSP00000244751*:Copine-like protein KIA	3.4 3.4
	433229	AB040925 R24595	Hs.91625 Hs.7122	KIAA1492 protein scrapie responsive protein 1	3.4
50	440274 436114	AA778232	Hs.19515	ESTs, Highly similar to NRG3_HUMAN PRO-N	3.4
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	417868 439793	AA018825	Hs.7934	Kruppel-like factor 4 (gut)	3.3
55	456209	W60633	Hs.297792		3.3 3.3
	421458	NM_003654 AA780243	Hs.104576 Hs.54647	carbohydrate (keratan sulfate Gal-6) sul ESTs	3.3
	438201 400302		Hs.1915	folate hydrolase (prostate-specific memb	3.3
	425897	AA935315	Hs.48965	Homo sapiens cDNA: FLJ21693 fis, clone C	3.3 3.3
60	423169 415539		Hs.21837 Hs.72472	ESTs, Weakly similar to KIAA0927 protein BMP-R1B	3.3
	450337		Hs.202427	7 ESTs	3.3
	408447	AK002089	Hs.45080	Homo sapiens cDNA FLJ11227 fis, clone PL	3.3 3.3
65	423420		Hs.128382 Hs.19561		3.3
05	429084 440435		Hs.21273	transcription factor NYD-sp10	3.3
	453785		Hs.28373	2 ESTs, Moderately similar to ALU1_HUMAN A	3.3 3.3
	448048		Hs.17040 Hs.12845		3.3
70	436207 404632		FG.12043	NM 022490:Homo sapiens hypothetical prot	3.3
. 3	411565	S AW851728		ab:MR2-CT0222-011199-007-d06 CT0222 Homo	3.3 3.3
	416849		Hs.29378		3.3 3.3
	436267 426625		3 Hs.18011 Hs.30064		3.3
75	40127			C9000559*:gij12314195jemb/CAB99338.1] (A	3.3
	43507	1 D60683	Hs.35495		3.3 3.3
	43312 42692				3.3
	42366		Hs.1311	38 neurotensin receptor 2	3.3
80	43505	6 AW02333			3.3 3.3
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	42501 44526				3.3
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	421094	AW978202	Hs.289064	hypothetical protein FLJ22251	3.3
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	411048 432488	AK001742 AA551010	Hs.67991 Hs.216640	hypothetical protein DKFZp434G0522 ESTs	3.3 3.3
5	443672	AA323362	Hs.9667	butyrobetaine (gamma), 2-oxoglutarate di	3.3
•	412719	AW016610	Hs.816	ESTs	3.3
	420050	AL118615	Hs.94653	neurochondrin	3.3
	410082 408554	AA081594 AA836381	Hs.158311 Hs.315111	Musashi (Drosophila) homolog 1 nuclear receptor co-repressor/HDAC3 comp	3.3 3.3
10	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	3.2
	434574	A1424458	Hs.33470	ESTs	3.2
	432715	AA247152	Hs.200483	ESTs, Weakly similar to KIAA1074 protein	3.2
	426757	AW205640	Hs.158206	ESTS	3.2 3.2
15	428167 451597	AA770021 AW295250	Hs.16332 Hs.207536	ESTs ESTs	3.2
	400362	AF068294	Hs.272414	Horno sapiens HDCMB45P mRNA, partial cds	3.2
	417675	AI808607	Hs.3781	similar to murine leucine-rich repeat pr	3.2
	429550	AW293055	Hs.119357	ESTS	3.2 3.2
20	404120 417123	BE326521	Hs.159450	C5000537*:gi 3298595 gb AAC41376.1 (AF0 ESTs	3.2
20	450313	AI038989	Hs.332633	Bardet-Biedl syndrome 2	3.2
	425999	AW513051	Hs.332981	ESTs, Weakly similar to I38022 hypotheti	3.2
	430526	AF181862	Hs.242407	G protein-coupted receptor, family C, gr	3.2
25	452619 415558	AW298597 AA885143	Hs.61884 Hs.125719	Horno sapiens, clone IMAGE:4298026, mRNA, ESTs	3.2 3.2
23	451996	AW514021	Hs.245510	ESTs	3.2
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20	417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	3.2 3.2
30	414300 437834	A1304870 AA769294	Hs.188680 Hs.283854	eSTs gb:nz36g03.s1 NCL_CGAP_GCB1 Homo sapiens	3.2
	430694	AA810624	Hs.30936	ESTs, Weakly similar to H28H_HUMAN HISTO	3.2
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40	430809	AI791150	Hs.262009	ESTs, Moderately similar to I38022 hypot	3.2
40	445858	AL133811	U- 04027	solute carrier family 1 (glial high affi	3.2 3.2
	450692 439039	H50603 Al656707	Hs.94037 Hs.48713	hypothetical protein FLJ23053 ESTs	3.2
	401720		113.701 10	NM_014587°:Homo sapiens SRY (sex determi	3.2
	453740	AL120295	Hs.311809	ESTs, Moderately similar to PC4259 ferri	3.2
45	451032	W03692	Hs.323079	Homo sapiens mRNA; cDNA DKFZp564P116 (fr	3.2 3.2
•	413834	BE296896 R98299	Hs.224179 Hs.177502	ESTs, Wealthy similar to 138022 hypotheti ESTs	3.2
	438138 436338	W92147	Hs.118394	ESTs	3.2
	417169	R13550	Hs.246773	ESTs	3.2
50	424066	Z99348	Hs.112461	ESTs, Wealthy similar to I38022 hypotheti	3.2
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	415314 448475	N88802 BE613134	Hs.5422 Hs.247474	glycoprotein M6B hypothetical protein FLJ21032	3.2
	414699	AI815523	Hs.76930	synuclein, alpha (non A4 component of am	3.2
55	438549	BE386801	Hs.21858	trinucleotide repeat containing 3	3.2
	453896	AW293483	Hs.255205	KIAA1853 protein	3.2 3.1
	419539 428832	AF070590 AA578229	Hs.90869 Hs.324239	Homo sapiens clones 24622 and 24623 mRNA ESTs, Moderately similar to ZN91_HUMAN Z	3.1
	446636	AQ002563	Hs.15767	citron (rho-interacting, serine/threonin	3.1
60	429046	X57436	Hs.194772	oligodendrocyte myelin glycoprotein	3.1
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	413995	BE048146	Hs.75671 Hs.82572	syntaxin tA (brain) ESTs	3.1 3.1
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65	427712	AI368024	Hs.283696	ESTs	3.1
	406481			Target Exon	3.1
	453204	R10799	Hs.191990		3.1 3.1
	422890 422991	Z43784 H10940	Hs.48965	ankyrin 3, node of Ranvier (ankyrin G) Homo sapiens cDNA: FLJ21693 fis, clone C	3.1
70	421030	AW161357	113.40303	microtubule-associated protein tau	3.1
•	423603	AB007880	Hs.129883	Homo sapiens KIAA0420 mRNA, complete cds	3.1
	413985	AJ018666	Hs.75667	synaptophysin	3.1
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80	453324	W26592	Hs.232089	ESTs ob:HSC300041 normalized infant brain cDN	3.1 3.1
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	414884	R54418	Hs.183745	hypothetical protein FLJ13456	3.1
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                           AL 096711
               431431
                                                           GCN1 (general control of amino-acid synt
hypothetical protein FLJ20093
                                                                                                                                     3.0
  40
                           BE620886
              447881
                                                                                                                                     3.0
               454042
                           H22570
                                                                                                                                     3.0
                                                           ESTs, Weakly similar to JC5238 galactosy
                                            Hs 146589
                           AA984682
               429168
                                                                                                                                      3.0
                                            Hs.40568
                                                           ESTs
                           AA017410
               451391
                                                                                                                                     3.0
                           AW014022
                                            Hs.170953
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                                                                                                                                     3.0
3.0
  45
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                                            Hs.181451
                                                           ESTs
               430251
               420658
                            AW965215
                                            Hs.130707
                                                           ESTs
                                                                                                                                      3.0
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                           BE549773
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                                             Hs.40510
               454119
                                                                                                                                      3.0
                                             Hs.247324
                                                           mitochondrial ribosomal protein S14
               451018
                                                                                                                                      30
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                            R16814
                                             Hs.112062
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                                                            ADP-ribosylation factor domain protein 1
   50
               412494
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                                             Hs.792
                                            Hs.133483
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                                                                                                                                      3.0
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                            AL137326
                                                            KIAA1201 protein
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                                                                                                                                      3.0
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                                             Hs.145626
                                                            ESTs
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                                             Hs.7117
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                            AW590171
                                             Hs.101413
                                                            ĔŞTs
               446809
                                                                                                                                      3.0
                                                            similar to murine leucine-rich repeat or
                            AK001991
                                             Hs.3781
                434269
                                                                                                                                      3.0
                                                            paired box gene 6 (aniridia, keratitis)
                                             Hs.89506
               418951
                            F07809
                                                            hypothetical protein MGC1780
                            RF613280
                                             Hs.77550
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                                                                                                                                       3.0
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                Pkey:
CAT number:
    65
                                       Gene cluster number
                                       Genhank accession numbers
                             CAT Number
                                              AW954272 A1003154 AA059300 AA046911

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    70
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                             117647_1
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    75
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                 411565
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AW885592 AW885594 AW885579 AW885651
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                 412021
                                               AI267606 AA121045 AA126521
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                 412799
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                              132943 1
                 412811
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                 412820
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5	420352 421030	192979_1 19864_1	BE258835 AW968316 AA258918 AW843305 R14744 AI580388 BE071923 R36280 AW161357 AI879062 AI928938 AW161097 AW161167 BE314465 AA351715 F07096 AA179034 F08510 F00653 AI936671 AA476718 AW772454
,	421030	13004_1	AIB07703 R44253 AA976667 AI985186 AI650254 H38942 R84829 AA018724 AA001000 H85934 AA019126 H85609 AA017000 AA339355 AW950556
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			A1984613 A1934765 A1796172 AW157488 A1929191 R85523 D51221 D53851 H85610 A1749674 F21582 AA323145 AA019127 AA687444 T06745
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10			A1990023 A1935669 AW005821 AA324581 H17335 R37659 R42802 R46242 R60936 R59731 H28993 AA479907 R44570 A1890696 AA308884
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15			18/20/A356013 H10064 A1904/9 A050316 A060323 BE215003 BE046020 A196039/ A4605007 23503 F02003 226/34 F04/01 F10/F3/F10/F03
13	423476	22861_1	AL035633 F11794 F11783 H18042 T66089 H29379 R19493 AW134660 Al299437 AL133995 AA057405 N78357 AA917450 Al002692 T09262 T65008
	460410	22001_1	H29290 AJ200874 AA894415 AJ732887 AJ791768 AJ733447 AA988785 N62128 T09261 AW956936
	424009	234177_1	F11690 AW965370 AA333586 D30830
••	424572	24097_1	M19650 R18810 R18721 AW896146 AW889520 AA192362 AA176814 F12085 BE255264 BE251393 T65248 AA380585 AA380465 BE408684
20			AA459037 AW498869 AA776107 BE274289 D45269 M51958 AA378818 AW663180 AW672958 H08611 M78164 BE393721 AA348660 R36303
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25			AI217251 AA775807 BE390071 AA303517 AA001050 BE515169 N44066 AL133684 AI807085 AA808009 AA915914 F00007 AA019749 AL121560
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			R11203 AA019133 N94772 N71842 N29047 AA778138 AA554336 AA179865 N59453 T65212 AA054270 AW806630 AA533375 D13146 AA349487
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	429007	298301_1	AI085630 AA731340 D80642 AA443145 AL119015 AW904500
	429421	30431_1	AL031658 Al693758 AL040619 AW977914 AAB11957 AL352198 AW104364 AA648367 AA897604 AW341668 AL201382 AL040620
40	430183	31412_2	REDIOD38 AA676833 AI311783 T86895 W68032 BE064393 BE064394 BE157228 BE183282 AI936370 AA552514 T67280 AA039909
. •	430676	32168_1	AF084866 AF084870 AF084864 AF084867 AF084869 AF084865 AF084868 AW818206 AW812038 BE144813 BE144812 AW812041 AW812040
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	430968	326269_1	AW972830 AA527647 AA489820 AA570362
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65			T33623 A1222556 T33511 T33785 A1419606 D55612
	452454	918306_1	AW820480 AW820288 AI902522
	453739	979419_1	· · · · · · · · · · · · · · · · · · ·
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	45.44	4040040	F01659 Z38381 AA708886 AU81305 R53955 AAQ41432 W77787 AAV64037 AURG-1270 AURG-1267 AURG-1261 AURG-1261 7
	454171 455388	1049240_ 1287904_	
75	455646	1348557_	
	458912	823104_1	
	459079	888710_1	
80	TABLE 1		inique number corresponding to an Eos probeset
30	Pkey: Ret:	,	equence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et at." refers to the publication entitled "The DNA
	r vQ1.	5	equence of human chromosome 22" Dunham, et al. (1999) <u>Natura</u> 402:489-495.
	Strand:	b	dicates DNA strand from which exons were predicted.

	Alt nocition:	Indicate	s nucleatide po	sitions of predicted exons.	
	Nt_position:	_	-	a position	
				77132-277595	
5				3525-73644	
,				0745-71121	
				8374-98509	
				783-8468	
				13086-114800	
10	402604		Ptus 2	0393-20767	
10	402605		Minus 4	7680-47973	
	402855		Minus 5	9763-59909	
	403022	3132351	Plus 9	2097-92864	
	403142	9444521		9286-90131	
15	403341	8569175		0699-30910	
	403696	3135242		43457-143634	
	404120			35775-136000	
	404185			29171-129327	
20	404283			19460-99564 193455-193554	
20	404541			103456-103664 138651-139153	
	404584		P4	1500C 45200	
	404632	9796668	Plus Plus	16223_16319_16427_16513.16736-16859.16941-1707	5,17170-17287,17389-17529,18261-18357,18443-18578
	404819	4678240 7249119		51728-51836	
25	405238 405239	7249119	Plus	144345-144464,144690-144836,151750-151883,1524	107-152484
25	405233	2914717		43310-43462	
	405819	4007557		2830-2967	
	406481	9864741		91439-91579	
	100.0.				•
30				TO NOT THE REPORT OF THE PERSON OF THE PERSO	DOMAL CENTRAL NERVOUS SYSTEM
				EGULATED IN GLIOBLASTOMA COMPARED TO NO	
	Table 14A	lists about 1111	genes up-regu	ated in glioblastonia cumpareu w normal central nov	as greater than or equal to 2.5. The "average" glioblastoma level was set to the 85th
25	percentile	amongst various	brain tumois.	the 108 compatible value amongst various 600-0	adignant tissues was subtracted from both the numerator and the denominator before
35	backgrour	nd levels of non-s	pecinc nyonaiz	audit, the to-percental value attempt values to	
		ras evaluated.	io Ens nimbese	t identifier number	
	Pkey: ExAcon:	Even	ntar Accession	number, Genbank accession number	
	Unigeneil		ene number		
40	Unigene 1		ene gene title		
	R1:		of GLIOBLAS	TOMA to CNS	
					R1
	Pkey	ExAccn	UnigenelD	Unigene Title	32.8
	422737	M26939	Hs.119571	collagen, type III, alpha 1 (Ehlers-Dani	28.0
45	423961	D13666	Hs.136348	periostin (OSF-20s)	25.3
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	24.3
	414555	N98569	Hs.76422	phospholipase A2, group IIA (platelets,	22.6
	424800	AL035588	Hs.153203	MyoD family inhibitor KIAA0101 gene product	22.2
50	417308	H60720	Hs.81892 Hs.58446	ESTs	20.7
50	449539	W80363	Hs.32964	SRY (sex determining region Y)-box 11	18.7
	453392	U23752 X06370	Hs.77432	epidermal growth factor receptor (avian	18.6
	414825 444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	17.2
	412420	AL035668	Hs.73853	bone morphogenetic protein 2	16.7
55	417130	AW276858	Hs.81256	\$100 calcium-binding protein A4 (calcium	16.7
"	414217	Al309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	14.3
	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone CO	14.3
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	14.1
	446584	U53445	Hs.15432	downregulated in ovarian cancer 1	13.9 13.6
60	422672	X12784	Hs.119129	collagen, type IV, alpha 1	13.6
	402604			Target Exon	13.0
	424635	AA420687	Hs.115455	Homo sapiens cDNA FLJ14259 fis, clone PL	12.9
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin, chromosome 8 open reading frame 4	12.5
65	434078	AW880709	Hs.283683	enhancer of zeste (Drosophila) homolog 2	12.4
65	414761	AU077228	Hs.77256	hypothetical protein FLJ23468	12.2
	442432		Hs.38178 Hs.127792	The state of the s	12.1
	456759 409638		Hs.21335	ESTs	11.5
	441269		Hs.178784		10.5
70	435020		Hs.301855		10.5
, ,	422163		Hs.112360		10.1
	444969		Hs.160628	ESTs	10.1
	430132		Hs.234149	hypothetical protein FLJ20647	9.9
	433437		Hs.3280	caspase 6, apoptosis-related cysteine pr	9.4
75	445101		Hs.12314	Homo sapiens mRNA; cDNA DKFZp586C1019 (I	9.2
	41392	BE501689	Hs.75617	collagen, type IV, alpha 2	9.1 0.1
	425187			ESTs	9.1 8.9
	44972		Hs.23960	cyclin B1	8.9
00	44961		Hs.19707		8.9
80			Hs.2250	teukemia inhibitory factor (cholinergic Homo sapiens cDNA: FLJ23241 fis, clone C	8.9
	41923		Hs.18459 Hs.14541		8.8
	44373		NS. 1434 N	NM_001839*:Homo sapiens calponin 3, acid	8.7
	40285	•			0
				22	u

	447242	Al199268	Lin 10330	Harman State City to DWCN aCttl 2010	0.0
	447342 410102	AW248508	Hs.19322 Hs.279727	Homo sapiens, Simitar to RIKEN cONA 2010 ESTs; homologue of PEM-3 [Ciona savignyi	8.6 8.5
	420602	AF060877	Hs.99236	regulator of G-protein signalling 20	8.4
	417426	NM_002291	Hs.82124	taminin, beta 1	8.4
5	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	8.3
	417061	A1675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	8.1
	409451	AA382169	Hs.54483	N-myc (and STAT) interactor	8.1
	414622	AJ752666	Hs.76669	nicotinamide N-methyltransferase	8.1
10	430691	C14187	Hs.103538	ESTs	8.0
10	447725	AL137638	Hs.19368	matriin 2	8.0
	417043 447004	NM_004369 AW296968	Hs.80988 Hs.157539	collagen, type VI, alpha 3 ESTs	7.9 7.9
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	7.8
	426075	AW513691	Hs.270149	ESTs, Wealdy similar to 2109260A B cell	7.8
15	419938	AU076772	Hs.1279	complement component 1, r subcomponent	7.7
	419508	AW997938	Hs.90786	ATP-binding cassette, sub-family C (CFTR	7.7
	411411	AA345241	Hs.55950	ESTs, Weakly similar to KIAA1330 protein	7.5
	436291	BE568452	Hs.344037	protein regulator of cytokinesis 1	7.5
20	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	7.5
20	406972	M32053	At- 0720	gb:Human H19 RNA gene, complete cds.	7.4
	442802 427581	AL133035 NM_014788	Hs.8728 Hs.179703	hypothetical protein DKFZp434G171 KIAA0129 gene product	7.4 7.3
	409142	AL136877	Hs.50758	SMC4 (structural maintenance of chromoso	7.3 7.3
	409902	Al337658	Hs.156351	ESTs	7.3
25	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	7.2
	449961	AW265634	Hs.133100	ESTs	7.2
	418203	X54942	Hs.83758	CDC28 protein kinase 2	7.2
	424840	D79987	Hs.153479	extra spindle potes, S. cerevisiae, homo	7.2
30	428728	NM_016625	Hs.191381	hypothetical protein	7.1
30	429183 439451	AB014604 AF086270	Hs.197955	KIAA0704 protein	7.1 7.1
	422106	D84239	Hs.278554 Hs.111732	heterochromatin-like protein 1 Fc tragment of IgG binding protein	7.0
	406850	AI624300	Hs.172928	collagen, type I, alpha 1	7.0
	453941	U39817	Hs.36820	Bloom syndrome	6.9
35	425234	AW152225	Hs.165909	ESTs, Wealdy similar to 138022 hypotheti	6.9
	421977	W94197	Hs.110165	ribosomai protein L26 homotog	6.8
	411078	AI222020	Hs.182364	CocoaCrisp	6.7
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	6.7
40	448769	N66037	Hs.38173	ESTs	6.7
40	418400	BE243026	Hs.301989	KIAA0246 protein	6.6
	408161 440210	AW952912 AW674562	Hs.300383 Hs.125296	hypothetical protein MGC3032 ESTs	6.6 6.6
	437036	A1571514	Hs.133022	ESTs	6.6
	411968	AJ207410	Hs.69280	Homo sapiens, clone IMAGE:3636299, mRNA,	6.6
45	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	6.6
	449300	AI656959	Hs.346514	ESTs	6.5
	440052	AI633744	Hs.195648	ESTs, Weakly similar to 138022 hypotheti	6.5
	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	6.5
50	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	6.5
30	452451	N78223	Hs.108106	transcription factor	6.5 6.5
	408243 424954	Y00787 NM_000546	Hs.624 Hs.1846	interleukin 8 tumor protein p53 (Li-Fraumeni syndrome)	6.4
	450375	AA009647	113.1040	e disintegrin and metalloproteinase doma	6.4
	406478			Target Exon	6.4
55	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	6.4
	439710	AF086543		gb:Homo sapiens full length insert cDNA	6.4
	458814	AI498957	Hs.170861	ESTs, Wealdy similar to Z195_HUMAN ZINC	6.4
	410276	AI554545	Hs.68301	anglopoietin-2	6.4
60	425289 427871	AW139342 AW992405	Hs.155530 Hs.59622	interferon, gamma-inducible protein 16 Homo sapiens, clone IMAGE:3507281, mRNA,	6.3 6.3
	436895	AF037335	Hs.5338	carbonic anhydrase XII	6.3
	447458	AI741082	Hs.158961	ESTs	6.3
	447439	AA313565	Hs.145020	ESTs, Weakly similar to KIAA1205 protein	6.3
65	413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	6.3
65	449969	AW295142	Hs.180187	Homo sapiens cDNA FLJ14337 fis, clone PL	6.2
	440704	M69241	Hs.162	insulin-like growth factor binding prote	6.2
	400419	AF084545	11. 77576	Target	6.2
	412140 409731	AA219691 AA125985	Hs.73625 Hs.56145	RAB6 interacting, kinesin-like (rabkines thymosin, beta, identified in neuroblast	6.2 6.2
70	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	6.2
	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	6.1
	430630	AW269920	Hs.2621	cystatin A (stefin A)	6.0
	410064	X53416	Hs.195464	filamin A, alpha (actin-binding protein-	6.0
75	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	6.0
75	413627	BE182082	Hs.246973		6.0
	413063	AL035737	Hs.75184	chilinase 3-like 1 (cartilage glycoprote	5.9
	421899 407182	AJ011895 AA312551	Hs.109281 Hs.230157	Nef-associated factor 1 ESTs	5.9 5.9
	410286	AI739159	Hs.61898	DKFZP586N2124 protein	5.9
80	409829	M33552	Hs.56729	lymphocyte-specific protein 1	5.9
	446657	AI335191	Hs.260702	ESTs, Weakly similar to 2109260A B cell	5.8
	418097	R45137	Hs.21868	ESTs	5.8
	428450	NM_014791	Hs.184339	KIAA0175 gene product	5.8

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					5.7
				biquitin carrier protein E2-C :STs	5.7
	421988 422283			CDC45 (cell division cycle 45, S.cerevis	5.7
_	416111	AA033813	Hs.79018 (thromatin assembly factor 1, subunit A (5.7 5.7
5	434846			ESTs Homo sapiens cione 24651 mRNA sequence	5.7
	412567 452372			ESTs	5.6
	443247			c-Myc target JPO1	5.6
	423198	M81933		cell division cycle 25A	5.6 5.6
10	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-4 gb:ny91c01.s1 NCI_CGAP_GC81 Homo sapiens	5.6
	437034 429447	AA742643 AW812452	Hs.83286	ESTs, Weakly similar to S14747 sphingomy	5.6
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	5.6 5.6
1.5	437695	AA769202		ESTs collagen, type I, alpha 1	5.6
15	426935 453361	NM_000088 AA035197		ESTs	5.5
	418293	AI224483	Hs.16063	hypothetical protein FLJ21877	5.5
	405348			C7001664:gij12698061 dbj BAB21849.1 (AB	5.5 5.4
20	458079	AI796870	Hs.54277 Hs.213786	DNA segment on chromosome X (unique) 992 ESTs	5.4
20	452799 448935	A1948829 AL078596	Hs.22591	nuclear receptor subfamily 2, group E, m	5.4
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	5.4 5.4
	442547	AA306997	Hs.217484	ESTs, Weakly similar to ALU1_HUMAN ALU S gb:HSC300041 normalized infant brain cDN	5.4
25	424009 440332	F11690 Al218517	Hs.188051	ESTs	5.4
23	422094	AF129535	Hs.272027	F-box only protein 5	5.4
	443884	N20617	Hs.194397	leptin receptor	5.4 5.4
	422493	AW474183	Hs.250173 Hs.287820	hypothetical protein FLJ13158 fibronecfin 1	5.4
30	432731 426108	R31178 AA622037	Hs.166468	programmed cell death 5	5.3
50	407624	AW157431	Hs.248941	ESTS	5.3 5.3
•	411048	AK001742	Hs.67991	hypothetical protein DKFZp434G0522 endothetial cell growth factor 1 (platel	5.3
	412471 414020	M63193 NM_002984	Hs.73946 Hs.75703	small inducible cytokine A4 (homologous	5.2
35	414774	X02419	Hs.77274	plasminogen activator, urokinase	5.2 5.2
-	413786	AW613780	Hs.13500	ESTs	5.2 5.2
	454860	AW835767	Hs.89230	gb:QV4-LT0016-240200-110-b08 LT0016 Homo potassium intermediate/small conductance	5.2
	428037 420311	N47474 AW445044	Hs.38207	Human DNA sequence from clone RP4-530(15	5.1
40	416737	AF154335	Hs.79691	LIM domain protein	5.1 5.1
	445837	AI261700	Hs.145544	ESTs absent in melanoma 1	5.1
	425882 415682	U83115 Al347128	Hs.161002 Hs.191870	ESTs	5.1
	414053	BE391635	Hs.75725	transgelin 2	5.1 5.1
45	453884	AA355925	Hs.36232	KIAA0186 gene product	5,1
	431512	BE270734 AW301003	Hs.2795 Hs.51483	lactate dehydrogenase A ESTs, Wealdy similar to hypothetical pro	5.0
	432593 433323	AA805132	Hs.159142	ESTs	5.0
	443744	A1084326	Hs.271548		5.0 5.0
50	410434	AF051152	Hs.63668 Hs.94376	toll-like receptor 2 proprotein convertase subtilisin/kexin t	5.0
	420018 419485	U56387 AA489023	Hs.99807	ESTs, Weakly similar to unnamed protein	4.9
	446131	NM_000929	Hs.290	phospholipase A2, group V	4.9 4.9
55	412777	Al335773	Hs.270123	ESTs hypothetical protein FLJ 10983	4.9
55	449246 433244	AW411209 AB040943	Hs.23363 Hs.271285		4.9
	407235		Hs.169407		4.9 4.9
	445118		Hs.345572	ESTs pleckstrin homology-like domain, family	4.9
60	417404 420092		0 Hs.82101 Hs.88045	ESTs	4.9
UU	412811			ESTs	4.9
	436607	AW661783			4.9 4.9
	438456		Hs.20594 Hs.9930	ESTs serine (or cysteine) proteinase inhibito	4.9
65	443883 431553		Hs.2799	cartilage linking protein 1	4.9
05	439999		Hs.6838	ras homolog gene family, member E	4.9 4.9
	411252				4.8
	444381 429433				4.8
70	403349			ephrin-83	4.8
	40227	4		C19000498*:gi 4567179 gb AAD23607.1 AC00	4.8 4.8
	42604		Hs.17029 Hs.31035		4.8
	42360 42590			4 novel C3HC4 type Zinc finger (ring finge	4.8
75	43111	7 AF003522	Hs.25050	0 delta (Drosophila)-like 1	4.8 4.7
	41805				4.7
	44170 43962			hypothetical protein FLJ21841	4.7
	44590	0 AF070526	Hs.1250	Homo sapiens clone 24787 mRNA sequence	4.7 4.7
80	43593	7 AA83089	3 Hs.1197	59 ESTs Target Exon	4.7 4.7
	40396 40786		7 Hs.3379		4.6
	40852				4.6

	403481			Tomat Case	4.6
	423529	T87318	Hs.120411	Target Exon ESTs	4.6
	416847	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do	4.6
5	453362	H14988	Hs.107375	ESTs	4.6
3	407013 423757	U35637 AL049337	Hs.132571	gb:Human nebulin mRNA, partial cds Homo sapiens mRNA; cDNA DKFZp564P016 (fr	4.6 4.6
	432363	AA534489	110.102011	gb:nf76g11.s1 NCI_CGAP_Co3 Homo sapiens	4.6
	408380	AF123050	Hs.44532	diubiquilin	4.6
10	429149	AW193360	Hs.197962 Hs.112432	ESTs, Weakly similar to 138022 hypotheti	4.6 4.6
10	422170 405558	A1791949	FIS.112432	anti-Mullarian hormone Target Exon	4.6
	410295	AA741357	Hs.5174	nidogen (enactin)	4.6
	450166	AA429504		ESTs	4.6
15	451418 420075	BE387790 AF142482	Hs.26369 Hs.203846	hypothetical protein FLJ20287 TEA domain family member 3	4.5 4.5
15	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	4.5
	457465	AW301344	Hs.122908	DNA replication factor	4.5
	436827	H72187	Hs.5322	guanine nucleotide binding protein (G pr	4.5
20	452620 424381	AA436504 AA285249	Hs.119286 Hs.146329	ESTs protein kinase Chk2	4.5 4.5
20	444656	A1277924	Hs.145199	ESTs	4.5
	450639	AJ703186	Hs.277174	ESTs	4.5
	424247	X14008	Hs.234734	lysozyme (renal amyloidosis) Homo sapiens mRNA; cDNA DKFZp564C142 (fr	4.5 4.5
25	423178 447072	AI033140 D61594	Hs.124983 Hs.17279	tyrosytprotein sufforansferase 1	4.5
	447444	AK000318	Hs.18616	hypothetical protein FLJ20311	4.4
	401454			NM_014226":Homo sapiens renal tumor anti	4.4
	420560 409205	AW207748 AI952884	Hs.59115 Hs.14832	ESTs Moderately similar to unnamed prot	4.4 4.4
30	451129	BE072881	ri3,14032	gb:RC2-8T0548-200300-012-e09 BT0548 Homo	4.4
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	4.4
	447752	M73700	Hs.105938	lactotransferrin	4.4
	429083 418283	Y09397 S79895	Hs.227817 Hs.83942	BCL2-related protein A1 cathepsin K (pycnodysostosis)	4.4 4.3
35	424736	AF230877	Hs.152701	microtubule-interacting protein that ass	4.3
	416379	N38857	Hs.203933	ESTs	4.3
	452994	AW962597	Hs.31305	KIAA1547 protein	4.3
	437834 441035	AA769294 AI694309	Hs.283854 Hs.126458	gb:nz35g03.s1 NCI_CGAP_GCB1 Homo sapiens ESTs	4.3 4.3
40	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	4.3
	418030	BE207573	Hs.83321	neuromedin B	4.3
	450811 438458	AI739486 AW975186	Hs.245497	ESTs gb:EST387294 MAGE resequences, MAGN Homo	4.3 4.3
	442201	AW515704	Hs.208726	ESTs	4.3
45	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	4.3
	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	4.3
	442832 449318	AW206560 AW236021	Hs.253569 Hs.78531	ESTs Homo sapiens, Similar to RIKEN cDNA 5730	4.3 4.2
	421027	AA761198	Hs.55254	ESTs	4.2
50	414300	AI304870	Hs.188680	ESTs	4.2
	452874 444161	AK001061 N52543	Hs.30925 Hs.142940	hypothetical protein FLJ10199	4.2 4.2
	416908	AA333990	Hs.80424	ESTs coagulation factor XIII, A1 polypeptide	4.2
	418483	W26076	Hs.221847	ESTs	4.2
55	443318	AI051603	Hs.133141	ESTs	4.2
	415079 416871	R43179 H98716	Hs.22895	hypothetical protein FLJ23548 gb:yx13d08.s1 Soares melanocyte 2NbHM Ho	4.2 4.2
	423678	AW963357	Hs.7847	ESTs	4.2
60	429643	AA455889	Hs.167279	FYVE-finger-containing Rab5 effector pro	4.2
60	438875 428600	AA827640 AW863261	Hs.189059 Hs.242413	ESTs hypothetical protein DKFZp434K1421	4.2 4.2
	430968	AW972830	rt5.242413	gb:EST384925 MAGE resequences, MAGL Horno	4.2
	406872	A1760903		gb:wi09h08.x1 NCI_CGAP_CLL1 Homo sapiens	4.2
65	403790	05010071		NM_001334*:Homo sapiens cathepsin O (CTS	4.1
U3	409112 435703	BE243971 AW630133	Hs.50649 Hs.83313	quinone oxidoreductase homolog GK003 protein	4.1 4.1
	432625	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	4.1
	404407			Target Exon	4.1
70	412568	A1878826 X58968	Hs.74034 Hs.111301	caveolin 1, caveolae protein, 22kD matrix metalloproteinase 2 (gelatinase A	4,1 4,1
,,	422087 435143	R12375	Hs.194600		4.1
	447497	AW167254	Hs.205722	ESTs	4.1
	456304	AI820973		gb:nc21c02.y5 NCI_CGAP_Pr1 Homo sapiens	4.1
75	427676 436608	AA394062 AA628980	Hs.300772	tropomyosin 2 (beta) down syndrome critical region protein DS	4,1 4,1
, ,	453331	AA62656U AI240665		ESTs	4.0
	420004	AW975532	Hs.164039	ESTs, Moderately similar to 138022 hypot	4.0
	412125	Y17114	Hs.73393	eyes absent (Orosophila) homolog 4	4.0
80	426215 407603	AW963419 AW955705	Hs.155223 Hs.62604	stanniocalcin 2 Homo sapiens, clone IMAGE:4299322, mRNA,	4.0 4.0
- •	450581	AF081513	Hs.25195	TGF-beta 4	4.0
	415323	BE269352	Hs.949	neutrophil cytosolic factor 2 (65kD, chr	4.0
	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	4.0

					4.0
	432058			ESTs, Weakly similar to ALU1_HUMAN ALU S	4.0
				ESTs ESTs	4.0
			HS.202300 HS.135474	ESTs, Weakly similar to DDX9_HUMAN ATP-D	4.0
5				ESTs	4.0
•		AA687376		ESTs	4.0 4.0
				ESTs	4.0
	4100.		Hs.200266 Hs.111460	ESTs calcium/calmodulin-dependent protein kin	4.0
10	433556 458946	W56321 AA009716	Hs.42311	ESTs	4.0
10	449655	AI021987	Hs.59970	ESTS	4.0 4.0
	426649	AI914936	Hs.97152	ESTs	4.0
	457292	AI921270	Hs.281462	hypothetical protein FLJ14251 transcription factor NYD-sp10	4.0
15	440435	AL042201 AK000252	Hs.21273 Hs.169758	hypothetical protein FLJ20245	4.0
13	456977 420649	AR000232 AI866964	Hs.124704	ESTs, Moderately similar to S65657 alpha	4.0
	416406	D86961	Hs.79299	lipoma HMGIC fusion partner-like 2	4.0 3.9
	446291	BE397753	Hs.14623	interferon, gamma-inducible protein 30	3.9
20	449256	AA059050	Hs.59847 Hs.106300	ESTs Homo sapiens clone 23556 mRNA sequence	3.9
20	421637	AF035290 AA225313	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	3.9
	456306 438372	AI140189	Hs.123191	ESTs	3.9
	427375	AL035460	Hs.177536	metallocarboxypeptidase CPX-1	3.9 3.9
	415131	D61119		gb:HUM158C11B Clontech human fetal brain Homo sapiens mRNA; cDNA DKFZp434N079 (fr	3.9
25	439231	AW581935	Hs.141480 Hs.154138	chitinase 3-like 2	3.9
	424998 433376	U58515 Al249361	Hs.74122	casnasa 4. apoptosis-related cysteine pr	3.9
	455104	BE064863	,	gb:RC1-BT0313-110300-015-f06 BT0313 Homo	3.9 3.9
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	3.9
30	419594	AA013051	Hs.91417	topoisomerase (DNA) Il binding protein phosphoribosylghycinamide formyltransfer	3.9
	417576	AA339449 AA188775	Hs.82285 Hs.292453	ESTs	3.9
	416857 434784	AA649051	Hs.164007	ESTs	3.8
	438898	AI819863	Hs.106243	ESTs	3.8 3.8
35	408102	U46351	Hs.621	tectin, galactoside-binding, soluble, 3	3.8
	422081	AW136820	Hs.196011	ESTs gb:EST365510 MAGE resequences, MAGB Homo	3.8
	411688 447343	AW953440 AA256641	Hs.236894		3.8
	406395	707250041		Target Exon	3.8 3.8
40	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	3.8
	403696		11. 04000	C4001100":gij5852342 gb AAD54015.1 (AF0	3.8
	443740	R56434 U10564	Hs.21062 Hs.75188	ESTs wee1 (S. pombe) homolog	3.8
	413076 409189	AA125984	15.73100	gb:zn27h06.r1 Stratagene neuroepithelium	3.8
45	444326	AI939357	Hs.270710	ESTs .	3.8 3.8
	436899	AA764852	Hs.291567		3.8
	445075	Al651827	Hs.344767 Hs.80409	P ESTs growth arrest and DNA-damage-inducible,	3.8
	416892 429163	L24498 AA884766	115.00403	gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	3.8
50	416114	Al695549	Hs.18386	B glucuronidase, beta	3.8 3.8
• •	417018	M16038	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related	3.8
	446839	BE091926	Hs.16244 Hs.40368		3.8
	454117 416664	BE410100 H72780	Hs.20289	ESTs	3.8
55	449444			solute carrier family 16 (monocarboxylic	3.8 3.8
•	419735				3.7
	448275		Hs.20830	kinesin-lika 2 zinc finger protein 200	3.7
	405141 411537			gb:MR0-BT0551-060300-102-e05 BT0551 Homo	3.7
60	422648		Hs.11889		3.7 3.7
•	449145		Hs.1984		3.7
	428060		Hs.2494	33 ESTs Target Exon	3.7
	404584		1 Hs.2933	77 FSTs	3.7
65	418596 458072		Hs.2719	23 Homo sapiens cONA: FLJ22785 fis, clone K	3.7
05	445908		Hs.1343	6 Homo sapiens clone 24425 mRNA sequence	3.7 3.7
	439979				3.7
	431770) Hs.2685 Hs.1808		3.7
70	42780 43667			18 low molecular mass ubiquinone-binding pr	3.7
, 0	41345		Hs.7537	2 N.acetvinalactosaminidase, alpha-	3.7 3.7
	43446	7 BE55236			3.7
	44804				3.7
75	42279 40208		Hs.345	C18000743*:gij6678363 ref NP_033416.1 t	3.7
, ,	44801		34 Hs.195	541 ESTs, Moderately similar to 138022 hypot	3.7 3.7
	42887	3 AJ701609	Hs.989	D8 ESTs	3.7
	43732	23 AA37114			3.7
80	41309				3.7
60	42513 45227				3.7
	4395	74 A146978I	B Hs.165	190 ESTs	3.7 3.7
	4088		042 Hs.483		3.7
				222	

	407838	BE146411	Hs.40342	putative nuclear protein	3.7
	437748	AF234882	Hs.5814	suppression of turnorigenicity 7	3.6
	437470	AL390147	Hs.134742	hypothetical protein DKFZpS47D065	3.6
•	400288	X06256	Hs.149609	integrin, alpha 5 (fibronectin receptor,	3.6
5	453438	AH69935	Hs.22792	ESTS	3.6
	415024 419713	AI983981 AW968058	Hs.189114 Hs.92381	ESTs nudix (nucleoside diphosphate linked moi	3.6 3.6
	441523	AW514263	Hs.301771	ESTs, Wealthy similar to ALUF_HUMAN !!!!	3.6
	416427	BE244050	Hs.79307	Rac/Cdc42 guanine exchange factor (GEF)	3.6
10	448002	Y15227	Hs.20149	deteted in lymphocytic teukemia, 1	3.6
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	3.6
	456534	X91195	Hs.100623	phospholipase C, beta 3, neighbor pseudo	3.6
	402239			Target Exon	3.6
15	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	3.6 3.6
13	443715 403011	AI583187	Hs.9700	cyclin E1 ENSP00000215330*:Probable serine/threoni	3.6
	428403	AI393048	Hs.326159	leucine rich repeat (in FUI) interactin	3.6
	425202	AW962282	Hs.152049	ESTs, Weakly similar to I38022 hypotheti	3.6
	409557	BE182896	Hs.211193	ESTs	3.6
20	453948	Al970797	Hs.64859	ESTs	3.6
	440225	BE295782	Hs.159	tumor necrosis factor receptor superfami	3.6
	425331	AW962128	15-404042	gb:EST374201 MAGE resequences, MAGG Homo	3.6
	442326 437640	H92962 AA764893	Hs.124813 Hs.272155	hypothetical protein MGC14817 ESTs, Weakly similar to (38022 hypotheti	3.6 3.6
25	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	3.6
	406481	72710200	12.130111	Target Exon	3.6
	433835	AI806185		gb:wf26a10.x1 Soares_NFL_T_GBC_S1 Homo s	3.6
	456052	BE311901	Hs.28935	gb:601142614F1 NIH_MGC_14 Homo sapiens c	3.6
20	453857	AL080235	Hs.35861	DKFZP586E1621 protein	3.5
30	439726	AW449893	Hs.293707	ESTs, Weakly similar to 138598 zinc fing	3.5
	416913	AW934714	U- 00004	gb:RC1-DT0001-031299-011-a11 DT0001 Homo	3.5
	419402	268155	Hs.90291	laminin, beta 2 (laminin S) ENSP00000241415":Hypothetical 67.7 kDa p	3.5 3.5
	403108 426509	M31166	Hs.2050	pentaxin-related gene, rapidly induced b	3.5
35	418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	3.5
	432188	Al362952	Hs.2928	solute carrier family 7 (cationic amino	3.5
	448789	BE539108	Hs.22051	hypothetical protein MGC15548	3.5
	427299	AA830210	Hs.214263	ESTs, Moderately similar to ALU1_HUMAN A	3.5
40	425212	AW962253	Hs.171618	ESTs	3.5
40	422938	NM_001809	Hs.1594	centromere protein A (17kD)	3.5 3.5
	442264 407253	AI278777 AA411175	Hs.263455 Hs.141939	ESTs, Weakly similar to ALU1_HUMAN ALU S ESTs, Moderately similar to S65657 alpha	3.5
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	3.5
	452682	AA456193	Hs.9071	progesterone membrane binding protein	3.5
45	421247	BE391727	Hs.102910	general transcription factor IIH, polype	3.5
	418049	AA211467	Hs.190488	Homo sapiens, Similar to nuclear localiz	3.5
	453792	AL134539	Hs.254129	KIAA1678	3.5
	416426	AA180256	Hs.210473	Homo sapiens cDNA FLJ14872 fis, clone PL	3.5 3.5
50	412014 440370	A1620650 AA884000	Hs.43761 Hs.8173	ESTs, Weakly similar to A46010 X-linked hypothetical protein FLJ 10803	3.5
50	407729	T40707	Hs.270862	ESTs	3.5
	438527	AI969251	Hs.115325	RAB7, member RAS oncogene family-like 1	3.5
	455646	BE064420		gb:RC4-BT0311-241199-012-c08 BT0311 Homo	3.5
e e	418630	Al351311	Hs.251946	poly(A)-binding protein, cytoplasmic 1-l	3.5
55	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.5
	424503	NM_002205	Hs.149609 Hs.263024	integrin, alpha 5 (fibronectin receptor, ESTs	3.4 3.4
	449932 427700	A1675444 AA262294	Hs.180383	dual specificity phosphatase 6	3.4
	403849	74401254	113.100000	Target Exon	3.4
60	429747	M87507	Hs.2490	caspase 1, apoptosis-related cysteine pr	3.4
	451446	AI826288	Hs.171637	hypothetical protein MGC2628	3.4
	434589	AF147363		gb:Homo sapiens full length insert cDNA	3.4
	403361	41606064	11-04003	NM_002210°:Homo sapiens Integrin, alpha	3.4 3.4
65	420841 438206	AI625251 AA780385	Hs.94037 Hs.187885	hypothetical protein FLJ23053 ESTs	3.4
Ų,	425295	AA431366	Hs.37251	ESTs	3.4
	411789	AF245505	Hs.72157	Adlican	3.4
	440948	AW188311	Hs.128619	ESTs	3.4
3 0	439518	W76326		gb:zd60d04.r1 Soares_fetal_heart_NbHH19W	3.4
70	418821	AA436002	Hs.183161		3.4
	459660	M79082		ESTs	3.4 3.4
	404209 443950	NM_001425	Hs.9999	Yarget Exon epithelial membrane protein 3	3.4
	430694	AA810624	Hs.30936	ESTs, Weakly similar to H2BH_HUMAN HISTO	3.4
75	425300	AW601773	Hs.270259		3.4
-	420300	AA258245	Hs.127573	Homo sapiens FKSG41 (FKSG41) mRNA, compl	3.4
	458438	Al141520	Hs.151464		3.4
	444911	U06117	Hs.250	xanthene dehydrogenase	3.4
80	421064	A1245432	Hs.101382		3.4 3.4
ou	441287 446960	AW293132 AW294936	Hs.131373 Hs.156762		3.4
	405605	H11201300	1-0-100102	C2001342:gij127814 sp[P26434 MAH4_RAT SO	3.4
	433791	AA719352	Hs.112718		3.4

					3.4
	405238		T 25440	arget Exon	3.4
		X81120 H AA143654	4s.75110 c	annabinoid receptor 1 (brain) b:2065a02.r1 Stratagene pancreas (93720	3.4
			Hs.11090 r	nembrane-spanning 4-domains, subfamily A	3.4
5				ibosomal protein S2	3.4 3.4
-				STS MCC3M0	3.4
			Hs.280740 Hs.45184	rypothetical protein MGC3040 Homo sapiens cDNA FLJ12284 fis, clone MA	3.4
	456060 435005		Hs.306094	rinucleotide repeat containing 12	3.4
10	421674		Hs.296355	hypothetical protein FLJ23138	3.4
•	425242	D13635	Hs.155287	KIAA0010 gene product	3.4 3.4
	436805		Hs.270751	ESTs a disintegrin and metalloproteinase doma	3.4
	418641		Hs.86947 Hs.262009	ESTs, Moderately similar to I38022 hypot	3.4
15	430809 428878			ESTs	3.3
13	413774	AA131782	He 182314	ESTs	3.3 3.3
	400533			ENSP00000209376*:PRED65 protein (Fragmen	3.3
	422448	AW372922	Hs.116774 Hs.135150	integrin, alpha 1 lung type-I cell membrane-associated gly	3.3
20	423905 430637	AW579960 BE160081	Hs.256290	S100 calcium-binding protein A11 (calgiz	3.3
20	427899	AA829286	Hs.332053	serum amyloid A1	3.3
	434206	AW136973	Hs.180479	ESTs, Wealdy similar to S69890 mitogen i	3.3 3.3
	453387	AI990741	Hs.252809	ESTs	3.3
25	436265	AA731331 AA889628	Hs.190668 Hs.35125	ESTs ESTs	3.3
25	412971 441701	AW339828	Hs.127497	ESTs	3.3
	418967	NM_001725	Hs.89535	bactericidal/permeability-increasing pro	3.3 3.3
	434577	R37316	Hs.179769	Homo sapiens cDNA: FLJ22487 fis, clone H	3.3
20	418216	AA662240	Hs.283099 Hs.133512	AF15q14 protein ESTs	3.3
30	436137 428715	AI056769 AW293716	Hs.53126	ESTs	3.3
	449249	T52285	Hs.193115	Homo sapiens mRNA for KIAA1764 protein,	3.3 3.3
	440074	AA863045	Hs.10669	ESTs, Weakly similar to T00050 hypotheti	3.3 3.3
25	405046		Hs.280699	C3000978:gij9280045 dbj BAB01579.1 (AB0 ESTs	3.3
35	437816 401272	AI823445	HS.200033	C9000559*:gi[12314195]emb[CAB99338.1] (A	3.3
•	408896	AI610447	Hs.48778	niban protein	3.3 3.3
	432343	NM_002960	Hs.2961	S100 catcium-binding protein A3	3.3 3.3
40	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot Homo sapiens cDNA FLJ11477 fis, clone HE	3.3
40	439978	BE139460 AW978202	Hs.124673 Hs.289064	hypothetical protein FLJ22251	3.3
	421094 428722	U76456	Hs.190787	tissue inhibitor of metalloproteinase 4	3.3
	446134	AW161234	Hs.13993	TBP-like 1	3.3 3.3
	412281	AI810054	Hs.14119	ESTs ESTs, Moderately similar to ALU1_HUMAN A	3.3
45	436282	R91913	Hs.272104	transporter 1, ATP-binding cassette, sub	3.3
	452203 421307	X57522 BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f	3.3
	409463	AI458165	Hs.17296	hynothetical protein MGC2376	3.3 3.3
	411565	AW851728		gb:MR2-CT0222-011199-007-d06 CT0222 Homo Homo sapiens, clone MGC:15203, mRNA, com	3.3
50	410422	AL042014	Hs.63348	fibroblast activation protein, alpha	3.3
	450506 451254	NM_004460 AI571016	Hs.172967	FSTs	3.3
	423784	AK000039	Hs.132826		3.3 3.3
	433325	AW206986	Hs.143905	ESTs gb:HSZ99362 DKFZphamy1 Homo sapiens cDNA	3.3 3.3
55	419896	Z99362	Hs.98806	hypothetical protein	3.3
	420552 451778		Hs.62954	ESTs. Weakly similar to zinc finger prot	3.3
	427584		Hs.179718		3.2 3.2
	433507	AI817336	Hs.191791	ESTs	3.2
60	418661		Hs.1189 Hs.14287	E2F transcription factor 3 FSTs	3.2
	440933 426746		Hs.2057	uridine monophosphate synthetase (orotat	3.2
	404120			C5000537*:gi 3298595 gb AAC41376.1 (AF0	3.2 3.2
	453920	AI133148	Hs.36602		3.2 3.2
65	437014		Hs.22253		3.2
	424479 413278		Hs.14909 Hs.833	interferon-stimulated protein, 15 kDa	3.2
	42592		Hs.16275	1 Homo sapiens mRNA; cDNA DKFZp761E2423 (f	3.2
	407304		Hs.27164		3.2 3.2
70				ESTs gb:601117374F1 NIH_MGC_16 Homo sapiens c	3.2
	42035 45476			gb:RC5-ST0293-140200-014-H05-ST0293-Homo	3.2
	41040		Hs.63287	carbonic anhydrase IX	3.2
	41249	0 AW803564	Hs.2888	io Homo sapiens cDNA: FLJ22528 fis, clone H	3.2 3.2
75	43456	3 AW083994		pleckstrin homology domain-containing, f	3.2
	41712				3.2
	40737 43976		Hs.2274	t hypothetical protein MGC13105	3.2
	44593	6 BE543594	Hs.6147	B hypothetical protein FLJ22329	3.2 3.2
80	44652	3 NM_0030	63 Hs.3346		3.2 3.2
	40606		3 Hs.2741	Target Exon 70 Opa-interacting protein 2	3.2
	43225 43726				3.2

	****	AMOCOOFT	LL 27520	FOT- 144-44-4-4-3-4- AF000044 4 DD0000	3.2
	449115 425146	AW959952 AW954627	Hs.37528	ESTs, Wealthy similar to AF090944 1 PRO06 gb:EST366697 MAGE resequences, MAGC Horno	3.2 3.2
	436210	AI825420	Hs.197824	ESTs	3.2
	437698	R61837	Hs.7990	ESTs, Moderately similar to 184505 calci	3.2
5	444371	BE540274	Hs.239	forkhead box M1	3.2
•	410006	AW732308	Hs.57783	eukaryotic translation initiation factor	3.2
	445828	F05802	Hs.81907	ESTs	3.2
	450810	8E207588	Hs.334360	transforming growth factor beta 1 induce	3.2
• •	439533	W76021		gb:zd64c04.r1 Soares_fetal_heart_NbHH19W	3.2
10	418079	R40058	Hs.6911	ESTs	3.2
	418781	T41160	Hs.8404	ESTs	3.2
	422765	AW409701	Hs.1578	bacutoviral IAP repeat-containing 5 (sur	3.2 ·
	431319	AA873350 AA151342	Hs.302232	ESTs CCI 147 ambie	3.2 3.2
15	445413 424947	R77952	Hs.12677	CGI-147 protein ESTs, Wealdy similar to alternatively sp	3.2
13	429490	AI971131	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	3.2
	426765	AA743603	Hs.172108	nucleoporin 88kD	3.2
	419726	U50330	Hs.1274	bone morphogenetic protein 1	3.2
	425849	AJ000512	Hs.296323	serum/glucocorticoid regulated kinase	3.1
20	439566	AF086387		gb:Homo saciens full length insert cONA	3.1
	452574	AF127481	Hs.301946	lymphoid blast crisis oncogene	3.1
	439753	BE262233	Hs.7423	hypothetical protein from EUROIMAGE 2168	3.1
	435256	AF193766	Hs.13872	cytokine-like protein C17	3.1
26	439570	T79925	Hs.269165	ESTs, Wealty similar to ALU1_HUMAN ALU S	3.1
25	443431	AI056847	Hs.20654	ESTs	31
	428289	M26301	Hs.2253	complement component 2	3.1 3.1
	415849	R20529 AL157485	Hs.6806 Hs.91973	ESTs	3.1
	419652	X78565	Hs.289114	hypothetical protein hexabrachion (tenascin C, cytotactin)	3.1
30	429500 457579	AB030816	Hs.36761	HRAS-like suppressor	3.1
50	420579	AA278449	Hs.137429	ESTs	3.1
	408116	AA251393	Hs.289052	Homo sapiens, Similar to RIKEN cDNA 5430	3.1
	408247	AA053451	Hs.225632	leucine zipper protein 3	3.1
	405183			NM_016358*:Homo sapians iroquois homeobo	3.1
35	420676	AI434780	Hs.4248	vav 2 oncogene	3.1
	440286	U29589	Hs.7138	cholinergic receptor, muscarinic 3	3.1
	431176	AI026984	Hs.293662	ESTs	3.1
	417918	AA209205	Hs.163754	hypothetical protein FLJ12606	3.1
40	437945	T78519		gb:yd68c08.r1 Soares fetal liver spleen	3.1
40	404632		40000	NM_022490:Homo sapiens hypothetical prot	3.1
	428917	AA437337	Hs.16689	ESTs	3.1 3.1
	429940	W25215		gb:zb87a09.r1 Soares_senescent_fibroblas	3.1
	444016	AA448154	Un 202071	gb:zw82h09.r1 Soares_testis_NHT Homo sap	3.1
45	430701	A1760833 BE262804	Hs.293971	ESTs mitochondrial ribosomal protein S2	3.1
43	402229 454177	AW807321		gb:MR4-ST0062-240300-003-g05 ST0062 Homo	31
	400090	A1100/321		Eos Control	3.1
	419326	W94915	Hs.42419	ESTs	3.1
	435644	AA700867	Hs.269659	ESTs	3.1
50	433042	AW193534	Hs.281895	Homo sapiens cDNA FLJ11660 fis, clone HE	3.1
	458810	BE407125	Hs.231510	EST\$	3.1
	414403	AW969551	Hs.76064	ribosomal protein L27a	3.1
	449670	F07693	Hs.85603	Homo sapiens mRNA; cDNA DKFZp434K2172 (f	3.1
55	403288		•	C1001737*:gi[7511201 pir T27904 hypothe	3.1
55	430535	AW968485		gb:EST380561 MAGE resequences, MAGJ Homo	3.1 3.1
	455899	BE155112		gb:PM1-HT0350-151299-003-a03 HT0350 Homo	3.1
	432044 443105	AW972727 X96753	Hs.9004	gb:EST384819 MAGE resequences, MAGL Homo chondroitin suffate proteoglycan 4 (mela	3.1
	423789	AK002084	Hs.132851	hypothetical protein FLJ11222	3.1
60	439538	AA837323	Hs.56407	ESTs	3.1
•	437681	AI207958	Hs.166556	Homo sapiens, Similar to TEA domain fami	3.1
	433577	AW007080	Hs.284192	ESTs	3.1
	443021	AA368546	Hs.8904	lg superfamily protein	3.1
	433894	AI907682	Hs.243293	ESTs	3.1
65	414884	R54418	Hs.183745	hypothetical protein FLJ13456	3.1
	408996	AI979168	Hs.344096	glycoprotein (transmembrane) rimb	3.1
	449162	AI632740	Hs.10476	ESTs	3.1
	417893	AA290605	Hs.190002		3.1
70	433578	BE336886	Hs.3416	adipose differentiation-related protein	3.0
70	438380	T06430	Hs.6194	chondroitin sullata proteoglycan BEHAB/b	3.0 3.0
	450756 422631	AI733488	Hs.144062 Hs.118793	ESTs hypothetical protein FLJ10688	3.0
	414733	8E218919 8E514535	Hs.77171	minichromosome maintenance deficient (S.	3.0
	431019	NM_005249	Hs.2714	forthead box G1B	3.0
75	434503	T96231	Hs.17762	ESTs	3.0
	455481	AW948317		gb:RC0-MT0015-280300-021-a09 MT0015 Homo	3.0
	427413	BE547647	Hs.177781	hypothetical protein MGC5618	3.0
	414396	BE548266	Hs.76057	galactose-4-epimerase, UDP-	3.0
	458760	AJ498631	Hs.111334	ferritin, light polypeptide	3.0
80	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	3.0
	411543	AW851248		gb:IL3-CT0220-160200-066-F01 CT0220 Homo	3.0
	435375	AI733610	Hs.187832		3.0
	407047	X65965		gb:H.sapiens SOD-2 gene for manganese su	3.0

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	422065	AA401039 1	Hs.2903 o	rotein phosphatase 4 (formerly X), cata	3.0
			Hs.302908 E	STs	3.0
	433062		Hs.281348 h	hypothetical protein FLJ 10895	3.0 3.0
_	412135	AW895309	Un 07407 (b:QV4-NN0038-300300-155-e07 NN0038 Homo tuman clone IMAGE:35527 unknown protein	3.0
5	418669 449385			ESTs	3.0
	426384		Hs.303662	hypothetical protein FLJ13189 (FLJ13189)	3.0
	436267	AW450938		STs	3.0 3.0
10	440388			ESTs ESTs	3.0
10	427235 420116			FH1/FH2 domain-containing protein	3.0
	419764		Hs.93183	vasodilator-stimulated phosphoprotein	3.0
	406673	M34996		major histocompatibility complex, class	3.0 3.0
	445921	AW015211		ESTs	3.0
15	427695	R88483		ESTs ESTs	3.0
	453324 404272	W26592	Hs.232089	Target Exon	3.0
	428538	AA446440	Hs.98643	FSTs	3.0
	442786	H50733		ESTs, Moderately similar to ALU8_HUMAN A	3.0 3.0
20	444396	T65213	Hs.4257	ESTs	3.0
	440483	AI200836 AI423317	Hs.150386 Hs.164680	ESTs ESTs	3.0
	429973 450125	AA005418	Hs.158186	ESTs	3.0
	417409	BE272506	Hs.82109	syndecan 1	3.0 3.0
25	429569	AA454993	Hs.138343	ESTs, Wealthy similar to 178885 serine/th	3.0
	455778	BE088746	Hs.247551	gb:CM2-BT0693-210300-123-d09 BT0693 Homo metaxin 1	3.0
	427954 422418	J03060 AK001383	Hs.116385	hypothetical protein FLJ10521	3.0
	427527	AI809057	Hs.293441	immunoglobulin heavy constant mu	3.0
30	416677	T83470	Hs.334840	ESTs, Moderately similar to 178885 serin	3.0 3.0
_	451130	AI762250	Hs.345554	ESTs Human DNA sequence from clone RP3-403A15	3.0
	431431	AL096711	Hs.252953 Hs.252766	ESTs	3.0
	425248 422757	AW957442 AI909935	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	3.0
35	431836	AF178532	Hs.271411	beta-site APP-cleaving enzyme 2	3.0
	416355	H49875	Hs.268906	ESTs	3.0 3.0
	426406	AI742501	Hs.169756 Hs.115185	complement component 1, s subcomponent ESTs, Moderately similar to PC4259 terri	3.0
	419829	A!924228 NM_006825	Hs.74368	transmembrane protein (63kD), endoplasmi	2.9
40	412646 423869	BE409301	Hs.134012	C1q-related factor	2.9
-10	422710	AW936566	Hs.201876	ESTs	2.9 2.9
	445906	N28939	Hs.13434	Homo sapiens clone 24418 mRNA sequence	2.9
	429751	M55210	Hs.214982	laminin, gamma 1 (formerly LAMB2) small inducible cytokine A5 (RANTES)	2.9
45	430413 443433	AW842182 R44743	Hs.241392 Hs.301667	ESTs	2.9
73	444145	BE153823	Hs.282385	ESTs, Weakly similar to 2004399A chromos	2.9
	425262	D87119	Hs.155418	GS3955 protein	2.9 2.9
	442476	AF069475	Un 122222	gb:AF069475 Homo sapiens astrocytoma lib ESTs	2.9
50	443361 427144	A1792628 X95097	Hs.133273 Hs.2126	vasoactive intestinal peptide receptor 2	2.9
50	415709	AA649850	Hs.278558	ESTs	2.9
	453385	AW296101	Hs.252806		2.9 2.9
	442609	AL020996	Hs.8518	setenoprotein N proteasome (prosome, macropain) subunit,	2.9
55	443378 414416	AW392550 AW409985	Hs.9280 Hs.76084	hypothetical protein MGC2721	2.9
))	443502		Hs.133949	ESTs	2.9
	444143		Hs.160999	ESTs, Moderately similar to A56194 throm	2.9 2.9
	416308		Hs.23628	3 beta-hydroxy-della 5-C27-steroid oxido cyclin-dependent kinase 2	2.9
60	447674 408989		Hs.19192 Hs.49500	KIAA0746 protein	2.9
00	427418		Hs.325520	LAT1-3TM protein	2.9
	408788		Hs.213956		2.9 2.9
	426827		Hs.17266	methylenetetrahydrofolate dehydrogenase C10001011*:gi 4758212tref NP_004411.1 d	2.9
65	403290		Hs.2699	glypican 1	2.9
05	430890 441217		Hs.21324		2.9
	418287		Hs.78935		2.9
	443836		Hs.14055		2.9 2.9
70	45152				2.9
70	41811		Hs.21775	ESTs, Weakly similar to T29012 hypotheti	2.9
	42088 43937			1 ESTs	2.9
	42619	7 AA004410	Hs.10000	9 acyl-Coenzyme A oxidase 1, palmitoyl	2.9 2.9
	40667	9 AA070786	i .	gb:zm66b07.r1 Stratagene neuroepithelium	2.9 2.9
75	45412				2.9
	45724 43203			ra interleutin 20	2.9
	45736			gb:EST383123 MAGE resequences, MAGK Horno	2.9
	43786	O AA333063	Hs.2798		2.9 2.9
80				14 Homo sapiens cDNA FLJ14209 fis, clone NT ab:fL3-CT0214-150300-085-H06 CT0214 Homo	2.9
	45496 43752		b Hs.1697		2.9
	40085			Target Exon	2.9
				237	,

	428896	AW291932	Hs.98936	ESTs	2.9
	426140	AF131798	Hs.343768	Homo sepiens clone 25119 mRNA sequence	2.9
	408872	AJ476139	Hs.13291	ESTs	2. 9 2.9
5	414799 406646	A1752416 M33600	Hs.77326 Hs.308026	insulin-like growth factor binding prote major histocompatibility complex, class	2.9
,	416569	H64891		gb.yr68h03.r1 Soares fetal liver spleen	2.9
	439130	AA306090	Hs.124707	ESTs	2.9
	451433	AA021140	Hs.269265	ESTs, Wealdy similar to A46010 X-linked	2.9 2.9
10	430314 424308	AA369601 AW975531	Hs.239138 Hs.154443	pre-B-cell colony-enhancing factor minichromosome maintenance deficient (S.	29
10	420172	AA601122	Hs.95655	secreted and transmembrane 1	29
	442485	BE092285	Hs.29724	hypothetical protein FLJ13187	2.9
	416505	H66470	Hs.16004	ESTs	2.9 2.9
15	415198 420674	AW009480 NM_000055	Hs.943 Hs.1327	natural killer cell transcript 4 butyrylcholinesterase	29
10	452139	AA099969	Hs.16331	Homo sapiens cDNA: FLJ21482 fis, clone C	2.8
	447499	AW262580	Hs.147674	protocadherin beta 16	2.8
	411373	BE326276	Hs.8861	ESTs	28 28
20	456816 414232	AK001509 W86946	Hs.144391 Hs.238246	hypothetical protein FLJ 10547 hypothetical protein FLJ 22479	2.8
	416188	8E157260	Hs.79070	v-myc avian myelocytomatosis viral oncog	2.8
	447733	AF157482	Hs.19400	MAD2 (mitotic arrest deficient, yeast, h	2.8
	438624	AA889055	Hs.123468	ESTs	2.8 2.8
25	452102 408716	U04343 A1567839	Hs.27954 Hs.151714	CD86 antigen (CD28 antigen ligand 2, 87- Homo sapiens mRNA for KIAA1769 protein,	2.8
	424028	AF055084	Hs.153692	Homo sepiens cDNA FLJ14354 fis, clone Y7	2.8
	421679	AI475110	Hs.203933	ESTs	2.8
	450651	W79000	Hs.44545	ESTs, Weakly similar to B34087 hypotheti	2.8 2.8
30	452785 432842	AL359942 AW674093	Hs.296434 Hs.334822	erythroid differentiation and denucleati hypothetical protein MGC4485	28
50	403291	7.1107 1000	1-0.00	Target Exon	2.8
	453096	AW294631	Hs.11325	ESTs	2.8
	422545	X02761	Hs.287820	fibronectin 1	2.8 2.8
35	440296 427154	D30829 AL137262	Hs.180610 Hs.325630	splicing factor profine/glutamine rich (hypothetical protein MGC4289	2.8
55	422282	AF019225	Hs.114309	apolipoprotein L.	2.8
	434868	R50032	Hs.159263	collagen, type VI, alpha 2	2.8
	414727	BE466904	Hs.190162	gb:hz28f03.x1 NCI_CGAP_GC6 Homo sapiens	2.8 2.8
40	437437 427722	AA226869 AK000123	Hs.180479	hypothetical protein DKFZp762L0311 hypothetical protein FLJ20116	2.8
40	443623	AA345519	Hs.9641	complement component 1, q subcomponent,	2.8
	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	2.8
	448432	AI783586	Hs.208575	ESTs	2.8 2.8
45	453682 447527	T79703 AI702896	Hs.42091	gb:yd71e08.r1 Soares fetal liver spleen ESTs	2.8
73	418557	BE140602	Hs.246645	ESTs	2.8
	409157	AA064631		gb:zf72c03.s1 Soares_pineal_gland_N3HPG	2.8
	457653	AI820719	Hs.154662	DnaJ (Hsp40) homolog, subfamily A, membe	2.8 2.8
50	456908 439220	AI953671 AW295340	Hs.220994 Hs.130417	hypothetical protein FLJ14129 ESTs, Weakly similar to Z195_HUMAN ZINC	2.8
50	418312	AW972468	Hs.170307	Rai guanine nucleotide exchange factor R	2.8
	,454581	AW809189		gb:MR4-ST0118-261099-012-e10 ST0118 Homo	2.8
	419169	AW851980	Hs.262346	ESTs, Wealdy similar to \$72482 hypotheti	2.8 2.8
55	400645 413951	AW051200	Hs.75640	Target Exon natriuretic peptide precursor A	2.8
23	441360	AI091713	Hs.106597	Homo sapiens, Similar to RIKEN cDNA 1110	2.8
	404150			Target Exon	2.8
	402936	AMOT2455		ENSP00000217246*:DJ803K15.1 (novel prote gb:QV2-CT0261-261099-011-d11 CT0261 Homo	2.8 2.8
60	454457 439544	AW753456 W26354	Hs.28891	hypothetical protein FU11360; artemis p	2.8
••	403969	*******		ENSP0000034663:Zinc finger protein 131	2.8
	447183	AI554733	Hs.173182		2.8
	446566	H95741	Hs.17914 Hs.293972	membrane-spanning 4-domains, subfamily A ESTs	2.8 2.8
65	426141 440146	C05886 AW014231	Hs.90790	Homo sapiens cDNA: FLJ22930 fis, clone K	2.8
-	430335	D80007	Hs.239499		2.8
	447071	AW236867	Hs.244376		2.8
	428899	AA744610	Hs.194431	palladin ENSP00000237081*:KIAA1217 PROTEIN (FRAGM	· 28
70	400658 403942			Target Exon	2.8
	420565	AI806770	Hs.30258	ESTs	2.8
	409734	BE161664	Hs.56155	hypothetical protein	2.8
	456645	AF227156	Hs.110103	RNA polymerase I transcription factor RR NM_015113:Homo sapiens KIAA0399 protein	2.8 2.8
75	401841 447247	AW369351	Hs.287955		2.8
	450150	AI754391	Hs.23510	Kruppel-like factor 12	2.8
	409154	U72882	Hs.50842	interferon-induced protein 35	2.8
	410267	AW978005 R48700	Hs.12600 Hs.20733	N-ethylmateimide-sensitive factor attach Homo sapiens cDNA: FLJ22356 fis, clone H	2.8 2.8
80	448224 410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	2.8
- •	447512	AW958148	Hs.129454	ESTs	2.8
	417749	U09196	Hs.82520	polymerase (DNA-directed), delta 4	2.8 2.8
	415293	R49462	Hs.106541	ESTs	2.8

		0. 2745	U- 70077 I	tomo sapiens, clone MGC:2908, mRNA, comp	2.8
				exin 2 (conductin, axii)	2.8
	425128			umor protein D52-like 2	2.7 2.7
_	444491			ESTs	2.7
5	428311		Hs.183671 1 Hs.301865 (ryptophan 2,3-dioxygenase dopachrome tautomerase (dopachrome delta	2.7
	430377 417944		Hs.82985	collagen, type V, alpha 2	2.7
	444153	AK001610	Hs.10414	hypothetical protein FLJ 10748	2.7 2.7
10	438138			ESTs tetracycline transporter-like protein	2.7
10	425421 431070			transcription factor 19 (SC1)	2.7
	451748	AK001612	Hs.26962	Homo sapiens cDNA FLJ10750 fis, clone NT	2.7
	452085	AW239140		ESTs, Wealthy similar to PC4396 mucin 3 T	2.7 2.7
15	405941	BE564245		Target Exon integrin beta 3 binding protein (beta3-e	2.7
13	417395 449667	AB023227	Hs.23860	KIAA1010 protein	2.7
	428808	AA436007	Hs.188780	ESTs	2.7 2.7
	425843	BE313280	Hs.159627	death associated protein 3	2.7
20	438025 400924	AW501360	Hs.258910	ESTs Target Exon	2.7
20	412898	Al129903	Hs.74669	vesicle-associated membrane protein 5 (m	2.7
	413834	BE296896	Hs.224179	ESTs, Weakly similar to 138022 hypotheti	2.7 2.7
	453785	A1368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A ribosomal protein S2	2.7
25	406736 414280	AI254733 BE410769	Hs.182426 Hs.75873	zyxin	2.7
23	434203	BE262677	Hs.283558	hypothetical protein PRO1855	2.7
	442621	AI004333	Hs.130553	ESTs, Wealdy similar to ALUA_HUMAN IIII	2.7 2.7
	414591	AI888490	Hs.55902 Hs.268946	ESTs, Weakly similar to ALUB_HUMAN ALU S ESTs, Weakly similar to PC4259 ferritin	2.7
30	416547 416784	H62914 AA334592	Hs.79914	lumican	2.7
50	413851	AW897510	Hs.137387	ESTs	2.7 2.7
	451767	AJ625014	Hs.187328	ESTs	2.7
	441668	AI611973 AI032087	Hs.136313 Hs.269819	ESTs ESTs	2.7
35	435664 435046	AA662772	Hs.174330	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.7
22	439467	AW292275	Hs.158365	ESTs	2.7 2.7
	441329	A1203575	Hs.46821	hypothetical protein FLJ20086 Homo sapiens cDNA: FLJ22373 fis, clone H	2.7
	426925 427241	NM_001196 AA399988	Hs.315689 Hs.112087	Human DNA sequence from clone RP11-530N1	2.7
40	449919	AJ674685	Hs.200141	ESTs	2.7
	458070	AW503578	Hs.209406	ESTs, Weakly similar to I38600 zinc fing	2.7 2.7
	444794	AI419991	Hs.145225 Hs.165028	ESTs ESTs	2.7
	410781 449520	Al375672 R34993	Hs.226666	ESTs, Moderately similar to 154374 gene	2.7
45	439481	AF086294	Hs.125844	ESTs	2.7 2.7
	401702			NM_001171*:Homo sapiens ATP-binding cass	2.7
	432890	NM_014442 AA687415	Hs.279751 Hs.28107	siatic acid binding tg-like lectin 8 ESTs	2.7
	435545 416422	H60457	113,20101	ESTs, Moderately similar to ZN91_HUMAN Z	2.7
50	429415	NM_002593		procotlagen C-endopeptidase enhancer	2.7 2.7
	420982	AW576160	Hs.100729		2.7
	431421 444168	AW969118 AW379879	Hs.108144	gb:RC1-HT0256-081199-011-f01 HT0256 Homo	2.7
	419964		Hs.220913	ESTs	2.7 2.7
55	424480		Hs.205299		2.7
	436314		Hs.189226	ESTs ENSP00000200457*:Thyroid receptor intera	2.7
	405516 449340		Hs.195359	hypothetical protein MGC10954	2.7
	457876			ESTs, Moderately similar to ALU8_HUMAN A	2.7 2.7
60	423799			i 19A24 protein gb:EST379359 MAGE resequences, MAGJ Homo	2.7
	422551 404592			NM_022739":Homo sapiens E3 ubiquitin tig	2.7
	424200	AA337221		gb:EST41944 Endometrial tumor Homo sapie	2.7 2.7
15	428612		Hs.18877		2.7
65	446139 440478		Hs.39749 Hs.13000	7717	2.7
	429612		Hs.25258	7 pituitary tumor-transforming 1	2.7
	422530) AW972300		0 bone marrow stromal cell antigen 2	2.7 2.7
70	423713		?	gb:RC2-CT0321-131199-011-c01 CT0321 Homo ENSP00000251056":Plasma membrane calcium	2.7
70	402033 42418		Hs.28870		2.7
	40279	9		Target Exon	2.7 2.7
	42335	2 AA324808	_	6 ESTs gb:RC4-OT0071-090300-011-g11 OT0071 Homo	2.7
75	41202		2 Hs.18724		2.7
13	45861 40417		113.10124	NM 000636":Homo sapiens superoxide dismu	2.7
	41088	6 AW80932	4	gb:MR4-ST0121-141099-010-G06_1 ST0121 Ho	2.7 2.7
	41498		Hs.2628	gb:C17535 Human placenta cDNA (TFujiwara 9 ESTs	2.7
80	45032 45891		Hs.2526		2.7
00	40576	iÓ		Target Exon	2.7 2.7
	40678	9 AI041403		ribosomat protein L29 qb:EST51529 Gall bladder II Homo sapiens	2.7
	42468	36 AA345504	•	gn:E3131323 Gail Gaolle il Fronto sapens	

	400335	Y13187	Hs.248068	Homo sapiens dmd gene, intron 11	2.7
	435065	BE064391		gb:RC4-BT0310-110300-015-b08 BT0310 Homo	2.7
	419373	NM_003244 AA588061	Hs.90077	TG-interacting factor (TALE family homeo	2.7 2.7
5	406785 433006	BE242758	Hs.190223	gb:nk10d03.s1 NCI_CGAP_Co2 Homo sapiens ESTs, Moderately similar to T29285 hypot	27
_	428690	AI948490	Hs.98765	ESTs	2.7
	432692	AW974944	Hs.200577	ESTs	2.7
	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	2.7
10	452811	AA937079	Hs.118983	hypothetical protein FLJ12150	2.6 2.6
10	457035 427725	AA398074 U66839	Hs.119143 Hs.180533	ESTs, Moderately similar to KIAA1513 pro mitogen-activated protein kinase kinase	26
	433681	AI004377	Hs.200360	Homo sapiens cDNA FLJ13027 fis, clone NT	2.6
	423748	AI149048	Hs.30211	hypothetical protein FLJ22313	2.6
16	422764	AI767727	Hs.47522	EST8	2.6
15	403431			Target Exon	2.6
	439332 412749	AW842747 AA378417	Hs.300870 Hs.74564	Homo sapiens mRNA; cDNA DKFZp547M072 (fr signal sequence receptor, beta (transloc	2.6 2.6
	409703	NM_006187	Hs.56009	2-5-ciigoadenylate synthetase 3 (100 k	2.6
	405717			CX000838:gi 10092633fref NP_055314.1 pu	2.6
20	426503	AA380153		gb:EST93093 Skin tumor I Homo sapiens cD	26
	414039	M83221	Hs.858	v-rel avian reticuloendotheliosis viral	26 26
	452683 447587	AI089575 AW292139	Hs.9071 Hs.115789	progesterone membrane binding protein ESTs	26
	408605	AF025374	Hs.46465	T-cell, immune regulator 1	2.6
25	407103	AA424881	Hs.256301	hypothetical protein MGC13170	2.6
	427395	AW298741	Hs.97861	ESTs, Moderately similar to 138022 hypot	2.6
	435113	AA665469	Hs.117136	ESTS	2.6 2.6
	419015 427648	T79262 Al376722	Hs.14463 Hs.180062	ESTs proteasome (prosome, macropain) subunit,	2.6 2.6
30	453707	AW003879	Hs.126522	Homo sapiens, clone MGC:16722, mRNA, com	2.6
-	411927	BE274009	Hs.772	glycogen synthase 1 (muscle)	2.6
	404053			Target Exon	2.6
	415069	AA159831	Hs.29286	ESTs, Weakly similar to 149636 DNA-bindi	2.6 2.6
35	449625 438033	NM_014253 T26483	Hs.6059	odz (odd Oz/ten-m, Drosophila) homolog 1 EGF-containing fibulin-like extracellula	2.6
"	451593	AF151879	Hs.26706	CGI-121 protein	2.6
	435828	AA700705	Hs.13852	ESTs	2.6
	443753	AW36757B	Hs.134749	ESTs	2.6
40	416097	BE387371	Hs.118964	hypothetical protein FLJ20085	2.6 2.6
40	413986 439755	Z43567 AW748482	Hs.77873	gb:HSC1FC021 normalized infant brain cDN B7 homolog 3	26
•	408371	AF161545	Hs.44439	hypothetical protein	2.6
	445658	AI469062	Hs.172660	ESTs	2.6
	438166	N30158	Hs.122645	ESTs	2.6
45	449426	T92251	Hs.198882	ESTs	2.6 2.6
	422605	H16646 AW628686	Hs.118666 Hs.78851	hypothetical protein PP591 KIAA0217 protein	26
	415788 448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	2.6
	400295	W72838		Al905687:IL-BT095-190199-019 BT095 Homo	2.6
50	441128	AA570256		ESTs, Weakly similar to T23273 hypotheti	2.6
	420372	AW960049	Hs.293660	Homo sapiens, clone IMAGE:3535476, mRNA,	2.6 2.6
	428977 424278	AK001404 AK000723	Hs.194698 Hs.144517	cyclin B2 hypothetical protein FLJ20716	26
	445211	BE045601	Hs.118248	ESTs, Weakly similar to YC18_HUMAN HYPOT	2.6
55	412715	NM_000947	Hs.74519	primase, polypeptide 2A (58kD)	2.6
	417838	R24713	Hs.22514	ESTs	2.6
	420670	AW973577		ESTs	2.6 2.6
	403267 454354	AW389896		Target Exon gb:RC4-ST0173-191099-032-e12 ST0173 Homo	2.6
60	452903	AI953425	Hs.345291	ESTs, Weakly similar to 138022 hypotheti	2.6
	427830	AA416598	Hs.98233	ESTs	2.6
	435953	AI767087	Hs.114142		2.6 2.6
	430744 413335	AA485229 Al613318	Hs.105649 Hs.48442	ESTs ESTs	2.6
65	416370	N90470	Hs.203697		2.6
-	431865	AA521106	Hs.136375		2.6
	434274	AA628539	Hs.116252	_	2.6
	447854	AW138454	Hs.11594	ESTs	2.6 2.6
70	412799 455409	AI267606 AW936832		gb:eq91h03.x1 Stanley Frontal SB pool 1 gb:PM2-DT0023-050400-003-h03 DT0023 Homo	2.6
, 0	408212	AA297567	Hs.43728	hypothetical protein	2.6
	453055	AW291436	Hs.31917	Homo sapiens, clone MGC:9658, mRNA, comp	2.6
	443539	AI076182	Hs.134074		2.6 2.6
75	434898	AW500458	Hs.29956 Hs.346690	KIAA0460 protein ESTs	2.6 2.6
13	438118 431786	AW753311 AW452784	Hs.220718		2.6
	421689	N87820	Hs.106826	KIAA1696 protein	2.6
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	2.6
QΛ	424684	AW752714	Hs.5174	ribosomal protein S17	2.6 2.6
80	439823 411962	AW665287 AA099050	Hs.124514	ESTs gb:zk85d12.r1 Soares_pregnant_uterus_NbH	2.6
	445774	AI254165	Hs.339968		26
	400492			C10001573*:gi]7302749[gb[AAF57827.1] (AE	2.6

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	450625	AW970107	(b:EST382188 MAGE resequences, MAGK Homo	2.6 2.6
	426931			tinc finger protein 7 (KOX 4, clone HF.1	2.6
	440131			ESTs ESTs	2.6
5	438525 412247		Hs.73793	vascular endothelial growth factor	2.6
,	406662	X62006	Hs.172550	polypyrimidine tract binding protein (he	2.6
	443725	AW245680	Hs.9701	growth arrest and DNA-damage-inducible,	2.6
	402260			NM_001436*:Homo sapiens fibrillarin (FBL	2.6 2.6
10	429599	AA806106	Hs.123664	ESTS	2.6
10	429562	A1732767		Homo sapiens cDNA FLJ14673 fis, clone NT ESTs	2.6
	432527	AW975028 AA688278		hypothetical protein FLJ22578	2.6
	434420 452732	BE300078	Hs.80449	Homo sapiens, clone IMAGE:3535294, mRNA,	2.6
	424408	AI754813	Hs 146428	collagen, type V, atoha 1	2.6
15	413151	H47969	Hs.141971	ESTs, Wealty similar to ALU1_HUMAN ALU S	2.6
	416244	N39535	Hs.32748	ESTs	2.6
	403104			C8000064*:gi 10432393 emb CAC10283.1 (A	2.6 2.6
	400780			NM_007325*:Horno sapiens glutamata recept gb:nz24c08.s1 NCI_CGAP_GCB1 Horno sapiens	2.6
20	433009	AA761668	U= 120262	XIAP associated factor-1	2.6
20	424090	X99699	Hs.139262	NM_019595:Homo sapiens intersectin 2 (IT	2.6
	403212 407855	R54126	Hs.40500	similar to S. cerevisiae RER1	2.6
	406849	AA454809	Hs.172928	collagen, type I, alpha 1	2.6
	443462	AJ064690	Hs.171176	ESTs	2.6
25	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	2.6 2.6
	450089	A1681883	Hs.209546	ESTs, Weakly similar to 2109260A B cell	2.6
	419571	AW674962	Hs.91146	protein kinase D2	2.6
	448140	AF146761	Hs.20450 Hs.192805	BCM-like membrane protein precursor ESTs	2.6
30	444881	AI623288 AW965215	Hs.130707	ESTs	2.6
30	420658 437634	AW293046	Hs.255158	ESTs	2.6
	426894	AI204209	Hs.143911	ESTs	2.6
	428467	AK002121	Hs.184465	hypothetical protein FLJ11259	2.6
	434171	BE247688	Hs.347349	KIAA0948 protein	2.6 2.6
35	410174	AA306007	Hs.59461	DKFZP434C245 protein	2.5
	427245	AA421022	Hs.97739	ESTs	2.5
	437085	AA743935	Hs.202329 Hs.272414	ESTs Homo sapiens HDCMB45P mRNA, partial cds	2.5
	400352 452221	AF068294 C21322	Hs.288057	hypothetical protein FLJ22242	2.5
40	432221	AF085937	Hs.38348	ESTs	2.5
70	437287	AA748180	Hs.159346	hypothetical protein FLJ21369	2.5
	411852	AA528140	Hs.107515	ESTs, Weakly similar to T00329 hypotheti	2.5
	427624	AA406245	Hs.24895	ESTs	2.5 2.5
4.00	435177	Ai018174	Hs.42936	ESTS	2.5 2.5
45	449433	AI672096	Hs.9012	ESTs, Wealdy similar to S26650 DNA-bindi ESTs, Wealdy similar to AFG1_YEAST AFG1	2.5
	447853	A1434204 H77795	Hs.164285 Hs.39785	ESTs. Weakly Sitting to At Ot_1250 Fra G	2.5
	416704 401696	U11132	115.33103	Target Exon	2.5
	445677	H96577	Hs.6838	ras homotog gene family, member E	2.5
50	413840	AI301558	Hs.146381	RNA binding motif protein, X chromosome	2.5
	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	2.5 2.5
	420289	N55394	Hs.96398	8-oxoguanine DNA glycosylase	2.5
	421848	X15880 AA907153	Hs.108885 Hs.190060		2.5
55	421234 414598	AJ094221	Hs.135150		2.5
33	420162	BE378432	Hs.95577	cyclin-dependent kinase 4	2.5
	458199	AW136417		hypothetical protein FLJ14464	2.5
	433523			ESTs	2.5 2.5
7 0	429125		Hs.271004	ESTs, Wealthy similar to 138022 hypotheti	2.5
60	418399		Hs.84753	hypothetical protein FLJ12442 ENSP00000238177*:Similar to kynurenine 3	2.5
	404748 413507		Hs.190064		2.5
	418886		Hs.130858		2.5
	429359		Hs.2399	matrix metalloproteinase 14 (membrane-in	2.5
65	452367		Hs.29279	eyes absent (Drosophila) homolog 2	2.5
	436258				2.5 2.5
	459527				2.5
	450543		Hs.17029	5 Homo sapiens cDNA: FLJ22090 fis, clone H ESTs	2.5
70	434818		Hs.5996 Hs.42294		2.5
70	444534 452113		113.4227	gb:wm11a02.x1 NCI_CGAP_Ut4 Homo sapiens	2.5
	429115		Hs.28902		2.5
	434012		Hs.18625	6 ESTs	2.5
	447143	3 AW292408	Hs.15229		2.5
75	44950		Hs.19537		2.5 2.5
	41981			8 ESTs 0 Homo sapiens, clone IMAGE:4299555, mRNA,	2.5
	45798				2.5
	43145- 42501				2.5
80	42751		Hs.19248		2.5
	44131	8 AI078234	Hs.17613	D ESTs	2.5
	42483	0 AW27058			2.5 2.5
	41427	1 AK000275	Hs.75871	protein kinase C binding protein 1	2.5

	446089	AI860021	Hs.345028	ESTs, Moderately similar to A47582 B-cel	2.5
	415983	AJ436798	Hs.117078	Homo sapiens cDNA: FLJ23028 fs, clone L	2.5
	408292	AW178363		gb:RC3-HT0105-010999-002-H06 HT0105 Homo	2.5
5	446862	AV660697	Hs.282700	ESTs	2.5
3	448970 459200	AW138582 Y09306	Hs.30148	gb:UI-H-BI1-acw-a-06-0-UI.s1 NCI_CGAP_Su	2.5 2.5
	422627	BE336857	Hs.118787	homeodomain-interacting protein kinase 3 transforming growth factor, beta-induced	2.5
	433388	AJ432672	Hs.288539	hypothetical protein FLJ22191	2.5
	436222	AI208737	Hs.122810	Homo sapiens cONA FLJ11489 fis, clone HE	2.5
10	441255	R06350	Hs.171635	ESTs	25
	441627	AA947552	Hs.58086	branched chain aminotransferase 1, cytos	2.5 2.5
	438714 441020	AAB14859 W79283	Hs.294112 Hs.35962	ESTs ESTs	2.5 2.5
	418291	BE300369	Hs.289038	hypothetical protein MGC4126	2.5
15	434267	AI206589	Hs.116243	ESTs	2.5
	446821	W03766		tropomodulin 3 (ubiquitous)	2.5
	402615	HOESTO	U- 202700	C1003844*:gi[6912550]ref[NP_036483.1] ol	2.5 2.5
	416845 408253	H95279 AW807476	Hs.293788 Hs.21051	gb:yu20h02.s1 Soares fetal liver spleen Homo sepiens mRNA for FLJ00012 protein,	2.5 2.5
20	444884	AI201094	Hs.148540	ESTs	2.5
	440826	AW383618	Hs.346256	ESTs, Moderately similar to ALU2_HUMAN A	2.5
	431374	8E258532	Hs.251871	CTP synthase	2.5
	458093	AJ207788 AA568770	Hs.343628	sialytransferase 4B (beta-galactosidase	2.5 2.5
25	422484 442804	AW300118	Hs.123158 Hs.131257	Homo sapiens cDNA FLJ12830 fis, clone NT ESTs	2.5
	420949	AA934063	Hs.13836	ESTs, Weakly similar to 138022 hypotheti	2.5
	451350	AI791447		gb:ni13a05.y5 NCI_CGAP_Co4 Homo sapiens	2.5
	410855	X97795	Hs.66718	RAD54 (S.cerevisiae)-like	2.5
30	430426	AA478807	Hs.125173	ESTs	25
30	418526 406290	BE019020	Hs.85838	sotute carrier family 16 (monocarboxylic Target Exon	2.5 2.5
	442085	AA975688	Hs.159955	ESTs	2.5
	448148	NM_016578	Hs.20509	HBV pX associated protein-8	2.5
25	432888	T86823		gb:yd81a08.s1 Soares fetal liver spleen	2.5
35	424126	AA335635	Hs.96917	ESTs	2.5
	459727 407989	AI906494 AW135208	Hs.256092	gb:RC-BT113-060499-024 BT113 Homo sapien ESTs	2.5 2.5
	404571	AW 133200	113.230032	NM_015902°:Homo sapiens progestin induce	2.5
	429139	F09092	Hs.66087	ESTs	2.5
40	435232	NM_001262	Hs.4854	cyclin-dependent kinase inhibitor 2C (p1	2.5
	420608	BE548277	Hs.103104	ESTs	2.5
	432668 406871	AA558601 AA993857	Hs.43296 Hs.180842	ESTs	2.5 2.5
	443516	AA305821	Hs.9527	ribosomal protein L13 apoptosis related protein APR-3	2.5
45	445985	BE621800	Hs.29444	putative small membrane protein NID67	2.5
	424614	X54486	Hs.151242	serine (or cysteine) proteinase inhibito	2.5
	437267	AW511443	Hs.258110	ESTs	2.5
	458251 431198	AL040927 AL047634	Hs.210422 Hs.231913	ESTs ESTs	2.5 2.5
50	413944	AW001579	Hs.9645	Homo sapiens mRNA for KIAA1741 protein,	2.5
••	420796	L34355	Hs.99931	sarcoglycan, alpha (50kO dystrophin-asso	2.5
	428032	AW997704	Hs.11493	Homo sapiens cDNA FLJ13536 fis, clone PL	2.5
	422017	NM_003877		STAT induced STAT inhibitor-2	2.5
55	424662 423779	NM_002870 AW071837	Hs.151536 Hs.57971	RAB13, member RAS oncogene family ESTs	2.5 2.5
33	405863	A1107 1007	113.37371	Target Exon	2.5
	458421	AI279978	Hs.22547	ESTs	2.5
	439019	AF085902	Hs.271737	ESTs	2.5
60	412577	Z22968	Hs.74076	CD163 antigen	2.5 2.5
OU	404891 419043	T19167	Hs.89566	Target Exon ets variant gene 1	25
	448482	AW294078	Hs.171092		25
	426030	BE243933	Hs.108642		2.5
CE	429109	AL008637	Hs.196352		2.5
65	450597	AI701635	Hs.207077		2.5 2.5
	414386 440473	X00442 BE562314	Hs.75990 Hs.98711	haptoglobin Homo sapiens, clone IMAGE:3677165, mRNA,	2.5
	406851	AA609784	113.30711	major histocompatibility complex, class	2.5
~^	414821	M63835	Hs.77424	Fc tragment of IgG, high affinity Ia, re	2.5
70	417663	R07483	Hs.180461		2.5
	429341	X73874	Hs.2393	phosphorylase kinase, alpha 1 (muscle)	2.5
	450663 407198	H43540 H91679	Hs.25292	ribonuclease HI, large subunit qb:yv04a07.s1 Soares fetal liver spleen	2.5 2.5
	411742	AW247593	Hs.71819	eukaryotic translation initiation factor	2.5
75	409449	H11341	Hs.13366	Homo sapiens cDNA: FLJ23567 fis, clone L	2.5
	TABLE 1		ious Ess and a	set identifier number	
	Pkey: CAT nun		va cinster unur Line coe hione		
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	<u>-</u> .				
	Pkey 408292	1050507_1	F Accession	AW846011 AW845964 AW845988 AW845977 AW846002	
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	409189	110687_1	AA125984 AA127189 AA065075 AAU/0377 AA100017 AA073091 AA105091 AA075091
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	411565	1249756_1	AWR5172R AWR51607 AWR51621 AWR51702 AWR51647 AWR51727 AWR51030 AWR51017 AWR51020
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	413986	140720_1	7/43567 H2/4159 AA 134240 ·
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	416569 416871	1601567_1 1626761_1	
	416913	163001_1	H98716 N90792 N24283 AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499
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	424686	242486_1	AA345504 AA345251 AW963243 R77952 AA348809 AW959960 AW959962 AI565552 AW070702 AA973910 R85973
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45	433009	357371_1	AA761668 AA573621 R92814 R09670 H29882 AW665533 AW149901 AI572917 AA598500 AI686466 AI336390 AW864390 AW864320
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	439533		W76021 AF088052 W72465
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	44247	6 543547_1	
65	44401		AA48154 AV647571
	44416		AW379879 AI126285 H12014
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	44897		
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	45112	29 859870_	1 BE072881 BE072946 AI762181
80	4513		
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AJ820973 AJ734077 AJ820984 AA225796 AA225060 AA225101
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                                             Unique number corresponding to an Eos probeset
Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA
                Pkey:
                Ref:
                                              sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
                                              Indicates DNA strand from which exons were predicted.
                Strand:
                 Mt_position:
                                              Indicates nucleotide positions of predicted exons.
 35
                                                                           Nt_position
                                                       Strand
                Pkey
                 400492
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                 400533
                                  6981826
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                                                                           277132-277595
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                                   9926801
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                  402799
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7139839
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                   404170
                                    9930793
                                                          Plus
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                   404209
                                    5006246
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	404592	9943965	Minus	39067-39225
5	404632	9796668	Plus	45096-45229
_	404748	7263437	Plus	11446-11591
	404891	7329392	Plus	84974-85125
	405046	7596829	Minus	4373-4528
	405141	8980911	Plus	99861-100054
10	405183	7209940	Plus	12335-12653
	405238	7249119	Minus	51728-51836
	405348	2914717	Minus	43310-43462
	405516	9454624	Plus	112707-112876,113676-113854
	405558	1621110	Plus	4502-4644,5983-6083
15	405605	5836195	Minus	117070-117270
	405717	9588573	Plus	11275-11973
	405760	6066938	Minus	37424-38045
	405863	7657810	Plus	49410-49620
	405941	6758796	Plus	2798-3444
20	406060	6899623	Minus	20339-20746
	406290	5686274	Plus	8711-9358
	406395	9256242	Minus	20805-20960
	406478	9857502	Plus	68314-68523,68853-68950
	406481	9864741	Minus	91439-91579
25	.50.01			

TABLE 15A: ABOUT 1033 GENES UP-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT TISSUES
Table 15A ists about 1033 genes up-regulated in glioblastoma compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03
GeneChip array such that the ratio of "average" glioblastoma to "average" normal tissues was greater than or equal to 3.0. The "average" glioblastoma level was set to the 85th percentile amongst various non-malignant adult tissues. In order to remove genespecific background levels of non-specific hybridization, the 10th percentile value amongst the various non-malignant tissues was subtracted from both the numerator and the
denominator before the ratio was evaluated. 30 Menominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number

Exacon: Exemplar Accession number, Genbank accession number

35

ExAccn: UnigenelD: Unigene Title: R1: Unigene number

Unigene gene title Ratio of GLIOBLASTOMA to NORMAL ADULT TISSUES

	KI:	(Cano di Coloro di C			
	Pkey	ExAcco	UnigenelD	Unigene Title	R1
40	427343	AI880044	Hs.176977	protein kinase C binding protein 2	60.5
40	431917	D16181	Hs.2868	peripheral myelin protein 2	54.9
	418375	NM_003081	Hs.84389	synaptosomal-associated protein, 25kD	53.1
	418373	AI699994	Hs.2868	peripheral myelin protein 2	49.6
		AB007979	Hs.301281	Homo sapiens mRNA, chromosome 1 specific	45.4
45	409389	AL133731	Hs.4774	Homo sapiens mRNA; cDNA DKFZp761C1712 (f	43.9
43	435147	BE242870	Hs.75379	solute carrier family 1 (glial high affi	42.7
	413472	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	42.3
	415817	BE259150	Hs.127792	delta (Drosophila)-like 3	39.1
	456759	N46664	Hs.169395	hypothetical protein FLJ12015	37.9
50	430838		Hs.172717	ESTs	37.6
50	417183	R52089		myelin-associated oligodendrocyte basic	36.5
	426325	D28114	Hs.169309 Hs.169395	hypothetical protein FLJ12015	34.3
	425088	AA663372	ns.109393	gb:HUM092E09B Human fetal brain (TFujiwa	33.9
	429007	D80642	Hs.315369	Homo sapiens cDNA: FLJ23075 fis, clone L	33.9
<i></i>	449494	AW237014	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f	32.7
55	423849	AL157425	Hs.198612	G protein-coupled receptor 51	32.3
	429276	AF056085		fibroblast growth factor 1 (acidic)	29.0
	413333	M74028	Hs.75297	ESTs	27.9
	450133	AW969769	Hs. 105201	KIAA0080 protein	27.6
7 0	412733	AA984472	Hs.74554	NK-2 (Drosophila) homolog B	27.3
60	425842	AI587490	Hs.159623	catenin (cadherin-associated protein), d	27.1
	416829	AB013805	Hs.80220	myelin oligodendrocyte glycoprotein	25.2
	424140	248051	Hs.141308		24.3
	402604			Target Exon ESTs, Weakly similar to I55214 sativary	24.3
	437204	AL110216	Hs.22826		23.6
65	422656	AI870435	Hs.1569	LIM homeobox protein 2	23.3
	447359	NM_012093		adenylate kinase 5	22.9
	436878	BE465204	Hs.47448	ESTs	22.9
	435708	A1362949	Hs.75169	ESTs	22.7
=^	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	22.4
70	439239	A1031540	Hs.235331		22.2
	409395	U46745	Hs.336678		21.9
	425799	T08133	Hs.182906	Homo sapiens mixtua for Kitaanahila homof	21.3
	425057	AA826434	Hs.1619	achaete-scute complex (Drosophila) homol	21.2
	444378	R41339	Hs.47860	neurotrophic tyrosine kinase, receptor,	21.0
75	444513	AL120214	Hs.7117	glutamate receptor, ionotropic, AMPA 1	21.0
	419078	M93119	Hs.89584	insulinoma-associated 1	20.9
	425048	H05468	Hs.164502	ESTs	19.3
	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	19.3
~~	423853	AB011537	Hs.133466		19.2
80	418110	R43523	Hs.21775		18.6
	447004	AW296968			18.6
	439415	F05538	Hs.4273	ESTs	18.5
	441497	R51064	Hs.23172	ESTs	

	425523	AB007948	Hs.158244	KIAA0479 protein	18.3
	413597	AW302885	Hs.117183	ESTs .	18.2
	433551	AI985544	Hs.12450	protocadherin 9	17.7
5	428392 453642	H10233	Hs.2265 Hs.34074	secretory granute, neuroendocrine protei	17.3 17.3
3	418338	AJ370936 NM_002522	Hs.84154	dipeptidylpeptidase VI neuronal pentraxin I	17.1
	437268	A1754847	Hs.227571	regulator of G-protein signalling 4	16.8
	408604	D\$1408	Hs.21925	ESTs	16.6 16.6
10	424581 422980	M62062 N46569	Hs.150917 Hs.76722	catenin (cadherin-associated protein), a CCAAT/enhancer binding protein (C/EBP).	16.5
10	448302	AJ480208	Hs.182906	Homo sapiens mRNA for KIAA1872 protein,	16.4
	429466	M85835	Hs.12827	ESTs	16.3
	441350 448672	AB020690 Al955511	Hs.7782 Hs.225106	paraneoplastic antigen MA2 ESTs	15.9 15.8
15	448743	AB032962	Hs.21896	KIAA1136 protein	15.7
	415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	15.3
	441285	NM_002374	Hs.167	microtubule-associated protein 2	15.2 14.8
	431019 431941	NM_005249 AK000106	Hs.2714 Hs.272227	forthead box G18 Homo sapiens cDNA FLJ20099 fis, clone CO	14.3
20	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	14.3
	416370	N90470	Hs.203697	ESTs, Weakly similar to 138022 hypotheti	14.1 14.0
	439979 444471	AW600291 AB020684	Hs.6823 Hs.11217	hypothetical protein FLJ10430 KIAA0877 protein	13.9
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	13.8
25	448595	AB014544	Hs.21572	KIAA0644 gene product	13.6 13.6
	441440 428982	AI807981 NM_005097	Hs.30495 Hs.194704	ESTs leucine-rich, glioma inactivated 1	13.5
	424790	AL119344	Hs.13326	ESTs, Wealty similar to 2004399A chromos	13.3
20	459516	AJ049662	Hs.246858	EST	13.2
30	421264 428342	AL039123 AI739168	Hs.103042	microtubule-associated protein 18 Homo sapiens cDNA FLJ13458 fis, clone PL	13.2 13.1
	408562	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	12.9
	412959	D87458	Hs.75090	KIAA0282 protein	12.9
35	439199	R40373	Hs.26299	ESTS	12.8 12.5
33	423419 445495	R55336 BE622641	Hs.23539 Hs.38489	ESTs ESTs, Weakly similar to 138022 hypotheti	12.4
	415849	R20529	Hs.6806	ESTs	12.4
	452372	AI885742	Hs.228474	ESTs	12.4 12.3
40	452744 426344	AI267652 H41821	Hs.246107 Hs.322469	Homo sapiens mRNA; cDNA DKFZp434E082 (fr transcriptional activator of the c-fos p	12.3
	415734	NM_014747	Hs.78748	KIAA0237 gene product	12.1
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	12.1
	444119 409049	R41231 AI423132	Hs.184261 Hs.146343	ESTs, Weakly similar to 126686 hypotheti ESTs	12.0 11.9
45	434277	X77748	Hs.3786	glutamate receptor, metabotropic 3	11.9
	427897	NM_017413	Hs.303084	apelin; peptide ligand for APJ receptor	11.8
	453941	U39817	Hs.36820	Bloom syndrome	11.8 11.7
	424120 418738	T80579 AW388633	Hs.290270 Hs.6682	ESTs solute carrier family 7, (cationic amino	11.7
50	411305	BE241596	Hs.69547	myelin basic protein	11.7
	424945	AJ221919	11- 50445	hypothetical protein FLJ 10582	11.6 11.5
	449539 409638	W80363 AW450420	Hs.58446 Hs.21335	ESTs ESTs	11.5
	441016	AW138653	Hs.25845	ESTs	11.4
55	429037	X81895	Hs.194765	H.sapiens GENX-5624 mRNA, 3 UTR	11.3 11.2
	407034 446372	U84540 AB020644	Hs.14945	gb:Human dystrobrevin isoform DTN-3 (DTN long fatty acyl-CoA synthetase 2 gene	11.2
	425984	AW836277	Hs.165636	hypothetical protein DKFZp761C07121	11.2
60	424432	AB037821	Hs.146858	protocadherin 10 Homo sapiens cDNA FLJ13303 fis, clone OV	11.1 11.1
oo	424893 425649	AW295112 U30930	Hs.153648 Hs.158540	UDP glycosyltransferase 8 (UDP-galactose	11.1
	438380	T06430	Hs.6194	chondroitin sulfate proteoglycan BEHAB/b	11.1
	423678	AW963357	Hs.7847	ESTs	10.7 10.7
65	446692 430691	Z44514 C14187	Hs.103538	Homo sapiens mRNA for KIAA1763 protein, ESTs	10.7
05	428728	NM_016625			10.6
	427701	AA411101	Hs.243886		10.6
	431988 433896	AC002302 AW294729	Hs.77202 ·Hs.274461	protein kinase C, beta 1 ESTs	10.5 10.5
70	431467	N71831	Hs.256398		10.4
	419249	X14767	Hs.89768	gamma-aminobutyric acid (GABA) A recepto	10.3
	445041 446782	T64183 AI653048	Hs.282982 Hs.144006		10.3 10.2
	451952	AL120173	Hs.301663		10.2
75	446711	AF169692	Hs.12450	protocadherin 9	10.1
	438054	AA776626	Hs.169309		10.1 10.1
	443785 451099	AW449952 RS2795	Hs.190125 Hs.25954	interleukin 13 receptor, alpha 2	10.0
00	419863	AW952691	Hs.93485	Homo sapiens mRNA; cDNA DKFZp761D191 (fr	10.0
80	416857	AA188775	Hs.292453		10.0 10.0
	435191 419271	R15912 N34901	Hs.4817 Hs.238532	Homo sapiens clone 24461 mRNA sequence ESTs	9.9
	429927	NM_001115		adenylate cyclase 8 (brain)	9.9

					0.0
	415293	R49462	Hs.106541	ESTs	9.9 9.8
	440184 452526	AB002297 W38537	Hs.7022 Hs.280740	dedicator of cyto-kinesis 3 hypothetical protein MGC3040	9.8
	427304	AA761526	Hs.163853	ESTs	9.7
5	420547	AF155140	Hs.98738	gonadotropin-regulated testicular RNA he	9.6
	421659	NM_014459	Hs.106511	protocadhenn 17	9.6
	426847	S78723	Hs.298623	5-hydroxytryptamine (serotonin) receptor	9.6 9.5
	429656 447101	X05608 N72185	Hs.211584 Hs.44189	neurofilament, light polypeptide (68kD) ESTs	9.5
10	442613	AI004002	Hs.130522	Kv channel-interacting protein 1	9.5
	454027	R40192	Hs.21527	Human DNA sequence from clone GS1-115M3	9.5
	445102	AW204510	Hs.22270	ESTs	9.5
	435793	AB037734	Hs.4993	KIAA1313 protein ESTs	9.5 9.5
15	437948 438209	AA772920 AL120659	Hs.303527 Hs.6111	aryl-hydrocarbon receptor nuclear transi	9.4
10	415170	R44386	Hs.164578	ESTs	9.3
	415486	H12214	Hs.13284	ESTs, Weakly similar to 2109260A B cell	9.2
	435501	AW051819	Hs.129908	KIAA0591 protein	9.2 9.2
20	416072	AL110370 Al365130	Hs.79000 Hs.11307	growth associated protein 43 ESTs, Weakly similar to T19326 hypotheti	9.1
20	442910 438080	AA777381	Hs.291530	ESTs, Weakly similar to ALUC_HUMAN !!!!	9.1
	425187	AW014486	Hs.22509	ESTs	9.1
	424028	AF055084	Hs.153692	Homo sapiens cDNA FLJ14354 fis, clone Y7	9.0
25	430091	AB032958	Hs.233023	KIAA1132 protein	9.0 9.0
25	427540 447198	R12014 D61523	Hs.20976 Hs.283435	ESTs ESTs	9.0
	449611	AI970394	Hs.197075	ESTs	8.9
	444124	R43097	Hs.6818	ESTs	8.9
20	451996	AW514021	Hs.245510	ESTs	8.8
30	454048	H05626	Hs.6921	ESTs	8.8 8.8
	412266	N59006 AA708205	Hs.26133 Hs.100343	ESTs ESTs	8.7
	433597 447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	8.6
	450154	R15891	Hs.281587	Human (clone CTG-A4) mRNA sequence	8.6
35	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 (Ciona savignyi	8.5
•	423135	N67655	Hs.26411	ESTs ESTs	8.5 8.4
	418097 420602	R45137 AF060877	Hs.21868 Hs.99236	regulator of G-protein signalling 20	8.4
	419721	NM_001650	Hs.288650	aquaporin 4	8.4
40	449300	AI656959	Hs.346514	ESTS	8.4
	436954	AA740151	Hs.130425	ESTs	8.3 8.3
	425354	U62027	Hs.155935	complement component 3a receptor 1	8.3
	424997 442710	AL138167 AID15631	Hs.96920 Hs.23210	ESTs ESTs	8.2
45	449625	NM_014253	10.20210	odz (odd Oz/ten-m, Drosophila) homolog 1	8.2
	451625	R56793	Hs.106576	alanine-glyoxylate aminotransferase 2-li	8.2
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	B.O 8.0
	449605	AW138581	Hs.198416 Hs.100826	ESTs ESTs	8.0
50	407886 414175	AW969688 Al308876	Hs.103849	hypothetical protein DKFZp761D112	7.9
•	429946	R49390	Hs.254129	KIAA1678	7.9
	400293	N51002	Hs.306480		7.9
	455601	Al368680	Hs.816	SRY (sex determining region Y)-box 2 phosphoserine phosphatase-like	7.9 7.8
55	409799 415279	D11928 F04237	Hs.76845 Hs.1447	glial fibrillary acidic protein	7.8
-	429918	AW873986	Hs.119383		7.8
	449433	AI672096	Hs.9012	ESTs, Weakly similar to S26650 DNA-bindi	7.8
	422411	AW749443	Hs.22511 Hs.22543	ESTs Homo sapiens mRNA; cDNA DKFZp761I1912 (f	7.7 7.7
60	448902 452355	Z45998 N54926	Hs.29202	G protein-coupled receptor 34	7.7
•	492333	D82343	Hs.74376	neuroblastoma (nerve tissue) protein	7.7
	407168	R45175	Hs.117183	ESTs	7.6
	448555	AI536697	Hs.159863		7.6 7.6
65	428536	AI143139 AL080093	Hs.2288 Hs.49117	visinin-like 1 Homo sapiens mRNA; cDNA DKFZp564N1662 (1	7.6
05	408947 420362	U79734	Hs.97206	huntingtin interacting protein 1	7.6
	435624	AF218942	Hs.24889	formin 2	7.6
	440105	AA694010	Hs.6932	Homo sapiens clone 23809 mRNA sequence	7.6
70	412068	572043	Hs.73133	metallothionein 3 (growth inhibitory fac L KIAA1796 protein	7.6 7.5
70	445568 417160	H00918 N76497	Hs.268744 Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	7.5
	423361	AW170055	Hs.47628	ESTs	7.5
	456965	AW131888	Hs.172792		7.5
75	458332		Hs.220491		7.4 7.3
75	409902		Hs.15635 Hs.20912		7.3 7.3
	448321 420345		Hs.25231	ESTs	7.3
	402855			NM_001839*:Homo sapiens calponin 3, acid	7.2
٥٨	424481	R19453	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	7.2
80	425741		Hs.15941		7.2 7.2
	448986 415651		Hs.34731 Hs.3815	stathmin-tike-protein RB3	7.2
	412709		Hs.74518		7.1

	451621	AJ879148	Hs.26770	fatty acid binding protein 7, brain	7.1
	445745	AB007924	Hs.13245	KIAA0455 gene product	7.1
	439451	AF086270	Hs.278554	heterochromatin-like protein 1	7.1 7.1
5	418030 400292	BE207573 AA250737	Hs.83321 Hs.72472	neuromedin B 8MP-R1B	7.1
,	407748	AL079409	Hs.38176	KIAA0606 protein; SCN Circadian Oscillat	7.0
	440435	AL042201	Hs.21273	transcription factor NYD-sp10	7.0
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	7.0
10	417417 440152	F05745 AB002376	Hs.89512 Hs.7006	ATPase, Ca transporting, plasma membrane KIAA0378 protein	7.0 7.0
10	422960	AW890487	Hs.63984	cadherin 13, H-cadherin (heart)	7.0
	454293	H49739	Hs.134013	ESTs, Moderately similar to HK61_HUMAN H	7.0
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	7.0
15	426814	AF036943	Hs.172619	myelin transcription factor 1-like	6.9 6.9
13	416836 447350	D54745 A1375572	Hs.80247 Hs.172634	cholecystokinin ESTs	6.9
	440074	AA863045	Hs.10669	ESTs, Weakly similar to T00050 hypotheti	6.9
	436039	AW023323	Hs.121070	ESTs	6.9
20	444396	T65213	Hs.4257	ESTs	6.9
20	425234 438330	AW152225 AW450572	Hs.165909 Hs.257316	ESTs, Wealdy similar to I38022 hypotheti ESTs	6.9 6.8
	410305	AF030409	Hs.62185	solute carrier family 9 (sodium/hydrogen	6.8
	421141	AW117261	Hs.125914	ESTs	6.7
25	412788	AA120960	Hs.198416	ESTs	6.7
25	411078 443455	AI222020 AB001025	Hs.182364 Hs.9349	CocoaCrisp	6.7 6.7
	448769	N66037	Hs.38173	ryanodine receptor 3 ESTs	6.7
	441523	AW514263	Hs.301771	ESTs, Weakly similar to ALUF_HUMAN !!!!	6.7
20	414214	D49958	Hs.75819	glycoprotein M6A	6.6
30	439845	AL355743	Hs.56663	Homo sapiens EST from clone 41214, full	6.6
	437036 429239	A1571514 AA448419	Hs.133022 Hs.45209	ESTs ESTs	6.6 6.6
	434164	AW207019	Hs.148135	serine/threonine kinase 33	6.6
	412155	R38167	Hs.12449	Homo sapiens transmembrane protein HTMP1	6.5
35	452834	AI638627	Hs.105685	KIAA1688 protein	6.5
	441916	AA993571	Hs.129075	ESTs	6.5
	451516	AI800515 AF155108	Hs.12024 Hs.256150	ESTS	6.5 6.5
	434808 452461	N78223	Hs.108106	Homo sapiens, Similar to RIKEN cDNA 2810 transcription factor	6.5
40	450375	AA009647		a disintegrin and metalloproteinase doma	6.4
-	434811	AW971205	Hs.114280	ESTs	6.4
	424624	AB032947	Hs.151301	Ca2+dependent activator protein for secr	6.4
	429250	H56585	Hs.198308	tryptophan rich basic protein	6.3
45	414245 433447	BE148072 U29195	Hs.75850 Hs.3281	WAS protein family, member 1 neuronal pentraxin II	6.3
,,,	424922	BE386547	Hs.217112	hypothetical protein MGC10825	6.3
	426919	AL041228		ELAV (embryonic tethal, abnormal vision,	6.3
	411411	AA345241	Hs.55950	ESTs, Weakly similar to KIAA1330 protein	6.3
50	415669 449048	NM_005025 Z45051	Hs.78589 Hs.22920	serine (or cysteine) proteinase inhibito similar to S68401 (cattle) glucose induc	6.2 6.2
50	433929	AI375499	Hs.27379	ESTs	6.2
	423346	AI267677	Hs.127416	synaptojanin 1	6.2
	448148	NM_016578	Hs.20509	HBV pX associated protein-8	6.2
55	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	6.2 6.2
33	409731 420608	AA125985 BE548277	Hs.56145 Hs.103104	thymosin, beta, identified in neuroblast ESTs	6.2
	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	6.2
	422175	N79885	Hs.6382	ESTs, Highly similar to T00391 hypotheti	6.1
60	428845	AL157579	Hs.153610	KIAA0751 gene product	6.1
60	439274	AF086092	Hs.48372	ESTs	6.1 6.1
	447499 425977	AW262580 R15138	Hs.147674 Hs.165570	protocadherin beta 16 Horno sapiens clone 25052 mRNA sequence	6.1
	453924	R49295	Hs.24886	ESTs	6.1
65	449340	AW235786	Hs.195359	hypothetical protein MGC10954	6.1
65	420077	AW512260	Hs.87767	ESTs	6.1
	431721 433701	AB032996 AW445023	Hs.268044 Hs.15155	KIAA1170 protein ESTs	6.1 6.1
	430968	AW972830	113.13133	gb:EST384925 MAGE resequences, MAGL Horno	6.1
	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	6.1
70	456723	Z43902	Hs.4748	adenylate cyclase activating polypeptide	6.0
	448681	AL109781 AA460421	Hs.21754	Homo sapiens mRNA full length insert cDN	6.0 6.0
	429900 410909	AW898161	Hs.30875 Hs.53112	ESTs ESTs, Moderately similar to ALU8_HUMAN A	6.0
	432281	AK001239	Hs.274263		6.0
75	448243	AW369771	Hs.52620	integrin, beta 8	6.0
	416427	BE244050	Hs.79307	Rac/Cdc42 guanine exchange factor (GEF)	6.0
	419704	AA429104 AL134451	Hs.45057	ESTs EST-	6.0 6.0
	436936 428409	AL134451 AW117207	Hs.197478 Hs.98523	ESTs ESTs	6.0
80	433244	AB040943	Hs.271285	== -	6.0
-	439772	AL365406	Hs.10268	Homo sapiens mRNA tull length insert cDN	6.0
	408096	BE250162	Hs.83765	dihydrofolate reductase	6.0
	419929	U90268	Hs.93810	cerebral cavemous malformations 1	6.0

	422544	AB018259		KIAA0716 gene product	6.0 6.0
	413627	BE182082 H66373		ESTs ESTs, Highly similar to bA393J16.3 [H.sa	6.0
	419985 410366	Al267589	Hs.302689	hypothetical protein	6.0
5	429183	AB014604	Hs.197955	KIAA0704 protein	5.9
	430188	AL049242	Hs.234794	Homo sapiens mRNA; cDNA DKFZp564B083 (fr	5.9 5.9
	441102 448533	AA973905 AL119710	Hs.21365	intermediate filament protein syncollin nucleosome assembly protein 1-like 3	5.9
	407182	AA312551	Hs.230157	ESTs	5.9
10	437372	AA323968	Hs.283631	hypothetical protein DKFZp547G183	5.9 5.9
	433523	H29882	11- 10141	ESTs hypothetical protein FLJ11236	5.9
	444165 424343	AL137443 AW956360	Hs.10441 Hs.4748	adenylate cyclase activating polypeptide	5.9
	420156	AW449258	Hs.6187	ESTs	5.9
15	422864	AA318323	Hs.12827	gb:EST20390 Retina II Homo sapiens cDNA	5.8 5.8
	446727	AB011095	Hs.16032	KIAA0523 protein Homo sapiens mRNA; cDNA DKFZp586P1124 (f	5.6 5.8
	448543 430132	AW897741 AA204686	Hs.21380 Hs.234149	hypothetical protein FLJ20547	5.8
	425782	U66468	Hs.159525	cell growth regulatory with EF-hand doma	5.8
20	419629	AB020695	Hs.91662	KIAA0888 protein	5.8 5.8
	452279	AA286844	Hs.61260	hypothetical protein FLJ13164	5.8
	407808 414737	AA663559 Al160386	Hs.279789 Hs.125087	histone deacetylase 3 ESTs	5.8
	432154	AI701523	Hs.112577	ESTs	5.8
25	410099	AA081630		KIAA0036 gene product	5.8 5.8
	411379	AI816344	Hs.12554	ESTs, Weakly similar to NPL4_HUMAN NUCLE hypothetical protein DKFZp547J036	5.7
	440492 424560	R39127 AA158727	Hs.21433 Hs.150555	protein predicted by clone 23733	5.7
	424300	AL036591	Hs.20887	hypothetical protein FLJ10392	5.7
30	436643	AA757626	Hs.10941	ESTs, Weakly similar to IPP1_HUMAN PROTE	5.7
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (5.7 5.7
	419088	A1538323 AA922153	Hs.52620 Hs.132760	integrin, beta 8 hypothetical protein MGC15729	5.7
	436109 428588	F12101	Hs.185701	Homo sapiens mRNA full length insert cDN	5.7
35	451752	AB032997	Hs.26966	KIAA1171 protein	5.7
	413492	D87470	Hs.75400	KIAA0280 protein	5.7 5.6
	414683	\$78296	Hs.76888	hypothetical protein MGC12702	5.6
	418079 445873	R40058 AA250970	Hs.6911 Hs.251946	ESTs poly(A)-binding protein, cytoplasmic 1-l	5.6
40	437034	AA742643	113.201310	gb:ny91c01.s1 NCI_CGAP_GCB1 Homo sapiens	5.6
• • •	419544	AI909154		gb:QV-BT200-010499-007 BT200 Homo sapien	5.6 5.6
	452785	AL359942	Hs.296434	erythroid differentiation and denucleati	5.6
	408081 436887	AW451597 AW953157	Hs.167409 Hs.193235	ESTs hypothetical protein DKFZp547D155	5.6
45	413589	AW452631	Hs.313803		5.6
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	5.6 5.5
	433556	W56321	Hs.111460 Hs.20887	catcium/calmodulin-dependent protein kin hypothetical protein FLJ 10392	5.5
	448299 425154	AA497044 NM_001851			5.5
50	447773	AI423930	Hs.36790	ESTs, Weakly similar to putative p150 [H	5.5
	422421	AA325138	Hs.235873		5.5 5.5
	453128	AW026516	Hs.31791 Hs.32452	acylphosphatase 2, muscle type Homo sapiens mRNA for KIAA1263 protein,	5.5
	453220 440866	AB033089 Ai703103	Hs.271360		5.4
55	428976	AL037824	Hs.194695	ras homolog gene family, member I	5.4
	419723	AL120193	Hs.339810		5.4 5.4
	452799	AI948829 AL023513	Hs.213786 Hs.194766		5.4
	429038 445255	NM_01484			5.4
60	424332	AA338919	Hs.10161		5.4
	440210	AW674562		ESTs	5.4 5.4
	414825	X06370 AL078596	Hs.77432 Hs.22591		5.4
	448935 452786		Hs.10664		5.4
65	408790			neurotrophic tyrosine kinase, receptor,	5.4
	423476			Human DNA sequence from clone RPS-1046G1	5.4 5.4
	448507		Hs.21333 Hs.48784		5.4
	419683 407728				5.4
70	453313				5.4
	422094				5.4 5.4
	452856				5.4
	434792 412190		Hs.27446		5.3
75	425588		Hs.46627	ESTs	5.3
	444190	AI878918	Hs.10526		5.3 5.3
	429698		Hs.26339) ESTs, Wealdy similar to S21348 probable myelin associated glycoprotein	5.3
	424456 446997		Hs.1780 Hs.16758		5.3
80	427302			Homo sapiens cDNA FLJ11554 fis, clone HE	5.3
	439607	7 BE540565	Hs.15946	50 ESTs	5.3 5.3
	448499				5.3
	41003	ADUZU/Z	, 15,,000		

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	451407	AA131376	Hs.343809	fibroblast growth factor 128	5.3
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	5.3
	428784	Y12851	Hs.193470	purinergic receptor P2X, ligand-gated to	5.3
5	418512 435538	AW498974 AB011540	Hs.4930	diacytglycerol tinase, zeta (104kD) tow density lipoprotein receptor-related	5.3 5.3
,	420285	AA258124	Hs.293878	ESTs, Moderately similar to ZN91_HUMAN Z	5.2
	407896	D76435	Hs.41154	Zic family member 1 (odd-paired Drosophi	5.2
	404819	AA2001E2		NM_002688*:Homo sapiens peanut (Drosophi	5.2 5.2
10	426503 405348	AA380153		gb:EST93093 Skin tumor 1 Homo sapiens cD C7001664:gi[12698061]dbj[BAB21849.1] (AB	5.2
10	431552	AI815863	Hs.259873	axonal transport of synaptic vesicles	5.2
	418677	S83308	Hs.87224	SRY (sex determining region Y)-box 5	5.2
	427250 428037	R35941 N47474	Hs.25418 Hs.89230	ESTs potassium intermediate/small conductance	5.2 5.2
15	445740	178281	Hs.13226	Homo sepiens clone 25181 mRNA sequence	5.2
	430130	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (5.2
	423869	BE409301	Hs.134012	C1q-related factor	5.2 5.2
	416220 457005	N49776 AJ007421	Hs.170994 Hs.172597	hypothetical protein MGC10946 sal (Drosophila)-like 3	5.1
20	447072	D61594	Hs.17279	tyrosytorotein sutfotransferase 1	5.1
	414372	AA143654		gb:zo65a02.r1 Stratagene pancreas (93720	5.1
	410631	AA086469	Hs.47171	ESTs	5.1 5.1
	414821 420133	M63835 AA426117	Hs.77424 Hs.155543	Fc tragment of IgG, high affinity Ia, re ESTs	5.1
25	453884	AA355925	Hs.36232	KIAA0186 gene product	5.1
	414922	D00723	Hs.77631	glycine cleavage system protein H (amino	5.1
	414727	BE466904 NM_003947	Hs.190162 Hs.8004	gb:hz28f03.x1 NCI_CGAP_GC6 Homo sapiens huntingtin-associated protein interactin	5.1 5.1
	441869 437387	Al 198874	Hs.28847	AD026 protein	5.0
30	400533	70,000, 4		ENSP00000209376*:PRED65 protein (Fragmen	5.0
	430979	A1479755	Hs.129010	ESTs	. 5.0
	448944	AB014605	Hs.22599 Hs.6996	atrophin-1 interacting protein 1; activi ESTs	5.0 5.0
	444600 453785	R41398 Al368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	5.0
35	428878	AA436884	Hs.48926	ESTS	5.0
	444670	H58373	Hs.332938	hypothetical protein MGC5370	5.0
	440471	AA886146	Hs.307944	ESTs toll-like receptor 2	5.0 5.0
	410434 441390	AF051152 Al692560	Hs.63668 Hs.131175	ESTs	4.9
40	448765	R15337	Hs.21958	Homo sapiens mRNA; cDNA DKFZp547D086 (fr	4.9
	422263	AA307639	Hs.129908	KIAA0591 protein	4.9
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	4.9 4.9
	407235 417404	D20569 NM_007350	Hs.169407 Hs.82101	SAC2 (suppressor of actin mutations 2, y pleckstrin homology-like domain, family	4.9
45	448548	R13209	Hs.21413	solute carrier family 12, (potassium-chl	4.9
	420092	AA814043	Hs.88045	ESTs	4.9
	449571	AW016812	Hs.200266	ESTS	4.9 4.9 ·
	412811 409100	H06382 H98216	Hs.42245	ESTs ESTs, Moderately similar to 138022 hypot	4.9
50	403142			NM_002706*:Homo sapiens protein phosphat	4.9
	414300	Al304870	Hs.188680	ESTs .	4.9 4.9
	436607 431553	AW661783 X78075	Hs.211061 Hs.2799	ESTs cartilage linking protein 1	4.9
	449328	AI962493	Hs.345303	ESTs	4.9
55	420805	L10333	Hs.99947	reticulon 1	4.9
	421688	AK000307	Hs.106825	hypothetical protein FLI20300	4.9 4.9
	452898 427958	AA814497 AA418000	Hs.78792 Hs.98280	ESTs potassium intermediate/small conductance	4.9
	432328	AI572739	Hs.195471	6-phosphofructo-2-kinase/fructose-2,6-bi	4.9
60	408453	AI369838	Hs.45127	chondroitin sulfate proteoglycan 5 (neur	4.8
	428841	AI418430	Hs.104935	ESTs ESTs	4.8 4.8
	416439 447458	AA180363 AI741082	Hs.118769 Hs.158961	ESTS	4.8
	429433	AA452899	Hs.213586		4.8
65	409746	NM_004794		RAB33A, member RAS oncogene family	4.8
	436511	AA721252	Hs.291502		4.8 4.8
	443392 423600	AI055821 AI633559	Hs.293420 Hs.310359		4.8
~ 0	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finge	4.8
70	414706	AW340125	Hs.76989	KIAA0097 gene product	4.8
	407385	AA610150 AB032436	Hs.272072 Hs.6535	ESTs, Wealdy similar to 138022 hypotheti brain-specific Na-dependent inorganic ph	4.8 4.7
	439340 427624	AA406245	Hs.24895	ESTs	4.7
-	413248	T64858	Hs.21433	hypothetical protein DKFZp547J036	4.7
75	408670	AF160967	Hs.46784	potassium large conductance calcium-acti	4.7
	440491 411555	R35252 AF113537	Hs.130558 Hs.70669	ESTs, Wealdy similar to 2109260A B cell HMP19 protein	4.7 4.7
	430471	AF064845	Hs.241523		4.7
00	413530	AA130158	Hs.19977	ESTs, Moderately similar to ALU8_HUMAN A	4.7
80	445900	AF070526	Hs.125036		4.7 4.7
	426457 459527	AW894667 AW977556	Hs.169965 Hs.291735		4.7 4.7
	453096		Hs.11325	ESTs	4.7
				250	1
				250	•

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		047000	II- 242567 -	would be account of managing workings	4.7
	409125 428001		Hs.343567 a Hs.219907 E	xonal transport of synaptic vesicles STs, Moderately similar to Transforming	4.7
	410276	AI554545	He 68301 2	naionnietia-2	4.7 4.7
5	421637			tomo sapiens clone 23556 mRNA sequence corting nexin 10	4.7
3	421633 440052	AF121860 AI633744	Hs 195648	ESTs. Weakly similar to 138022 hypotheti	4.7
	439566	AF086387	•	ab:Homo sapiens full length insert cONA	4.7 4.6
	432890	NM_014442		siatic acid binding Ig-like lectin 8 Farget Exon	4.6
10	402145 409892	AW956113	Hs.7149	gb:EST368183 MAGE resequences, MAGD Homo	4.6
	458760	AI498631	Hs.111334	territin, light polypeptide	4.6 4.6
	453362 436734	H14988 Al937612	Hs.107375 Hs.273758	ESTs hypothetical protein FLJ23112	4.6
	426925	NM_001196	Hs.315689	Homo sapiens cDNA: FLJ22373 fis, clone H	4.6
15	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	4.6 4.6
	428832 423770	AA578229 AW976766	Hs.324239 Hs.132776	ESTs, Moderately similar to ZN91_HUMAN Z Homo sapiens cDNA FLJ 10077 fis, clone HE	4.6
	410264	AK001853	Hs.61508	Homo sapiens cDNA FLJ 10991 fis, clone Pt.	4.6
20	429149	AW193360		ESTs, Wealdy similar to I38022 hypotheti	4.6 4.6
20	437762 439249	T78028 AF086060	Hs.154679 Hs.170053	synaptotagmin I G-protein coupled receptor 88	4.6
	416426	AA180256	Hs.210473	Homo sapiens cDNA FLJ14872 fis, clone PL	4.6
	425256	8E297611	Hs.155392	collapsin response mediator protein 1	4.6 4.6
25	415257 428186	F03016 AW504300	Hs.27513 Hs.295605	ESTs mannosidase, alpha, class 2A, member 2	4.6
23	458814	AM98957	Hs.170861	ESTs, Weakly similar to Z195_HUMAN ZINC	4.6 4.5
	451320	AW118072		diacylglycerol kinase, zeta (104kD)	4.5 4.5
	424998 422709	U58515 AA315331	Hs.154138 Hs.153485	chitinase 3-like 2 ESTs	4.5
30	420578	AA813546	Hs.99034	GTP-binding protein Rho7	4.5 4.5
	421977	W94197	Hs.110165	ribosomal protein L26 homolog DNA replication factor	4.5
	457465 427712	AW301344 Al368024	Hs.122908 Hs.283696	ESTs	4.5
	444656	Al277924	Hs.145199	ESTs	4.5
35	413409	A1638418	Hs.1440	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	4.5 4.5
	429399 450639	AA452244 A1703186	Hs.16727 Hs.277174	ESTs ESTs	4.5
	452106	AI141031	Hs.21342	ESTs	4.5 4.5
40	424240	AB023185	Hs.143535	catcium/calmodulin-dependent protein kin gb:nz24c08.s1 NCI_CGAP_GCB1 Homo sapiens	4.5
40	433009 446657	AA761668 AI335191	Hs.260702	ESTs, Weakly similar to 2109260A B cell	4.5
	428189	AA424030	Hs.46627	ESTs	4.5 4.5
	423178	AI033140	Hs.124983	Homo sapiens mRNA; cDNA DKFZp564C142 (fr	4.5 4.5
45	445133 418771	AW157646 AA807881	Hs. 198689 Hs. 25329	ESTs ESTs	4.4
73	438456	AA913381	Hs.20594	FSTs	4.4 4.4
	410386	W26187	Hs.3327	Homo sapiens cDNA: FLJ22219 fis, clone H ESTs, Weakly similar to 138022 hypotheti	4.4
	413834 419103	BE296896 240229	Hs.224179 Hs.96423	hypothetical protein FLJ23033	4.4
50	420560	AW207748	Hs.59115	ESTs	4.4 4.4
	439662	H97552	Hs.269060	ESTs ESTs, Highly similar to NRG3_HUMAN PRO-N	4.4
	408577 445034	H50572 AW293376	Hs.19515 Hs.143659		4.4
	402605			Target Exon	4.4 4.4
55	426271	AF026547 AA331517	Hs.169047 Hs.286055		4.4
	457561 430676		rs.200033	ob Homo sagiens envelope protein RIC-3 (4.4
	439570	179925	Hs.269165	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.4 4.4
60	452752 439108			KIAA0820 protein synaptogyrin 3	4.4
00	405819		115.0401	NM_002578:Homo sapiens p21 (CDKN1A)-acti	4.4
	446544	Al631932	Hs.7047	ESTs, Weakly similar to Unknown [H.sapie	4.4 4.4
	412530 420871		Hs.266273 Hs.65300	hypothetical protein FLJ13346 ESTs	4.4
65	408622				4.4
-	429269	AA449013		ESTs	4.3 4.3
	427463 425403		Hs.97900 Hs.24970	ESTs ESTs, Weakly similar to B34323 GTP-bindi	4.3
	41204		Hs.73088	RAS-related on chromsome 22	4.3
70	42719	4 AA399018	Hs.25083		4.3 4.3
	43783 40917		Hs.28385 Hs.12259		4.3
	40995			cadherin 18, type 2	4.3
	42696	8 U07616	Hs.17303	4 amphiphysin (Stiff-Mann syndrome with br	4.3 4.3
75	45209 43845			hypothetical protein FLJ11210 gb:EST387294 MAGE resequences, MAGN Homo	4.3
	43845 44693		Hs.47314	ESTs	4.3
	43393	2 AW95459	9 Hs.16933	O neuronal protein	4.3 4.3
80	42480 42198				4.3
50	44283			9 ESTs	4.3
	41658	36 D44643	Hs.14144		4.2 4.2
	40836	59 R38438	Hs.18257	5 Source carrier family 13 (FFFF transport	

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	450530	NM_006668	Hs.25121	cytochrome P450, subfamily 46 (cholester	4.2
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cONA 5730	4.2
	438624	AA889055	Hs.123468	ESTs	4.2 4.2
5	421027	AA761198	Hs.55254 Hs.5422	ESTs share-trip MSP	4.2
,	417632 419412	R20855 AW161058	Hs.90297	glycoprotein M6B synuclein, beta	4.2
	430228	AW950939	Hs.6382	ESTs, Highly similar to T00391 hypotheti	4.2
	450813	A1739625	Hs.203376	ESTs	4.2
10	412505	AA974491	Hs.21734	ESTs	4.2 4.2
10	440168 441707	AA868507 R42637	Hs.126141 Hs.21963	ESTs hypothetical protein DKFZp76180514	4.2
	438703	AI803373	Hs.31599	ESTs	4.2
	444127	N63620	Hs.13281	EST8	4.2
16	447397	BE247676	Hs.18442	E-1 enzyme	4.2 4.2
15	445523 415079	Z30118 R43179	Hs.293788 Hs.22895	ESTs, Moderately similar to unnamed prot hypothetical protein FLJ23548	· 4.2
	416871	H98716	NS.22033	gb:yx13d08.s1 Soares melanocyte 2NbHM Ho	4.2
	408838	AI669535	Hs.40369	ESTs	4.2
20	425287	R88249	Hs.155524	peanut (Drosophila)-like 2	. 4.2
20	404584	44702070	Un 400000	Target Exon ESTs, Wealthy similar to SYT5_HUMAN SYNAP	4.2 4.2
	436035 409091	AA703679 AW970386	Hs.106999 Hs.269423	ESTs Weakly similar to 5115_Howard 51104F	4.2
	437117	AL049256	Hs.122593	ESTs	4.2
~~	429643	AA455889	Hs.167279	FYVE-finger-containing Rab5 effector pro	4.2
25	439231	AW581935	Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	4.2 4.2
	408177 438875	A1241733 AA827640	Hs.43871 Hs.189059	ESTs ESTs	4.2
	447877	AI435184	Hs.164252	ESTs	4.2
	415402	AA164687	Hs.177576	mannosyl (alpha-1,3-)-glycoprotein beta-	4.2
30	434859	BE255080	Hs.299315	collapsin response mediator protein-5, C	4.2
	449714	AB033015	Hs.23941 Hs.175563	KIAA1189 protein Homo sapiens mRNA; cDNA DKFZp564N0763 (f	4.2 4.2
	427315 404541	AA179949	ns.113303	NM_030795:Homo sapiens stathmin-like 4 (4.1
	449969	AW295142	Hs.180187	Homo sapiens cDNA FLJ14337 fis, clone PL	4.1
35	422374	AW732869	Hs.1519	protein kinase, cAMP-dependent, regulato	4.1
	422253	W81526	Hs.118329	ESTs, Moderately similar to GAD_HUMAN GA ESTs	4.1 4.1
	440483 429421	Al200836 Al031658	Hs.150386	Human DNA sequence from clone RP1-310013	4.1
	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-ti	4.1
40	424001	W67883	Hs.137476	paternally expressed 10	4.1
	422170	A1791949	Hs.112432	anti-Mullerian hormone	. 4.1 4.1
	445292 450407	AV653264 NM_000810	Hs.13982 Hs.24969	Homo sapiens cDNA FLJ14666 fis, clone NT gamma-aminobutyric acid (GABA) A recepto	4.1
	429401	AW296102	Hs.99272	ESTs, Weakly similar to S32567 A4 protei	4.1
45	408950	AA707814	Hs.14945	long fatty acyl-CoA synthetase 2 gene	4.1
	415796	R87548	Hs.78854	ATPase, Na? transporting, beta 2 polypep	4.1 4.1
	446619	AU076643 AW972565	Hs.313 Hs.32399	secreted phosphoprotein 1 (osteopontin, ESTs, Wealdy similar to S51797 vasodilat	4.1
	457211 416547	H62914	Hs.268946	ESTs, Weakly similar to PC4259 ferritin	4.1
50	412777	Al335773	Hs.270123	ESTs	4.1
	445225	AJ216555	Hs.202398	ESTs	4.1
	408926	AF217525 BE266659	Hs.49002	Down syndrome cell adhesion molecule Horno sapiens, Similar to RIKEN cDNA A430	4.1 4.1
	417873 443301	AI733614	Hs.293659 Hs.220587	ESTs, Moderately similar to ALUS_HUMAN A	4,1
55	429281	AA830856	Hs.29808	Homo sapiens cDNA: FLJ21122 fis, clone C	4.1
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	4.1
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	4.1 4.1
	417355 410359	D13168 R38624	Hs.82002 Hs.106313	endothelin receptor type B ESTs	4.1
60	426529	AF090100	Hs.170241	Homo sapiens clone IMAGE 23915	4.1
	433323	AA805132	Hs.159142		4.1
	434933	R91095	Hs.4276	KIAA1701 protein	4,1 4.1
	453331 422661	AI240665 NM_014700	Hs.119004	ESTs KIAA0665 gene product	4.1
65	424726	AK001007	Hs.138760		4.0
	416805	F13271	Hs.79981	Human clone 23560 mRNA sequence	4.0
	441797	AI936933	Hs.214635		4.0 4.0
	424282	R76421	Hs.135694 Hs.39384		4.0
70	407792 425390	A1077715 A1092634	Hs.156114	putative secreted ligand homologous to f protein tyrosine phosphatase, non-recept	4.0
	435312	AJ243396	Hs.4865	voltage-gated sodium channel beta-3 subu	4.0
	424635	AA420687	Hs.115455		4.0
	423279	AW959861	Hs.290943		4.0 4.0
75	444001 410768	AI095087 AF038185	Hs.152299 Hs.66187	ESTs, Moderately similar to S65657 atpha Homo sapiens clone 23700 mRNA sequence	4.0
, ,	426413	AA377823	113.00107	gb:EST90805 Synovial sarcoma Homo sapien	4.0
	450581	AF081513	Hs.25195	TGF-beta 4	4.0
	435854	AJ278120	Hs.4996	putative ankyrin-repeat containing prote	4.0
80	433615	AA732982	Hs.269607 Hs.130729		4.0 4.0
30	432058 439774	AW665996 AL360257	Hs.213493		4.0
	445666		Hs.282388	S ESTs	4.0
	450582			G-rich RNA sequence binding factor 1	4.0

		437814	AI088192	Hs.135474	ESTs, Weakly similar to ODX9_HUMAN ATP-D	4.0
		451468	AW503398	Hs.293663	ESTs, Moderately similar to 138022 hypot	4.0 4.0
			AA001064	Hs.43670	ESTs Homo sapiens cDNA FLJ14459 fis, clone HE	4.0
	5		AA889416 AF070564	Hs.344043 Hs.13415	Homo saniens clone 24571 mRNA sequence	4.0
	,	420111	AA255652	1	gb:2s21h11.r1 NCI_CGAP_GCB1 Homo sapiens	4.0
		407198	H91679		gb:yv04a07.s1 Soares fetal fiver spleen	4.0 4.0
		422564	AI148006	Hs.222120 Hs.322922	ESTs	4.0
1	0	443992 435542	AW022228 AA687376	MS.J22922	ESTs ESTs	4.0
,	U	444153	AK001610	Hs.10414	hypothetical protein FLJ10748	4.0
		437748	AF234882	Hs.5814	suppression of turnorigenicity 7	4.0 4.0
		439285	AL133916	Hs.59970	hypothetical protein FLJ20093 ESTs	4.0
1	15	449655 458435	A1021987 A1418718	Hs.144121	ESTs, Wealdy similar to T46916 hypotheti	4.0
	13	412659	AW753865	Hs.74376	otfactomedin related ER localized protei	4.0
		423905	AW579960	Hs.135150	tung type-I cell membrane-associated gly	4.0 4.0
		432683	AW995441	Hs.10475	ESTs nucleosome assembly protein 1-like 2	4.0
,	20	410765 420649	A1694972 A1866964	Hs.66180 Hs.124704	ESTs, Moderately similar to S65657 alpha	4.0
•	20	450927	AI807804	Hs.134342		4.0
		448985	AA324885	Hs.22777	carbonic anhydrase XI	4.0 4.0
		416406	D86961	Hs.79299	lipoma HMGIC fusion partner-like 2 amyloid beta (A4) precursor-like protein	3.9
	25	412754 416340	AW160375 N31772	Hs.74565 Hs.79226	fasciculation and elongation protein zet	3.9
	23	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	3.9 3.9
		413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	3.9
		419687	AI638859	Hs.227699	ESTs, Weakly similar to T203_HUMAN TRANS	3.9
	30	453438 410082	AJ469935 AA081594	Hs.22792 Hs.158311	ESTs Musashi (Drosophila) homolog 1	3.9
	30	424736	AF230877	Hs.152701	microtubule-interacting protein that ass	3.9 3.9
		412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	3.9 3.9
		411666	AF106564	Hs.71346	neurofilament 3 (150kO medium) glutamate receptor, ionotropic, kainate	3.9
	35	439935 459278	S75105 AW294659	Hs.8358 Hs.34054	Homo sapiens cDNA: FLJ22488 fis, clone H	3.9
	55	432809	AA565509	Hs.131703	ESTs	3.9 3.9
		450568	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 fis, clone NT	3.9
		413951	AW051200	Hs.75640	natriuretic peptide precursor A ESTs	3.9
	40	435743 447937	T66861 AL109716	Hs.12962 Hs.20034	Homo sapiens mRNA full length insert cDN	3.9
	40	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	3.9
		448526	AB028946	Hs.21361	KIAA1023 protein	3.9 . 3.9
		445890	AF055019	Hs.21906	Homo sapiens clone 24670 mRNA sequence adolase C, tructose-bisphosphate	3.8
	45	425241 417333	AA324624 AL157545	Hs.155247 Hs.173179		3.8
	40	435832	AA425688	Hs.41641	Bruno (Drosophila) -like 4, RNA binding	3.8
		410592	R94088	Hs.43569	ESTs	3.8 3.8
		443361	A1792628	Hs.13327	3 ESTs C4001100*:gi 5852342 gb AAD54015.1 (AF0	3.8
	50	403696 437756	AA767537	Hs.19709		3.8
	50	433675	AW977653		ribonucleotide reductase M2 polypeptide	3.8 3.8
		414998	NM_00254		oxidised low density lipoprotein (lectin	3.8
		425652		Hs.32243		3.8
	55	437449 421040		Hs.20833 Hs.13528	M FSTs	3.8
	33	454171			gb:QV2-CT0261-201099-011-f05 CT0261 Homo	3.8
		443740	R56434	Hs.21062	2 ESTs	3.8 3.8
		441668		Hs.13631 Hs.34731		3.8
	60	423175 457183		Hs.11856		3.8
	00	438142		Hs.2696	51 ESTs	3.8
		408875	NM_0154			3.8 3.8
		436899				3.8
	65	456497 416892		6 Hs.1236 Hs.8040		3.8
	05	413199		Hs.7523	The second of the second states and the second states and the second states are second states and the second states are second states and the second states are second states	3.8
		410711	AB002316			3.8 3.8
		454117				3.8
	70	43894				3.8
	70	445071 424331			196 Homo sapiens cDNA FLJ13596 fis, clone PL	3.8
		43909		0 Hs.6462	protein kinase C and casein kinase subst	3.8 3.8
		44944				3.7
	75	41125				3.7
	13	44827 43426				3.7
		40077			NM_007325*:Homo sapiens glutamate recept	3.7
		41958	6 AI08848			3.7 3.7
	00	45807				3.7
	80	44590 44845		Hs.134 94 Hs.345	433 gb:Ul-H-BIOp-abh-g-09-0-Ul.s1 NCI_CGAP_S	3.7
		43018			gb:PM3-BN0176-100400-001-g04 BN0176 Homo	3.7
		43014		Hs.234	434 hairy/enhancer-of-split related with YRP	3.7

	458912	AI91 1066		ESTs	3.7
	428110	AJ312485	Hs.138294	ESTs, Moderately similar to Z195_HUMAN Z	3.7
	448048	BE281291	Hs.170408	ESTs, Moderately similar to A47582 B-cel	3.7 3.7
5	442326 422798	H92962 R92347	Hs.124813 Hs.34574	hypothetical protein MGC14817 ESTs, Wealdy similar to ALU1_HUMAN ALU S	3.7
•	428873	AI701609	Hs.98908	ESTs	3.7
	438208	AL041224	Hs.65379	ESTs	3.7
	414040	N58513	Hs.32171 Hs.40403	ESTs Cbp/p300-interacting transactivator, wil	3.7 3.7
10	407846 408829	AA426202 NM_006042	Hs.48384	heparan suffate (glucosamine) 3-0-suffot	3.7
••	425010	T16837	Hs.4241	ESTs	3.7
	427209	H06509	Hs.92423	KIAA1566 protein	3.7
	407603 410126	AW955705 BE169274	Hs.62604	Homo sapiens, clone IMAGE:4299322, mRNA, KIAA0036 gene product	3.6 3.6
15	426646	AA382787	Hs.122713	ESTs	3.6
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	3.6
	419390	AI701162	Hs.90207	hypothetical protein MGC11138	3.6 3.6
	441703 431725	AW390054 X65724	Hs.192843 Hs.2839	leucine zipper protein FKSG14 Norrie disease (pseudoglioma)	3.6
20	448425	AI500359	Hs.346112	ESTs	3.6
	423611	AB011163	Hs.129908	KIAA0591 protein	3.6
	438831	BE263273	Hs.6439	synapsin II neurotrimin	3.6 3.6
	419235 451027	AW470411 AW519204	Hs.288433 Hs.40808	ESTs	3.6
25	428483	AI908539	Hs.184592	KIAA0344 gene product	3.6
	424947	R77952		ESTs, Wealdy similar to alternatively sp	3.6
	404150 450297	AW901347	Hs.38592	Target Exon hypothetical protein FLJ23342	3.6 3.6
	443715	AI583187	Hs.9700	cyclin E1	3.6
30	435910	AI084152	Hs.21782	ESTs, Wealdy similar to ALU7_HUMAN ALU S	3.6
	418064	BE387287	Hs.83384	S100 calcium-binding protein, beta (neur	3.6 3.6
	432488 431342	AA551010 AW971018	Hs.216640 Hs.21659	ESTs ESTs	3.6
	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	3.6
35	412043	BE156622	Hs.333371	Homo sapiens clone TA40 untranslated mRN	3.6
	448448	NM_014954	Hs.21239 Hs.21906	KIAA0985 protein	3.6 3.6
	447818 445105	W79940 AF238869	Hs.283955	Homo sapiens clone 24670 mRNA sequence Homo sapiens clone GLSH-2 similar to gli	3.6
	409557	BE182896	Hs.211193	ESTs	3.6
40	425202	AW962282	Hs.152049	ESTs, Weakly similar to 138022 hypotheti	3.6
	451734	NM_006176	Hs.26944	naurogranin (protein kinase C substrate, gb:EST374201 MAGE resequences, MAGG Homo	3.6 3.6
	425331 412799	AW962128 AI267606		gb:aq91h03.x1 Stanley Frontal SB pool 1	3.6
	435040	AI932350	Hs.152825	ESTs	3.6
45	434149	Z43829	Hs.244624	hypothetical protein MGC5469	3.6 3.6
	415709 424051	AA649850 AL110203	Hs.278558 Hs.138411	ESTs Homo sapiens mRNA; cDNA DKFZp586J1922 (f	3.6
	437640	AA764893	Hs.272155	ESTs, Weakly similar to 138022 hypotheti	3.6
	445953	AI612775	Hs.145710		3.6
50	449256	AA059050	Hs.59847	ESTs	3.6 3.6
	424687 409327	J05070 L41162	Hs.151738 Hs.53563	matrix metalloproteinase 9 (gelatinase B collagen, type IX, alpha 3	3.6
	417675	AI808607	Hs.3781	similar to murine leucine-rich repeat pr	3.6
<i>c c</i>	423641	AL137256	Hs.130489		3.6 3.6
55	443912 424572	R37257 M19650	Hs.184780	ESTs 2,3-cyclic nucleotide 3' phosphodiasta	3.5
	424899	AL119387	Hs.119062		3.5
	439726	AW449893	Hs.293707	ESTs, Wealthy similar to 138598 zinc fing	3.5
60	416490	AF090116	Hs.79348	regulator of G-protein signafling 7 sin3-essociated polypeptide, 30kD	3.5 3.5
UU	458809 429084	AW972512 AJ001443	Hs.20985 Hs.195614		3.5
	407624	AW157431	Hs.248941		3.5
	419038	AW134924	Hs.190325		3.5 3.5
65	451489 428242	NM_005503 H55709	Hs.26468 Hs.2250	amytoid beta (A4) precursor protein-bind leukemia inhibitory factor (cholinergic	3.5
05	411048	AK001742	Hs.67991	hypothetical protein DKFZp434G0522	3.5
	435575	AF213457	Hs.44234	triggering receptor expressed on myeloid	3.5
	424340	AA339036	Hs.7033	ESTS	3.5 3.5
70	425790 432188	AW136286 Al362952	Hs.288448 Hs.2928	is ESTs solute carrier family 7 (cationic amino	3.5
, ,	453896	AW293483	Hs.255205		3.5
	434784	AA649051	Hs.164007	ESTS	3.5
	452449	AW068658	Hs.20943 Hs.171618		3.5 3.5
75	425212 407253	AW962253 AA411175	Hs.14193		3.5
	418049	AA211467	Hs.19048	Homo sapiens, Similar to nuclear localiz	3.5
	421247	BE391727	Hs.102910		3.5 3.5
	459311 439450	R40192 R51613	Hs.21527 Hs.12530		3.5 3.5
80	435545	AA687415	Hs.28107	ESTs	3.5
	445729	H21066	Hs.13223	Homo sapiens mRNA full length insert cDN	3.5
	448999		Hs.22791 Hs.13503		3.5 3.5
	412590	AL134388	rs.13303	Care, treast anime in worth ulbones	3.3

	400007	A1000261	Hs.115325	RAB7, member RAS oncogene family-like 1	3.5
	438527 441111			ESTs	3.5
	418630	AI351311	Hs.251946	poly(A)-binding protein, cytoplasmic 1-I	3.5 3.5
_	439920			neurotrimin	3.5 3.5
5	421268 432022	AI126821 AL162042	Hs.30514 Hs.272348	ESTs Homo sapiens mRNA; cDNA DKFZp761L1212 (1	3.5
	412719	AW016610	Hs 816	FSTs	3.5
	435092	AL137310	Hs.4749	Homo sapiens mRNA; cDNA DKFZp761E13121 (3.5 3.5
10	414178	AW957372	Hs.46791	ESTs, Weakly similar to 138022 hypotheti ESTs, Weakly similar to ALU1_HUMAN ALU S	3.5
10	437252 452108	AJ433833 AW135982	Hs.164159 Hs.203013	hypothetical protein FLJ12748	3.4
	421183	AL135740	Hs.102447	TSC-22-like	3.4
	441834	AL138034	Hs.7979	KIAA0736 gene product	3.4 3.4
1.5	413812	AW188687	Hs.44748	ESTs EST-	3.4
15	449932 447067	A1675444 R42098	Hs.263024 Hs.21964	ESTs ESTs	3.4
	408296	AL117452	Hs.44155	DKFZP586G1517 protein	3.4
	447028	AJ973128	Hs.167257	brain link protein-1	3.4 3.4
20	432715	AA247152	Hs.200483	ESTs, Weakly similar to KIAA1074 protein potassium voltage-gated channel, Shab-re	3.4
20	418358	L02840 H08370	Hs.84244 Hs.33067	ESTs	3.4
	417084 444534	AW271626	Hs.42294	ESTs	3.4
	440700	AW952281	Hs.296184	guanine nucleotide binding protein (G pr	3.4 3.4
25	436637	A1783629	Hs.26766	ESTs gb:CM3:BN0075-240200-101-d11 BN0075 Homo	3.4
25	412820	BE001236 AA773842	Hs.293799	ESTs	3.4
	428138 453033	AA325869	Hs.31463	KIAA0281 gene product	3.4
	453305	R39224	Hs.267997	EHM2 gene	3.4 3.4
20	459660	M79082		ESTs	3.4
30	418821	AA436002 W76326	Hs.183161	ESTs gb:zd60d04.r1 Soares_fetal_heart_NbHH19W	3.4
	439518 400379	NM_018432		Homo sapiens ovarian cancer related prot	3.4
	437085	AA743935	Hs.202329	ESTs	3.4 3.4
0.0	419852	AW503756	Hs.286184	hypothetical protein dJ551D2.5	3.4
35	430694	AA810624	Hs.30936 Hs.131373	ESTs, Weakly similar to H2BH_HUMAN HISTO ESTs	3.4
	441287 425870	AW293132 R13406	Hs.56782	ESTs	3.4
	443672	AA323362	Hs.9667	butyrobetaine (gamma), 2-oxoglutarate di	3.4 3.4
40	448044	A1458682		gb:tk13e01.x1 NCI_CGAP_Lu24 Homo sapiens	3.4
40	405238	AJ015881	Hs.324527	Target Exon mitochondrial ribosomal protein S5	3.4
	440404 453590	AF150278	Hs.33578	KIAA0820 protein	3.4
	450756	AI733488	Hs.144062	ESTs	3.4 3.4
	404283			ENSP00000244751*:Copine-like protein KIA	3.4
45	423257	AW161039	Hs.125878 Hs.133483	synapsin III ESTs, Wealdy similar to T34549 probable	3.4
	432149 412986	AW614326 X81120	Hs.75110	cannabinoid receptor 1 (brain)	3.4
	422809	AK001379	Hs.121028		3.4
	420050	AL118615	Hs.94653	neurochondrin	3.4 3.4
50	431789	H19500	Hs.269222 Hs.86122	mitogen-activated protein kinase 4 protein A	3.4
	408601 453740	U47928 AL120295	Hs.311809		3.4
	449919	AI674685	Hs.200141	ESTs	3.4 3.4
<i>E E</i>	426380	Al291267	Hs.149990		3.3
55	408554 443257	AA836381 Al334040	Hs.315111 Hs.11614	HSPC065 protein	3.3
	432731	R31178	Hs.287820		3.3
	421679	AI475110	Hs.203933	ESTs .	3.3 3.3
۲0	453169		Hs.32156	KIAA1394 protein hypothetical protein DKFZp761H039	3.3
60	437397 443310	AA349847 BE552018	Hs.4221 Hs.133152	P FSTs	3.3
	423169		Hs.21837	ESTs, Wealty similar to KIAA0927 protein	3.3
	433657	A1244368	Hs.8124	PH domain containing protein in retina 1	3.3 3.3
65	408449				3.3
03	417402 416677		Hs.13475 Hs.33484		3.3
	439753			hypothetical protein from EUROIMAGE 2168	3.3
	455648	BE064420		gb:RC4-BT0311-241199-012-c08 BT0311 Homo	3.3 3.3
70	450337		Hs.20242		3.3
70	423420 433238		Hs.12838 6 Hs.3221	regulator of G-protein signalling 6	3.3
	417868		Hs.12259	2 EŠTs	3.3
	436207	7 AA334774	Hs.12845	hypothetical protein MGC13159	3.3 3.3
75	44160			neuronal cell adhesion motecule 15 Homo sapiens mRNA for KIAA1764 protein,	3.3 3.3
75	449249 41821		Hs.19311 Hs.28309		3.3
	45606		Hs.45184	Homo sapiens cDNA FLJ12284 fis, clone MA	3.3
	44914	5 Al632122	Hs.19840	08 ESTs	3.3 3.3
80	41510		Hs.1445	34 ESTs C9000559*:gi[12314195 emb CAB99338.1] (A	3.3
80	40127 42029		Hs.8832		3.3
	41999				3.3
	44376				3.3
				25	-

	427317	A8028955	Hs.175780	KIAA1032 protein	3.3
	426920	AA393351	Hs.132121	ESTs	3.3
	433894	AI907682	Hs.243293	ESTs	3.3 3.3
5	454253 419647	AV660717 AA348947	Hs.47144 Hs.91816	DKFZP586N0819 protein hypothetical protein	3.3
,	439978	BE139460	Hs.124673	Homo sapiens cDNA FLJ11477 fis, clone HE	3.3
	407881	AW072003	Hs.40968	heparan sutfate (glucosamine) 3-O-sulfot	3.3
	428670	AA431682	Hs.134832	ESTS	33 33
10	435375 419043	AJ733610 T19167	Hs.187832 Hs.89566	ESTs ets variant gene 1	3.3
10	403341	:	. 4.0000	Target Exon	3.3
	436282	R91913	Hs.272104	ESTs, Moderately similar to ALU1_HUMAN A	3.3
	439627 456209	BE621702 W60633	Hs.29076 Hs.297792	hypothetical protein FLJ21841 ESTs	3.3 3.3
15	438810	AW897846	Hs.6421	hypothetical protein DKFZp761N09121	3.3
	411565	AW851728		gb:MR2-CT0222-011199-007-d06 CT0222 Homo	3.3
	418203	X54942	Hs.83758	COC28 protein kinase 2	3.3 3.3
	451254 435056	AI571016 AW023337	Hs.172967 Hs.5422	ESTs stycoprotein M5B	3.3
20	433842	AI652156	Hs.26346	ESTs	3.3
	433325	AW206986	Hs.143905	ESTs	3.3
	451066 436114	A1758660 AA778232	Hs.206132 Hs.19515	ESTs, Highly similar to NRG3_HUMAN PRO-N	3.3 3.3
	421686	AB011156	Hs.106794	KIAA0584 protein	3.3
25	429228	A1553633	Hs.326447	ESTs	3.3
	450325	A1935962 A1659306	Hs.26289	ESTs protein tyrosine phosphatase, non-recept	3.3 3.3
	412350 451778	AI826131	Hs.73826 Hs.62954	ESTs, Weakly similar to zinc finger prot	3.3
	435977	AL138079	Hs.5012	brain-specific membrane-anchored protein	3.2
30	450475	AW805634	Hs.205015	ESTs	3.2 3.2
	418661 436480	NM_001949 AJ271643	Hs.1189 Hs.87469	E2F transcription factor 3 putative acid-sensing ion channel	3.2
	407332	AI801565	Hs.200113	Homo sapiens cDNA FLJ11379 fis, clone HE	3.2
2.5	415131	D61119		gb:HUM158C11B Clontech human fetal brain	3.2
35	409248	AB033035	Hs.51965 Hs.256311	KIAA1209 protein granin-like neuroendocrine peptide pracu	3.2 3.2
	431462 434834	AW583672 AF156774	Hs.324020	1-acylglycerol-3-phosphate O-acyltransfe	3.2
	450358	AB010098	Hs.24907	coronin, actin-binding protein, 28	3.2
40	438461	AW075485	Hs.286049	phosphoserine aminotransferase	3.2 3.2
40	405239 407304	U89281 AA565832	Hs.271649	oxidative 3 alpha hydroxysteroid dehydro gb:nj32b03.s1 NCI_CGAP_AA1 Homo sapiens	3.2
	451697	AW449774	Hs.296380	POM (POM121 rat homolog) and ZP3 fusion	3.2
	435071	D60683	Hs.35495	ESTs	3.2
45	420352	BE258835	Hs.144057	gb:601117374F1 NIH_MGC_16 Homo sapiens c ESTs	3.2 3.2
43	412193 442320	AI684467 AI287817	Hs.129636	ESTS	3.2
	407378	AA299264	Hs.57776	ESTs, Moderately similar to 138022 hypot	3.2
	414528	AA148950	Hs.188836	ESTs	. 3.2 3.2
50	439764 410425	T26535 BE278367	Hs.22744 Hs.63510	hypothetical protein MGC13105 KIAA0141 gene product	3.2
50	429876	AB028977	Hs.225974		3.2
	427627	R87582	Hs.179915		3.2 3.2
	439039 447925	AI656707 AW292271	Hs.48713 Hs.250718	ESTs ESTs	3.2 3.2
55	447714	AW296313	Hs.255537		3.2
	434574	A1424458	Hs.33470	ESTs	3.2
	437269	AA334384 H95279	Hs.149420 Hs.293788		3.2 3.2
	416845 452234	AW084176	Hs.223296		3.2
60	440274	R24595	Hs.7122	scrapie responsive protein 1	3.2
	437698	R61837	Hs.7990	ESTs, Moderately similar to 184505 calci enhancer of zeste (Drosophila) homolog 2	3.2 3.2
	414761 445828	AU077228 F05802	Hs.77256 Hs.81907	ESTs	3.2
	423779	AW071837	Hs.57971	ESTs	3.2
65	403790	41 42 4520	15.054400	NM_001334*:Homo sapiens cathepsin O (CTS	3.2 3.2
	453792 428167	AL134539 AA770021	Hs.254129 Hs.16332	KIAA1678 ESTs	3.2
	445413	AA151342	Hs.12677	CGI-147 protein	3.2
70	415314	N88802	Hs.5422	glycoprotein M6B	3.2
70	425115 432625	R44664 A1243596	Hs.123956 Hs.94830	ESTs ESTs, Moderately similar to T03094 A-kin	3.2 3.2
	432625 412420	AL035668	Hs.73853	bone morphogenetic protein 2	3.1
	422772	AL119585	Hs.120228	KIAA0749 protein	3.1
75	437414	AW894071	Hs.48448	hypothetical protein DKFZp547C176 ESTs	3.1 3.1
13	427961 435256	AW293165 AF193766	Hs.143134 Hs.13872	cytokine-like protein C17	3.1
	428966	AF059214	Hs.194687	cholesteral 25-hydraxylase	3.1
	413995	BE048146	Hs.75671	syntaxin 1A (brain)	3.1 3.1
80	443431 414217	A1056847 A1309298	Hs.20654 Hs.27989	ESTs Horno sapiens cDNA: FLJ23165 fis, clone t	3.1
-	419617	AL008583	Hs.91622	neuronal pentraxin receptor	3.1
	444326	A1939357	Hs.270710		3.1 3.1
	436315	BE390513	Hs.27935	hypothetical protein MGC4837	3.1

PCT/US02/29560 WO 03/025138

	446131	NM_000929	Hs.290	phospholipase A2, group V	3.1
	423858	AL137326	Hs.133483	Homo sapiens mRNA; cDNA DKFZp434B0650 (f	3.1
	448475	BE613134	Hs.247474	hypothetical protein FLJ21032	3.1 3.1
_	432682	AI376400		ESTs	3.1
5	450661	AW952160	Hs.83849 Hs.191212	ESTs ESTs	3.1
	417636 417918	R08916 AA209205	Hs.163754	hypothetical protein FLJ12606	3.1
	454032	W31790	Hs.194293	ESTs, Weakly similar to 154374 gene NF2	3.1
	443150	AI034467	Hs.34650	ESTs	3.1
10	404632			NM_022490:Homo sapiens hypothetical prot	3.1 3.1
	425537	AB007913	Hs.158291	KIAA0444 protein	3.1
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr Eos Control	3.1
	400090 445424	AB028945	Hs.12696	cortactin SH3 domain-binding protein	3.1
15	422949	AA319435	110.12.000	gb:EST21657 Adrenal gland tumor Homo sap	3.1
	448750	U95020	Hs.21903	catcium channel, voltage-dependent, beta	3.1
	433560	AJ925195	Hs.130891	hypothetical protein MGC4400	3.1 3.1
	433042	AW193534	Hs.281895	Homo sapiens cDNA FLJ11660 fis, clone HE	3.1
20	449722	BE280074 AB023198	Hs.23960 Hs.158135	cyclin B1 KIAA0981 protein	3.1
20	425480 449670	F07693	Hs.85603	Homo sapiens mRNA; cDNA DKFZp434K2172 (f	3.1
	452619	AW298597	Hs.61884	Homo sapiens, clone IMAGE:4298026, mRNA,	3.1
	428722	U76456	Hs.190787	tissue inhibitor of metalloproteinase 4	3.1 3.1
0.5	405605			C2001342:gi 127814 sp P26434 NAH4_RAT SO	3.1
25	417565	A1203405	Hs.47831	ESTs ESTs	3.1
	439538 414117	AAB37323 W88559	Hs.56407 Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	3.1
	430818	AI311928	Hs.348156	gb:qo89h04.x1 NCI_CGAP_Kid5 Homo sapiens	3.1
	408508	AI806109	Hs.135736	KIAA1580 protein	3.1
30	414884	R54418	Hs.183745	hypothetical protein FLJ13456	3.1 3.1
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola citron (rho-interacting, serine/threonin	3.1
	446636 417169	AC002563 R13550	Hs.15767 Hs.246773	ESTs	3.1
	450202	AW969756	Hs.34145	ESTs, Weakly similar to B49647 GTP-bindi	3.1
35	428060	AA420616	Hs.249483	ESTs	3.1
	430526	AF181862	Hs.242407	G protein-coupled receptor, family C, gr	3.1 3.1
	421458	NM_003654	Hs.104576	carbohydrate (keratan suffate Gal-6) sul gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	3.0
	429163	AA884766	Hs.182874	guanine nucleotide binding protein (G pr	3.0
40	428180 422631	Al129767 BE218919	Hs.118793	hypothetical protein FLJ 10688	3.0
70	433290	R20077	Hs.302185	Homo sapiens clone 23618 mRNA sequence	3.0
	412507	L36645	Hs.73964	EphA4	3.0 3.0
	415827	H17462	Hs.23079	ESTs	3.0
45	429609	AF002246 A1479755	Hs.210863 Hs.129010		3.0
73	457358 441732	AW298818	Hs.127341		3.0
	459318	NM_000038		gb:Homo sapiens adenomatosis polyposis c	3.0
	426384	Al472078	Hs.303662		3.0 3.0
50	436267	AW450938	Hs.180115		3.0
50	450650 414865	T65617 AA157155	Hs.101257 Hs.274414		3.0
	459080	AW192083	Hs.290855		3.0
	412783	BE276738	Hs.74578	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	3.0
	432593	AW301003	Hs.51483	ESTs, Wealthy similar to hypothetical pro	3.0 3.0
55	443753	AW367578	Hs.134749		3.0
	445921 427695	AW015211 R88483	Hs.146181 Hs.172862		3.0
	438283		Hs.37282	ESTs	3.0
	453324		Hs.23208		3.0
60	421094				3.0 3.0
	433434		11. 20/01	gb:no22b03.s1 NCI_CGAP_Pr22 Homo sapiens ESTs, Moderately similar to A46010 X-lin	3.0
	452850 416658		Hs.22481 Hs.79432		3.0
	429569		Hs.13834		3.0
65	428600			3 hypothetical protein DKFZp434K1421	3.0
	443633	AL031290	Hs.9654	similar to pregnancy-associated plasma p	3.0 3.0
	433229		Hs.91625		3.0
	429046		Hs.19477 Hs.25295		3.0
70	431431 414430		Hs.76118		3.0
, •	42316		Hs.12491		3.0
	44026	M81886	Hs.7117	glutamate receptor, ionotropic, AMPA 1	3.0 3.0
	44136		6 Hs.12683	GO ESTS, Wealty similar to YD38_YEAST HYPOT gb:ok33a11.s1 Soares_NSF_F8_9W_OT_PA_P_S	3.0
75	43705		. Hs.1465		3.0
13	42916 45373			ESTs	3.0
	TABLE	E 158:	laiana Ean am	hoset identifier number	

TABLE 15B:
Pkey: Unique Eos probeset identifier number
CAT number: Gene chuster number
Accession: Genbank accession numbers 80

Pixey CAT Number Accession

	410099	117647_1	AAD81630 T08671 AI174254 D83874 AW959843 AA364503 AA693467 AW993370 BE327037 AA167714 N79906 AW901977 AW901980 W52882 T07735 AA484549 W60090 D52685 T23811 BE327043 AW901768 BE551237 AA917004 AA716027 AI439658 AA283724 AI805992 AI457096
_			AA084618 BE467736 AI092635 AI887863 AI697593 AA436618 AI167419 AI418634 T31586 AA436630 AA706191 AI041169 AI422304 T03534 AA211402 AI204899 AI366472 AW827081 AA788593 T32736 AI767935 AA167791 AA747914 AA663870 AI865504
5	410126	117761_1	BE169274 AW893230 AA210998 H24222 AA081774 BE000935 BE000834 AA334880
	411565	1249756_1	AW851728 AW851607 AW851621 AW851702 AW851647 AW851727 AW851658 AW851617 AW851628
	412799 412811	132817_1 132943_1	AI267606 AA121045 AA126221 H06382 AW957730 AA352014 R13591 AA121201 D60420 BE263253 BE047862 Z41952 AI424991 AI693507 AI863108 AA599060 AI091148 AA598689 R39887 AA813482 AW016452 H06383 R41807 AI364268 AA620528 AI241940 AW089149 AW090733 AW088875 Z38240 AA121202 R17734
10	412820	1330039_1	BE001236 BE001177 BE001180 BE001234
	414372	143909_1	AA143654 AW753140 AA213770 AW970865 AA569075 AA492132
	415131	1523680_1	D61119 D81508 D81734
	416871 418512	1626761_1 176394_1	H98716 N90792 N24283 AW498974 T09332 R58460 AA350990 T33786 T30936 AA350905 T08592 T09274 AA224297 D54678 T08951 R15346 AW953188 AA350074
15	410312	1/0354_1	AW330649
13	419544	185760 2	AI909154 AA526337 AA244193 AI909153
	420111	190755_1	AA255652 AA280911 AW967920 AA262684
	420352	192979_1	BE258835 AW968316 AA258918 AW843305 R14744 AI580388 BE071923 R36280
20	422949	223184_1	AA319435 N56456 AA319377 AW961532 T48452 AA894424 AL035633 F11794 F11783 H18042 T66089 H29379 R19493 AW134660 AI299437 AL133995 AA057405 N78357 AA917450 AI002692 T09262 T65008
20	423476	22861_1	ALD35633 F11794 F11783 H18042 166069 H29379 R19493 ART194000 AR259537 ACC150595 ACC1740 AR6037 ACC1740 ACC1740 ACC1740 ACC1740 ACC1740 ACC1740 ACC1740 ACC17
	424572	24097_1	M19650 R18810 R18721 AW896146 AW889520 AA192362 AA176814 F12085 BE255264 BE251393 T65248 AA380585 AA380465 BE408684
	424312	24031_1	AAAGOO37 AWAGRREG AA776107 RE2742R9 D45269 M61958 AA378818 AW663180 AW672958 H08611 M78164 BE393721 AA348660 R35303
			AWARRES AAN 1979 AAN 1977 AAN 1977 AAN 1977 AAN 1980 AAN 19132 AIBSB240 R73218 H30477 H17776 AA659570 BE276750 AL 118657
25			AARTERE1 AARERATT AWER1696 ALIALIRR NERTATA AAREA162 H17659 AL 120696 T28867 AW498868 AU355918 AA902349 AA569098 AU088231
			AIDAGGA AAGGGGG A AAGGGGGG AAGGGGGGGGGGG
			T15423 AW002084 AI824721 N36242 AI417281 AI018212 AA912337 F09722 AA749449 AW879172 AA885427 AA916639 AI872560 F00482 H45184
			AI217251 AA775807 BE390071 AA303517 AA001050 BE515169 N44066 AL 133684 AI807085 AA808009 AA915914 F00007 AA019749 AL 121560
20			AW675544 AW090233 AW072071 AI810932 AI089733 AW026222 AA770155 AI089647 AI085733 AW516061 AL037636 ALD37635 AI863947 H50420 R11203 AA019133 N94772 N71842 N29047 AA778138 AA554336 AA179865 N59453 T65212 AAD54270 AW806630 AA533375 D13146 AA349487
30			AU077160 BE 255671 BE276795 BE250823 AL 120301 BE311390 BE252483
	424945	245223_1	A1221010 710067 AA348780 AWG64077 AW166028 RES40193 N94800 AA452368 N99604 AI341345 AW298800 AA724961 AA931158 AI741227
	424543	243223_1	AI80660 AI982626 D81263 D53937 D52496 AA974487 AW043854 N50483 Z39997 AI492961 AI361526 F04002 AA452141 T23551 AI472655
			A1193667 A1341984 N92658 T32870 R52664 N50428 AW089291 A1934175 A1423737 D60665
35	424947	245247_1	R77952 AA348809 AW959960 AW959962 AI565552 AW070702 AA973910 R85973
	425331	250199_1	AW962128 AA355353 AA427363
	426413	266650_1	AA377823 AW954494 AI022688
	426503	268283_1	AA380153 AA380233 AW963529 AL041228 D82004 D61361 Al203314 Al990307 AW900295 Al018308 AW087473 AW183530 AA393346 H50055 AA935601
40	426919 428342	273507_1 290035_2	ALT39168 AA426249 AL199636 AW505198 AW977291 AA824583 AA883419 AA724079 AL015524 AL377728 AW293682 AL928140 AA731438 AL092404
40	420342	290033_2	A793100 AA731340
	429007	298301_1	D86642 AA443145 AL119015 AW904500
	429163	300543_1	AARRATGG AWOTADT1 AASGDOTS AAAATT312
4.0	429421	30431_1	AL031658 AI693758 AL040619 AW977914 AA811957 AI352198 AW104364 AA648367 AA897604 AW341668 AI201382 AL040620
45	430183	31412_2	BE010038 AA676833 AJ311783 T86895 W68032 BE064393 BE064394 BE157228 BE183282 AI936370 AA552514 T67280 AA039909
	430676	32168_1	AF684866 AF684870 AF684864 AF684867 AF684869 AF684865 AF684868 AW818206 AW812038 BE144813 BE144812 AW812041 AW812040 AW812067 BE051583 BE061604 T05808 AJ352469 AA580921 BE141783 BE141782 BE051501 AW814393 AW885029
	420000	200200 4	AW812067 BEUG1563 BEUG1604 105808 AU502469 AC560521 BE 141763 BE 141762 BEUG1601 ATTO 1455 ATTO
	430968 433009	326269_1 357371_1	AA761668 AA573621 R92814 R99670
50	433434	366095_1	AAS88429 AI972567 AW504832 AI299694
	433523	368873_1	H29882 AW665533 AW1499D1 AI572917 AA598500 AI686466 AI336390 AW864390 AW864320
	435542	407744_1	AA687376 H74234 AW975503
	437034	431713_1	AA742643 AA808575 AW976668
55	437056	432262_1	A1147061 AA743380 AA765223 AW976398 AI803927
))	438458 439285	457837_1 47065_1	AW975186 AA807807 D29548 AL133916 N79113 AF086101 N76721 AW950828 AA364013 AW955684 AL346341 AI867454 N54784 AI655270 AI421279 AW014882 AA775552
	439263	47003_1	N62351 N59253 AA626243 AI341407 BE175639 AA456968 AI358918 AA457077
	439518	47334_1	W76326 AF086341 W72300
	439566	47387_1	AF086387 W77884 W72711
60	441102	509604_1	AA973905 AI299888 AA917019 H53235 T90771
	446692	689623_1	Z44514 AI352097 AI803984 AW235923 AW196558 AI954637 AI336983
	447197	711623_1	R36075 Al366546 R36167 Al458682 H24240 R14537 R18426 AW867082
	448044 449625	747196_1 8113_1	NIA 014253 AC100772 RE088760 AL 022718 RE161779 AW86369 RE161640 AL 039060 RE168542 AW296554 AA323193 AA235370 AW779760
65	413023	0110_1	NAGEZA ALZZEGOZ GASAZZ DEGZAA ALZDIZIOZ FOZAGI RZEZEG RZEGGA ALGIZEGI ALAGRAGI TELEBAZ ALGIEGZO NASSZE TELATS AAJJIARO
•	450375	83327_1	AA009647 AA131254 AA374293 AW954405 H04410 AW606284 AA151166 BE157467 BE157601 H04384 W46291 AW663674 H04021 H01532
			AA190993 H03231 H59605 H01642 AA852876 AA113758 AA626915 AA746952 A1161014 AA099554 R69067
	450582	83933_1	AJ339732 AA010300 AW515041 AA768334 N29860 AA425874 AA425118 AA865829 AW936878 AW118072 AI631982 T15734 AA224195 AI701458 W20198 F26326 AA890570 N90552 AW071907 AI671352 AJ375892 T03517 R88265 AJ124088
70	451320	86576_1	AW118072 AIB31982 1157.34 AA224193 AI701436 W20198 P28536 AAB30310 N36532 AND 1307 AB7132 AO 1302 AND 1307 AB7132 AAA224388 AI084316 AI354686 T33652 AI140719 AI720211 T03490 AI372637 T15415 AW205836 AA630384 T03515 T33230 AA017131 AA443303
70			T23623 A1222556 T33511 T33785 A1419606 D55612
	453331	96214_1	A1240CCC TG2CQ1 N774GQ NG1923 AA147247 R75732 C184GN R73999 A1095755 T49904 H03868 AA411580 R33395 AA410586 T48869 U63292
	*****		D31091 H12408 H02668 AA036018 D75957 AIR03329 R27528 R36203 AIR0932 AIR08765 R78948 AA411449 AA976929 AI378760 AI3780 AI378760 AI
			R73906 R75632 H03612 AA909684 N50695 H02580 H12839 N58781 AA742532 AI360919 H03502 BE208298 R68588 AI350463 R31935 AW069127
75			AAA11621 R25671 R36105 H12451 H03869 H51263 AA035486 R25109 R25110 AA147933
	453739	979419_1	AL120266 AW269469 AW8690114 AMERICADO AMBERGET AMBERGES AW86R012 AW86R017
	454171	1049240_1	AW854832 AW854798 AW854857 AW854816 AW854834 AW854817 BE064420 BE064435 BE064429 BE064414 BE064400 BE064517
	455646 458912	1348557_1 823104_1	AI91 1066 AI933734 AI680888 AJ003599
80	-50312	~~.~.,	
	TABLE		
	Pkey:	· Un	ique number corresponding to an Eos probeset

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Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495. Indicates DNA strand from which exons were predicted.
            Ref:
            Strand:
                                    Indicates nucleotide positions of predicted exons.
            Nt_position:
 5
                                                           Nt_position
277132-277595
            Pkey
            400533
                          6981826
                                           Minus
                                                            70745-71121
            400777
                          8131663
                                            Plus
                                                            98374-98509
                          9797373
                                            Minus
            401272
                                                            113086-114800
10
                          8018280
            402145
                                                            20393-20767
             402604
                          9909420
                                            Plus
                                                            47680-47973
                          9909420
             402605
                                            Minus
                                                            59763-59909
                           9662953
                                            Minus
             402855
                           9444521
                                                            89286-90131
             403142
                                                            30699-30910
15
             403341
                           8569175
                                            Plus
                                                            143467-143634
                           3135242
                                            Minus
             403696
                                            Minus
                                                            87826-87947,89835-90002
                           8084957
             403790
             404150
                           7534008
                                            Plus
                                                            165811-165943
                                                            99460-99564
              404283
                           2276311
                                             Minus
20
                                                             103456-103664
             404541
404584
                           8318559
                                             Plus
                           9857511
                                                             138651-139153
                                             Plus
                           9796668
                                                             45096-45229
             404632
                                                             16223-16319,16427-16513,16736-16859,16941-17075,17170-17287,17389-17529,18261-18357,18443-18578
              404819
                           4678240
                                             Plus
                                             Minus
                                                             51728-51836
                           7249119
             405238
                                                             144345-144464,144690-144836,151750-151883,152407-152484
 25
                            7249119
                                             Plus
             405239
                                                             43310-43462
              405348
                            2914717
                                                             117070-117270
                                             Minus
              405605
                            5836195
                                                             2830-2967
                                             Plus
              405819
                            4007557
 30
              TABLE 16A: ABOUT 859 GENES UP-REGULATED IN GLIOBLASTOMA MULTIFORMA COMPARED TO NORMAL CENTRAL NERVOUS SYSTEM
              TABLE TOR: ABOUT 839 GENES UP-REGULATED IN GLIOBLASTOMA MULTIFORMA COMPARED TO NORMAL CENTRAL NERVOUS SYSTEM

Table 16A lists about 859 genes up-regulated in glioblastoma multiforma (GBM) compared to normal central nervous system (CNS). These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" LGG to "average" CNS issues was greater than or equal to 3.0. The "average" GBM level was set to the 85° percentile amongst various GBM timors. The "average" normal CNS tissue level was set to the 85° percentile amongst virious CNS tissues. In order to remove gene-specific background levets of non-specific hybridization, the 10° percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before
 35
              the ratio was evaluated.
                                      Unique Eos probeset identifier number
              Pkey:
                                      Exemplar Accession number, Genbank accession number
              ExAcon:
               UnigenelD:
                                      Unigene number
 40
              Unigene Title:
                                      Unicene gene title
                                       Ratio of GLIOBLASTOMA MULTIFORMA to CNS
               R1:
                                                                                                                                             R1
                                              UnigenelD
Hs.76422
                                                            Unigene Title
               Pkey
                             ExAccn
                                                                                                                                             47.2
                                                              phospholipase A2, group IIA (platelets,
                414555
                             N98569
                                               Hs.119571
                                                              collagen, type III, alpha 1 (Ehlers-Dani
  45
               422737
                             M26939
                                                                                                                                             33.3
                                               Hs.136348
                                                              periostin (OSF-2os)
                             D13666
                423961
                                                               clone HQ0310 PRO0310p1
                                                                                                                                             25.9
                             AF217513
                433001
                                               Hs.279905
                                                                                                                                             25.8
                                               Hs 58446
                                                               ESTs
                449539
                             W80363
                                                                                                                                              23.3
                                               Hs.81892
                                                               KIAA0101 gene product
               417308
424800
                             H60720
  50
                             AL035588
                                               Hs.153203
                                                               MyoD family inhibitor
                                                               epidermal growth factor receptor (avian
                                                                                                                                              19.6
                                               Hs.77432
                414825
                             X06370
                                                               Homo sapiens cDNA FLJ20099 fis, clone CO
                                                                                                                                              18.7
                                               Hs.272227
                431941
                              AK000106
                                                                                                                                               17.8
                                                               SRY (sex determining region Y)-box 11
                                               Hs.32964
                453392
                             1123752
                                                                                                                                               17.8
                                                               cysteine and glycine-rich protein 2
matrix metalloproteinase 7 (matrilysin,
$100 calcium-binding protein A4 (calcium
                                               Hs.10526
                              AI878918
                444190
                                                                                                                                               17.7
   55
                428330
                              L22524
                                               Hs.2256
                                                                                                                                               17.5
                              AW276858
                                               Hs.81256
                417130
                                                                                                                                               17.0
                                                               Homo sapiens cDNA: FLJ23165 fis, clone L
                                                Hs.279898
                414217
                              A1309298
                                                               leukemia inhibitory factor (cholinergic topoisomerase (DNA) II alpha (170kD)
                                                                                                                                               15.9
                                                Hs.2250
                428242
                              H55709
                                                                                                                                               156
                                               Hs.156346
Hs.115455
                              J04088
                425397
                                                                                                                                               15.2
   60
                                                               Homo sapiens cDNA FLJ14259 fis, clone PL
                              AA420687
Y00787
                424635
                                                                interleukin 8
                                                Hs.624
                408243
                                                                                                                                               14.7
                                                Hs.119129
                                                               collagen, type IV, alpha 1
                              X12784
                422672
                                                               chromosome 8 open reading frame 4 phosphoserine phosphatase-like
                                                                                                                                               14.6
                 434078
                               AW880709
                                                Hs.283683
                                                                                                                                               14.2
                 409799
                               D11928
                                                Hs.76845
                                                                                                                                               14.2
                                                                enhancer of zeste (Drosophila) homolog 2
    65
                               AU077228
                                                Hs.77256
                 414761
                                                                                                                                                14.1
                                                                hypothetical protein FLJ23468
                               BE093589
                                                Hs.38178
                 442432
                                                                                                                                               14.0
                                                Hs.15432
Hs.160628
                               U53445
                                                                downregulated in ovarian cancer 1
                 446584
                                                                                                                                               13.5
                                                                ESTs
                 444969
                               A1203334
                                                                                                                                                12.9
                                                Hs.103538
                                                                ESTs
                               C14187
                 430691
                                                                ESTs, Wealtly similar to 2109260A B cell
    70
                                                 Hs.270149
                 426075
                               AW513691
                                                                Homo sapiens mRNA; cONA DKFZp586C1019 (f
                                                                                                                                                12.1
                 445101
                                T75202
                                                 Hs.12314
                                                                                                                                                11.9
                               AW015206
                                                 Hs.178784
                                                                ESTs
                  441269
                                                                 laminin, beta 1
                               NM_002291
                                                 Hs.82124
                 417426
                                                                 hypothetical protein FLJ20647
                  430132
                               AA204686
                                                 Hs.234149
                                                                 prominin (mouse)-like 1
                                                                                                                                                11.3
     75
                  422163
                               AF027208
                                                 Hs.112360
                                                                 ESTs, Weakly similar to KIAA1330 protein
                                                                                                                                                11.3
                  411411
                                AA345241
                                                 Hs.55950
                                                                                                                                                11.2
                                                 Hs.23960
                                BE280074
                                                                 cyclin B1
                  449722
                                                                 protein regulator of cytokinesis 1
DiGeorge syndrome critical region gene 8
RAB6 interacting, kinesin-like (rabkines
                                                 Hs.344037
                                BE568452
                  436291
                                                                                                                                                 10.9
                  435020
                                AW505076
                                                 Hs.301855
                                                                                                                                                 10.9
     80
                  412140
                                AA219691
                                                  Hs.73625
                                                                                                                                                 10.6
                                                                  Homo sapiens cDNA: FLJ23241 fis, clone C
                                AA468183
                                                  Hs.184598
                  419239
                                                                 collagen, type VI, alpha 3
                  417043
                                NM_004369
                                                  Hs.80988
                                                                                                                                                 10.6
```

collagen, type IV, alpha 2

413929

BE501689

Hs.75617

	420602	AF060877	Hs.99235	regulator of G-protein signalling 20	10.6
	409142	AL136877	Hs.50758	SMC4 (structural maintenance of chromoso	10.4
	406972	M32053		gb:Human H19 RNA gene, complete cds.	10.4
5	412986	X81120	Hs.75110	cannabinoid receptor 1 (brain)	10.3 10.3
,	419508 449611	AW997938 AI970394	Hs.90786 Hs.197075	ATP-binding cassette, sub-family C (CFTR ESTs	10,1
	427581	NM_014788	Hs.179703	KIAA0129 gene product	10.1
	431512	BE270734	Hs.2795	lactate dehydrogenase A	9.9
10	429183	AB014604	Hs.197955	KIAA0704 protein	9.8 9.7
10	433437 424840	U20536 D79987	Hs.3280 Hs.153479	caspase 6, apoptosis-related cysteine pr extra spindle poles, S. cerevisiae, homo	9.7
	433800	AI034361	Hs.135150	tung type-I cell membrane-associated gly	9.7
	433647	AA603367	Hs.222294	ESTS	9.7
15	414622	A1752666	Hs.76669	nicotinamide N-methyltransferase	9.5 9.3
13	413719 409461	BE439580 AA382169	Hs.75498 Hs.54483	small inducible cytokine subfamily A (Cy N-myc (and STAT) interactor	9.3 9.3
	409902	AI337658	Hs.156351	ESTs	9.3
	450375	AA009647		a disintegrin and metalloproteinase doma	9.2
20	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-1	9.1 9.1
20	442802 452461	AL133035 N78223	Hs.8728 Hs.108106	hypothetical protein DKFZp434G171 transcription factor	9.1
	434846	AW295389	Hs.119768	ESTs	9.1
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	9.0
25	425187	AW014486	Hs.22509	ESTs	9.0
25	443247 458079	BE614387 AI796870	Hs.333893 Hs.54277	c-Myc target JPO1 DNA segment on chromosome X (unique) 992	8.7 8.7
	410276	A1554545	Hs.68301	angiopoletin-2	8.6
	402855			NM_001839*:Homo sapiens calponin 3, acid	8.6
20	439710	AF086543		gb:Homo sapiens full length insert cDNA	8.6
30	411968	AI207410 AW248508	Hs.69280 Hs.279727	Homo sapiens, clone IMAGE:3636299, mRNA, ESTs; homologue of PEM-3 [Ciona savignyi	8.6 8.6
	410102 436895	AF037335	Hs.5338	carbonic anhydrase XII	8.6
	418203	X54942	Hs.83758	CDC28 protein kinase 2	8.6
25	416892	L24498	Hs.80409	growth arrest and DNA-damage-inducible,	8.5
35	425234	AW152225	Hs.165909	ESTs, Wealthy similar to 138022 hypotheti	8.5 8.5
	449961 449444	AW265634 AW818436	Hs.133100 Hs.23590	ESTs solute carrier family 16 (monocarboxylic	8.4
	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	8.3
40	453884	AA355925	Hs.36232	KIAA0186 gene product	. 8.3
40	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	8.2
	419938 411078	AU076772 AJ222020	Hs.1279 Hs.182364	complement component 1, r subcomponent CocoaCrisp	8,1 8,1
	406850	A1624300	Hs.172928	collagen, type I, alpha 1	8.0
	447726	AL137638	Hs.19368	matrilin 2	8.0
45	439999	AA115811	Hs.6838	ras homolog gene family, member E	8.0
	416658	U03272 AF086270	Hs.79432 Hs.278554	fibrillin 2 (congenital contractural ara	7.9 7.9
	439451 458814	AI498957	Hs.170861	heterochromatin-like protein 1 ESTs, Weakly similar to Z195_HUMAN ZINC	7.9
	447004	AW296968	Hs.157539	ESTs	7.9
50	436140	W87355	Hs.269587	ESTs	7.9
	436607 422809	AW661783 AK001379	Hs.211061 Hs.121028	ESTs hypothetical protein FLJ 10549	7.8 7.7
	440052	AI633744	Hs.195648	ESTs, Weakly similar to I38022 hypotheti	7.7
	422106	D84239	Hs.111732	Fc fragment of IgG binding protein	7.7
55	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	7.7
	410286	AJ739159	Hs.61898	DKFZP586N2124 protein matrix metafloproteinase 9 (gelatinase B	7.7 7.6
	424687 422048	J05070 NM_012445	Hs.151738 Hs.288126	spondin 2, extracellular matrix protein	7.6
<i>~</i>	421988	AW450481	Hs.161333	ESTs	7.6
60	452620	AA436504	Hs.119286	ESTs	7.6
	453941	U39817	Hs.36820	Bloom syndrome LIM domain protein	7.5 7.5
	416737 425289	AF154335 AW139342	Hs.79691 Hs.155530	interferon, gamma-inducible protein 16	7.5
	418400	BE243026	Hs.301989		7.5
65	437036	Al571514	Hs.133022		7.5
	421899	AJ011895	Hs.109281	Nef-associated factor 1 thymosin, beta, identified in neuroblast	7.4 7.4
	409731 427528	AA125985 AU077143	Hs.56145 Hs.179565		7.4
	427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	7.3
70	448935	AL078596	Hs.22591	nuclear receptor subfamily 2, group E, m	7.3
	415079	R43179	Hs.22895	hypothetical protein FLJ23548	7.3
	449571 427899	AW016812 AA829286	Hs.200266 Hs.332053		7.3 7.3
	447458	A1741082	Hs.158961		7.3
75	430630	AW269920	Hs.2621	cystatin A (slefin A)	7.2
	411252	AB018549	Hs.69328	MD-2 protein	7.2
	432731 454117	R31178 BE410100	Hs.287820 Hs.40368	fibronectin 1 adaptor-related protein complex 1, sigma	7.2 7.2
	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-0-sulfot	7.2
80	428728	NM_016625	Hs.191381	hypothetical protein	7.1
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (7.1 7.1
	432281 410434	AK001239 AF051152	Hs.274263 Hs.63668	hypothetical protein FLJ10377 to0-like receptor 2	7.1 7.1
	-10-0-				***

			LL 04270 -	roprotein convertase subtilisin/kexin t	7.1
	420018 418293		Hs.94376 p Hs.16063 h	roprotein convertise submishingering to the protein FLJ21877	7.1
	424954		Hs.1846 t	umor protein p53 (Li-Fraumeni syndrome)	7.0
-	445900		Hs.125036 I	Iomo sapiens clone 24787 mRNA sequence	7.0 7.0
5	419741	NM_007019 AW411307		ubiquitin carrier protein E2-C CDC45 (cell division cycle 45, S.cerevis	7.0
	422283 434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	6.9
	416847	L43821	Hs.80261 (enhancer of filamentation 1 (cas-like do	6.9 6.9
10	424381	AA285249		protein kinase Chk2 filamin A, alpha (actin-binding protein-	6.9
10	410064 415682	X53416 Al347128		ESTs	6.9
	421977	W94197	Hs.110165	ribosomal protein L26 homolog	6.8
	429447	AW812452		ESTs, Weakly similar to S14747 sphingomy	6.8 6.8
15	423198	M81933 BE182082		cell division cycle 25A ESTs	6.8
13	413627 412777	Al335773		ESTs	6.8
	409829	M33552		lymphocyte-specific protein 1	6.8 6.8
	451129	BE072881	U- 002742	gb:RC2-BT0548-200300-012-e09 BT0548 Homo ESTs, Wealdy similar to S64054 hypotheti	6.7
20	444381 446131	BE387335 NM_000929	Hs.283713 Hs.290	phospholipase A2, group V	6.7
20	441703	AW390054	Hs.192843	leucine zipper protein FKSG14	6.7
	420311	AW445044	Hs.38207	Human DNA sequence from clone RP4-530115	6.7 6.7
	425202	AW962282 AW952912	Hs.152049 Hs.300383	ESTs, Wealdy similar to 138022 hypotheti hypothetical protein MGC3032	6.7
25	408161 440704	M69241	Hs.162	insufin-like growth factor binding prote	6.7
	407182	AA312551	Hs.230157	ESTs	6.7 6.6
	445837	AI261700	Hs.145544	ESTs caspase 4, apoptosis-related cysteine pr	6.6
	433376 431211	AI249361 M86849	Hs.74122 Hs.323733	gap junction protein, beta 2, 26kD (conn	6.6
30	447439	AA313565	Hs.145020	ESTs, Weakly similar to KIAA1205 protein	6.5
•	407235	D20569	Hs.169407	SAC2 (suppressor of actin mutations 2, y	6.5 6.5
	450506	NM_004460	Hs.51483	fibroblast activation protein, alpha ESTs, Wealdy similar to hypothetical pro	6.5
	432593 418054	AW301003 NM_002318	Hs.83354	lysyl oxidase-like 2	6.5
35	452799	AI948829	Hs.213786	ESTs	6.5 6.4
	446657	AJ335191	Hs.260702	ESTs, Wealdy similar to 2109260A B cell	6.4
	424247 443884	X14008 N20617	Hs.234734 Hs.194397	lysozyme (renal amyloidosis) leptin receptor	6.4
	420560	AW207748	Hs.59115	ESTs	6.4
40	419485	AA489023	Hs.99807	ESTs, Weakly similar to unnamed protein	6.3 6.3
	420649	AI866964	Hs.124704	ESTs, Moderately similar to S65657 alpha DNA replication factor	6.3
	457465 440332	AW301344 AI218517	Hs.122908 Hs.188051	ESTs	6.3
	449246	AW411209	Hs.23363	hypothetical protein FLJ10983	6.3
45	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	6.2 6.2
	448275 440286	BE514434 U29589	Hs.20830 Hs.7138	kinesin-like 2 cholinergic receptor, muscarinic 3	6.2
	439518	W76326	115.7130	gb:zd60d04.r1 Soares_fetal_heart_NbHH19W	6.1
	412567	AI750979	Hs.74034	Homo sapiens clone 24651 mRNA sequence	6.1 6.1
50	426935	NM_000088		oollagen, type 1, alpha 1 hypothetical protein FLJ20245	6.1
	456977 428450	AK000252 NM_014791	Hs.169758 Hs.184339	KIAA0175 gene product	6.0
	412125	Y17114	Hs.73393	eyes absent (Drosophila) homolog 4	6.0 6.0
<i>E E</i>	413786	AW613780	Hs.13500	ESTs a disintegrin and metalloproteinase doma	5.9
55	410555 400419	U92649 AF084545	Hs.64311	Target	5.9
	408380		Hs.44532	diubiquitin	5.9
	426108	AA622037	Hs.166468	programmed cell death 5	5.9 5.9
60	414774		Hs.77274 Hs.192142	plasminogen activator, urokinase ESTs	5.8
00	437695 409463		Hs.17296	hypothetical protein MGC2376	5.8
	411048	AK001742	Hs.67991	hypothetical protein DKFZp434G0522	5.8 5.8
	443731		Hs.145418) ESTs Target Exon	5.8
65	405558 422094		Hs.272027	F-box only protein 5	5.8
00	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	5.8 5.8
	425882		Hs.161002		5.8
	412471 429149		Hs.73946 Hs.19796		5.8
70	436827		Hs.5322	guanine nucleotide binding protein (G pr	5.7
	425905	5 AB032959			5.7 5.7
	414053				5.7 5.7
	43680: 44220				5.7
75	45336		Hs.10737	5 ESTs	5.6
	42908	3 Y09397	Hs.22781		5.6 5.6
	42649 42308				5.6
	42300			gb:Human nebutin mRNA, partial cds	5.5
80	40647	8		Target Exon	5.5 5.5
	43593 45336		Hs.11976 Hs.10737	75 ESTs	5.5
	45336 44996				5.5

	442547	AA306997	Hs.217484	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.5
	443883	AA114212	Hs.9930	serine (or cysteine) proteinase inhibito	5.5
	429643	AA455889 DEE49367	Hs.167279	FYVE-finger-containing Rab5 effector pro	5.5 5.4
5	407862 407624	BE548267 AW157431	Hs.337986 Hs.248941	Homo sapiens cDNA FLJ10934 fis, clone OV ESTs	5.4
-	448769	N66037	Hs.38173	ESTs	5.4
	417124	BE122762	Hs.25338	ESTs	5.4
	422493	AW474183	Hs.250173	hypothetical protein FLJ13158	5.4
10	457292	AI921270	Hs.281462	hypothetical protein FLJ14251	5.3 5.3
10	418596 410295	AW976721 AA741357	Hs.293327 Hs.5174	ESTs nidogen (enactin)	5.3
	433323	AA805132	Hs.159142	ESTs	5.3
	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	5.3
1.5	418630	AJ351311	Hs.251946	poly(A)-binding protein, cytoplasmic 1-l	5.3
15	420075	AF142482	Hs.203846	TEA domain family member 3	5.2 5.2
	427676 407729	AA394062 T40707	Hs.300772 Hs.270862	tropomyosin 2 (beta) ESTs	5.2
	416908	AA333990	Hs.80424	coagulation factor XIII, A1 polypeptide	5.2
	414372	AA143654		gb:zo65a02.r1 Stratagene pancreas (93720	5.2
20	433556	W56321	Hs.111460	calcium/catmodulin-dependent protein kin	5.2
	424998 407603	U58515 AMOS 5706	Hs.154138 Hs.62604	chitinase 3-like 2 Homo sapiens, clone IMAGE:4299322, mRNA,	5.2 5.2
	445118	AW955705 AI208762	Hs.345572	ESTs	5.2
	408523	AW833259	Hs.314287	ESTs	5.2
25	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	5.2
	449300	AI656959	Hs.346514	ESTs	5.2 5.2
	429732 423757	U20158 AL049337	Hs.2488 Hs.132571	hymphocyte cytosofic protein 2 (SH2 doma Homo sapiens mRNA; cDNA DKFZp564P016 (fr	5.1
	439570	T79925	Hs.269165	ESTs, Wealty similar to ALU1_HUMAN ALU S	5.1
30	415323	BE269352	Hs.949	neutrophil cytosolic factor 2 (65kD, chr	5.1
	443604	C03577	Hs.9615	myosin regulatory light chain 2, smooth	5.1 5.1
	421247 416913	BE391727 AW934714	Hs.102910	general transcription factor (IH, polype gb:RC1-DT0001-031299-011-a11 DT0001 Homo	5.1 5.1
	419968	X04430	Hs.93913	interleukin 6 (interferon, beta 2)	5.0
35	424009	F11690		gb:HSC30D041 normalized infant brain cDN	5.0
	418283	S79895	Hs.83942	cathepsin K (pycnodysostosis)	5.0
	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	5.0 5.0
	417404 408829	NM_007350 NM_006042	Hs.82101 Hs.48384	pleckstrin homotogy-like domain, family heparan sulfate (glucosamine) 3-O-sulfot	5.0
40	418097	R45137	Hs.21868	ESTs	5.0
	453331	A1240665		ESTs	4.9
	429433	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein ESTs	· 4.9
	426044 444161	AA502490 N52543	Hs.170290 Hs.142940	ESTs	4.9
45	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	4.9
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	4.9
	447752 439627	M73700 BE621702	Hs.105938 Hs.29076	lactotransferrin hypothetical protein FLJ21841	4.9 4.9
	402274	DEGETTOE	143.23410	C19000498*:gij4567179[gbjAAD23607.1]AC00	4.9
50	444656	AJ277924	Hs.145199	ESTs	4.9
	422087	X58968	Hs.111301	matrix metalloproteinase 2 (gelatinase A	4.9 4.9
	443744 416871	AI084326 H98716	Hs.271548	ESTs, Weakly simitar to 178885 serine/th gb:yx13d08.s1 Soares melanocyte 2NbHM Ho	4.9
	409112	BE243971	Hs.50649	quinone oxidoreductase homolog	4.8
55	403481			Target Exon	4.8
	443740	R56434	Hs.21062	ESTs	4.8
	435005 429163	U80743 AAB84766	Hs.306094	trinucleotide repeat containing 12 gb:am20a10.s1 Soares_NFi_T_GBC_S1 Horno s	4.8 4.8
	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	4.8
60	428403	AI393048	Hs.326159	leucine rich repeat (in FLII) interactin	4.8
	430968	AW972830		gb:EST384925 MAGE resequences, MAGL Horno	4.8
	425212	AW962253	Hs.171618	ESTs	4.8 4.8
	409205 431176	A1952884 A1026984	Hs.14832 Hs.293662	ESTs, Moderately similar to unnamed prot ESTs	4.8
65	420092	AA814043	Hs.88045	ESTs	4.8
	437834	AA769294	Hs.283854		4.8
	432363	AA534489		gb:nf76g11.s1 NCI_CGAP_Co3 Homo sapiens	4.8 4.7
	403011 405348			ENSP00000215330":Probable serine/threoni C7001664:gi[12698061[dbi][BAB21849.1] (AB	4.7
70	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	4.7
• -	443318	AI051603	Hs.133141		4.7
	421027	AA761198	Hs.55254	ESTs	4.7
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730 dual specificity phosphatase 4	4,7 4.7
75	429170 411852	NM_001394 AA528140	Hs.2359 Hs.107515		4.7
	450166	AA429504		ESTs	4.7
	438456	AA913381	Hs.20594	ESTs	4.7
	446839	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	4,7 4,7
80	438527 458946	AI969251 AA009716	Hs.115325 Hs.42311	RAB7, member RAS oncogene family-like 1 ESTs	4.7
50	454860		10.76011	gb:QV4-LT0016-240200-110-b08 LT0016 Homo	4.7
	424736	AF230877	Hs.152701		4.7
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	4.6

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	422648			Melanoma associated gene	4.6 4.6
	431319			ESTs	4.6
	445666 416406	R59960 D86961		ESTs lipoma HMGIC fusion partner-like 2	4.6
5	422887	AI751848		ESTs	4.6
•	422938	NM_001809		centromere protein A (17kD)	4.6
	405141	Y14443		zinc finger protein 200	4.6 4.6
	440210	AW674562		ESTs	4.6
10	432527	AW975028	Hs.102754 Hs.293707	ESTs ESTs, Weakly similar to 138598 zinc fing	4.6
10	439726 435143	AW449893 R12375	Hs.194600	ESTs	4.6
	422170	Al791949	Hs.112432	anti-Mullerian hormone	4.6
	452874	AK001061	Hs.30925	hypothetical protein FLJ 10199	4.6
	408996	AI979168	Hs.344096	glycoprotein (transmembrane) nmb	4.6 4.5
15	412568	AI878826	Hs.74034	caveolin 1, caveolae protein, 22kD stanniocalcin 2	4.5
	426215 413076	AW963419 U10564	Hs.155223 Hs.75188	wee1 (S. pombe) homolog	4.5
	456759	BE259150	Hs.127792	delta (Drosophila)-like 3	4.5
	419735	AW750056	Hs.169577	Homo sapiens cDNA FLJ14743 fis, clone NT	4.5
20	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	4.5
	441217	AI922183	Hs.213246	ESTs	4.5 4.5
	435542	AA687376 AL042201	Hs.21273	ESTs transcription factor NYD-sp10	4.5
	440435 400288	X06256	Hs.149609	integrin, alpha 5 (fibronectin receptor,	4.5
25	416114	AI695549	Hs.183868	glucuronidase, beta	4.5
	437323	AA371145	Hs.194397	leptin receptor	4.5
	425139	AW630488	Hs.25338	protease, serine, 23	4.5 4.5
	423678	AW963357	Hs.7847	ESTs	4.5
30	403961 443462	A1064690	Hs.171176	Target Exon ESTs	4.5
30	418483	W26076	Hs.221847	ESTs	4.5
	428873	AI701609	Hs.98908	ESTs	4.5
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	4.5
25	408298	A1745325	Hs.271923	Homo sapiens cONA: FLJ22785 fis, clone K	4.5 4.4
35	449145	AI632122	Hs.198408	ESTs ESTs	4.4
	439574 423905	A1469788 AW579960	Hs.165190 Hs.135150	tung type-I cell membrane-associated gly	4.4
	453387	AI990741	Hs.252809	ESTs	4.4
	447444	AK000318	Hs.18616	hypothetical protein FLJ20311	4.4
40	433507	AI817336	Hs.191791	ESTs	4.4
	448048	BE281291	Hs.170408	ESTs, Moderately similar to A47582 B-cel	4.4 4.4
	421064	A1245432	Hs.101382	turnor necrosis factor, alpha-induced pro Target Exon	4.4
	402604 445291	BE397753	Hs.14623	interferon, gamma-inducible protein 30	4.4
45	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	4.4
	423600	AI633559	Hs.310359	ESTs	4.4
	403361			NM_002210*:Homo sapiens integrin, alpha	4,4 4,4
	408432	AW195262	674476	gb:xn67b05.x1 NCI_CGAP_CML1 Homo sapiens	4.3
50	424489 442264	T48851 Al278777	Hs.274470 Hs.263455	D-siglec precursor, ESTs, Weakly similar to ALU1_HUMAN ALU S	4.3
50	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	4.3
	417018	M16038	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related	4.3
	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	4.3
55	439566	AF086387	11. 455003	gb:Homo sapiens full length insert cDNA	4.3 4.3
55	425242	D13635 T87318	Hs.155287 Hs.120411	KIAA0010 gene product ESTs	4.3
	423529 439538	AAB37323	Hs.56407	ESTs	4.3
	453682	179703	1,0,00	gb:yd71e08.r1 Soares fetal fiver spleen	4.3
	425259	AL049280	Hs.155397		4.3
60	417918	AA209205	Hs.163754	hypothetical protein FLJ 12606	4.3 4.3
	426649	AI914936	HS.97152	ESTS	4.3
	438875 445868	AA827640 BE169357	Hs.189059 Hs.207428		4.3
	426509	M31166	Hs.2050	pentaxin-related gene, rapidly induced b	4.3
65	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	4.3
	432058	AW665996	Hs.130729	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.3 4.3
	430694	AA810624	Hs.30936	ESTs, Weakly similar to H28H_HUMAN HISTO ESTs, Weakly similar to ALUF_HUMAN !!!!	4.2
	441523 443950			epithelial membrane protein 3	4.2
70	419896		3 115.5355	gb:HSZ99362 DKFZphamy1 Homo sapiens cDNA	4.2
, ,	452994		Hs.31305	KIAA1547 protein	4.2
	420841	A1625251	Hs.94037	hypothetical protein FLJ23053	4.2
	441255		Hs.17163		4.2 4.2
75	416426		Hs.21047	3 Homo sapiens cDNA FLJ14872 fis, clone PL Adlican	4.2
13	411789 409638		Hs.72157 Hs.21335		4.2
	439192				4.2
	440684		Hs.12735	6 ESTs, Highly similar to S21424 nestin (H	4.2
00	437470	AL390147	Hs.13474		4.2
80	432343		0 Hs.2961	S100 calcium-binding protein A3 NM_014226*:Homo sapiens renal tumor anti	4.2 4.2
	401454 431770		Hs.26855		4.2
	442326		Hs.12481		4.2

	419402	Z68155	Hs.90291	taminin, beta 2 (taminin S)	4.2
	435703	AW630133	Hs.83313	GK003 protein	4.2 4.2
	444609 404407	AW571659	Hs.278081	ESTs Target Exon	4.2
5	450581	AF081513	Hs.25195	TGF-beta 4	4.2
	407838	BE146411	Hs.40342	putative nuclear protein	4,1
	410407	X66839	Hs.63287	carbonic anhydrase IX	4.1 4.1
	418883 438898	BE387036 AI819863	Hs.1211 Hs.106243	acid phosphalase 5, tartrate resistant ESTs	4.1
10	421674	T10707	Hs.296355	hypothetical protein FLJ23138	4,1
••	445921	AW015211	Hs.146181	EST8	4.1
	453055	AW291436	Hs.31917	Homo sapiens, clone MGC:9658, mRNA, comp	4.1
	413450	Z99716	Hs.75372	N-acetylgalactosaminidase, alpha-	4.1 4.1
15	427463 450639	AA442224 AI703186	Hs.97900 Hs.277174	ESTs ESTs	4.1
10	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	4.1
	437269	AA334384	Hs.149420	ESTs	4.1
	415688	AA166963	Un 40000A	gb:zo86d01.s1 Stratagene ovarian cancer	4.1 4.1
20	414300 413278	A1304870 BE563085	Hs.188680 Hs.833	ESTs interferon-stimulated protein, 15 kDa	4.1
20	415024	AI983981	Hs.189114	ESTs	4.1
	408102	U46351	Hs.621	lectin, galactoside-binding, soluble, 3	4.1
	448019	AW947164	Hs.195641	ESTs, Moderately similar to 138022 hypot	4.1 4.1
25	451433 446523	AA021140 NM_003063	Hs.269265 Hs.334629	ESTs, Wealdy similar to A46010 X-linked sarcolipin	4.1
23	427700	AA262294	Hs. 180383	dual specificity phosphatase 6	4.1
	402239			Target Exon	4.1
	423713	AW754182		gb:RC2-CT0321-131199-011-c01 CT0321 Homo	4.1 4.1
30	437814	AI088192 C15240	Hs.135474 Hs.182155	ESTs, Weakly similar to DDX9_HUMAN ATP-D ESTs	4.0
50	414948 421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f	4.0
	427375	AL035460	Hs.177536	metallocarboxypeptidase CPX-1	4.0
	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	4.0
35	449655	AI021987	Hs.59970	ESTs Horno sapiens cDNA FLJ11477 fis, clone HE	4.0 4.0
33	439978 432842	BE139460 AW674093	Hs.124673 Hs.334822	hypothetical protein MGC4485	4.0
	422282	AF019225	Hs.114309	apolipoprotein L	4.0
	452574	AF127481	Hs.301946	lymphoid blast crisis oncogene	4.0
40	449256	AA059050	Hs.59847	ESTs	4.0 4.0
40	453385 443715	AW296101 AI583187	Hs.252806 Hs.9700	ESTs cyclin E1	4.0
	451778	AJ826131	Hs.62954	ESTs, Wealthy similar to zinc finger prot	4.0
	441287	AW293132	Hs.131373	ESTs	4.0
15	418661	NM_001949	Hs.1189	E2F transcription factor 3	4.0 4.0
45	420894	AA744597 AB032990	Hs.88854 Hs.40719	ESTs hypothetical protein KIAA1164	4.0
	454120 441627	AA947552	Hs.58086	branched chain aminotransferase 1, cytos	4.0
	453948	AI970797	Hs.64859	ESTs	4.0
50	444170	AW613879	Hs.102408	ESTs	4.0
50	427221	L15409	Hs.174007	von Hippel-Lindau syndrome ESTs	4.0 4.0
	418821 418216	AA436002 AA662240	Hs.183161 Hs.283099		4.0
	435106	AA100847	Hs.5978	ESTs, Highly similar to AF174600 1 F-box	4.0
	430890	X54232	Hs.2699	glypican 1	3.9
55	429490	AI971131	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	3.9 3.9
	425292 436265	NM_005824 AA731331	Hs.155545 Hs.190668		3.9
	407304	AA565832	Hs.271649		3.9
	433244	AB040943	Hs.271285	KIAA1510 protein	3.9
60	446960	AW294936	Hs.156762		3.9 3.9
	406627 420552	T64904 AK000492	Hs.163780 Hs.98806	ESTs hypothetical protein	3.9
	402082	A1000432	113.30000	C18000743*:gij6678363 ref[NP_033416.1] t	3.9
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	3.9
65	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	3.9
	427527	AI809057	Hs.293441		3.9 3.9
	422564 418781	AI148006 T41160	Hs.222120 Hs.8404	ESTS	3.9
	431820	AW410408	Hs.271167		3.9
70	413095	AA494359	Hs.30715	potassium voltage-gated channel, tsk-rel	3.9
	430637	8E160081	Hs.256290		3.9 3.9
	443539 422173	AI076182 BE385828	Hs.134074 Hs.250619		3.9
	433388	AI432672	Hs.288539		3.8
75	403849			Target Exon	3.8
	406646	M33600	Hs.308026		3.8 3.8
	445075 420004	AI651827 AW975532	Hs.344767 Hs.164039		3.8 3.8
	420004 449670	F07693	Hs.85603		3.8
80	424479	AF064238	Hs.149098	B smoothelin	3.8
	449625	NM_014253		odz (odd Oz/ten-m, Orosophila) homolog 1	3.8
	418641	BE243136 AW600291	Hs.86947 Hs.6823	a disintegrin and metalloproteinase doma hypothetical protein FLJ10430	3.8 3.8
	439979	WALDOOTAL	rts.0023	Hypothesis protein FC/10400	3.0

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			0400	. 14	3.8
	427286 453920		Hs.2132 Hs.36602	epidermal growth factor receptor pathway I factor (complement)	3.8
	453920		Hs.35861	DKFZP586E1621 protein	3.8
_	406872	AI760903		gh:wi09h08.x1 NCI_CGAP_CLL1 Homo sapiens	3.8 3.8
5	403696			C4001100*:gi 5852342 gb AAD54015.1 (AF0	3.8
	417791 418036	AW965339 Z37976		ESTs latent transforming growth factor beta b	3.8
	404209	23/3/0	113.00007	Target Exon	3.8
	431454	AW975980	Hs.292918	ESTs	3.8 3.8
10	410422	AL042014	Hs.63348	Homo sapiens, clone MGC:15203, mRNA, com	3.8
	406739 450810	AI566709 BE207588	Hs.182426 Hs.334360	ribosomal protein S2 transforming growth factor beta 1 induce	3.8
	457876	AI821940	113.304000	ESTs, Moderately similar to ALU8_HUMAN A	3.8
	435718	R06569	Hs.269534	ESTs	3.8 3.8
15	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	3.8 3.8
	442710	AI015631 X91195	Hs.23210 Hs.100623	ESTs phospholipase C, beta 3, neighbor pseudo	3.8
	456534 419764	BE262524	Hs.93183	vasodilator-stimulated phosphoprotein	3.8
	436674	AA725002	Hs.272018	low molecular mass ubiquinone-binding pr	3.8
20	408896	AI610447	Hs.48778	niban protein	3.8 3.8
	425300	AW601773 BE159028	Hs.270259 Hs.279704	ESTs chromatin accessibility complex 1	3.8
	432886 424090	X99699	Hs.139262	XIAP associated factor-1	3.7
	420202	AL036557	Hs.95910	putative lymphocyte G0/G1 switch gene	3.7
25	427584	BE410293	Hs.179718	v-myb avian myeloblastosis viral oncogen	3.7 3.7
	420579	AA278449	Hs.137429	ESTs zinc finger protein 200	3.7
	406038 412590	Y14443 AL134388	Hs.135033	ESTs, Weakly similar to I38022 hypotheti	3.7
	406714	Al219304	Hs.266959	hemoglobin, gamma G	3.7
30	412014	A1620650	Hs.43761	ESTs, Wealdy similar to A46010 X-linked	3.7 3.7
	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi ESTs, Weakly similar to AF090944 1 PR006	3.7
	449115 408955	AW959952 BE315170	Hs.37528 Hs.8087	Target CAT	3.7
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	3.7
35	413774	AA131782	Hs.182314	ESTs	3.7 3.7
	440225	BE295782	Hs.159	tumor necrosis factor receptor superfami	3.7
	414528 436137	AA148950 AI056769	Hs.188836 Hs.133512	ESTs ESTs	3.7
	414733	BE514535	Hs.77171	minichromosome maintenance deficient (S.	3.7
40	406785	AA588061		gb:nk10d03.s1 NCI_CGAP_Co2 Homo sapiens	3.7 3.7
	443361	A1792628	Hs.133273	ESTs	3.7 3.7
	434868	R50032	Hs.159263 Hs.211193	collagen, type VI, alpha 2 ESTs	3.7
	409557 420300	BE182896 AA258245	Hs.127573		3.7
45	427695	R88483	Hs.172862	ESTs	3.7
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	3.6 3.6
	437916	BE566249	Hs.20999	hypothetical protein FLJ23142 pleckstrin homology domain-containing, f	3.6
	434563 444371	AW083994 BE540274	Hs.9469 Hs.239	forkhead box M1	3.6
50	437816	AI823445	Hs.280699	ESTs	3.6
	405605			C2001342:gi 127814 sp P26434 NAH4_RAT SO	3.6 3.6
	444794	A1419991	Hs.145225 Hs.106357		3.6
	430540 429747	AW245422 M87507	Hs.2490	caspase 1, apoptosis-related cysteine pr	3.6
55	453785	AI368236	Hs.283732		3.6
	403267			Target Exon	3.6 3.6
	440370	AA884000	Hs.8173 Hs.205722	hypothetical protein FLJ10803 PESTs	3.6
	447497 428600	AW167254 AW863261	Hs.242413		3.6
60	428715	AW293716	Hs.53126	ESTs	3.6
	416097		Hs.118964		3.6 3.6
	453438	A1469935	Hs.22792 Hs.21426	ESTs S ESTs, Moderately similar to ALU1_HUMAN A	3.6
	427299 434577		Hs.17976		3.6
65	452785		Hs.29643	4 erythroid differentiation and denucleati	3.6
	434467	BE552368	Hs.23185		3.6 3.6
	435523		Hs.11090		3.6
	418287 422156		Hs.78935	gb:yy56d10.s1 Soares_multiple_sclerosis_	3.6
70	441224		Hs.7753	calumenin	3.6
	458072	AI890347	Hs.27192	3 Homo sapiens cDNA: FLJ22785 fis, clone K	3.6 3.6
	435677		Hs.29372		3.6
	433325		Hs.14390 Hs.27130		3.6
75	420683 443206		Hs.9075	serine/threonine kinase 17a (apoptosis-i	3.6
	454078		Hs.22209	secreted modular calcium-binding protein	3.6
	404584	٠		Target Exon	3.5 3.5
	428311				3.5
80	425927 41513		Hs.16275	gb:HUM158C11B Clontech human fetal brain	3.5
	41297		Hs.35125	5 ESTs	3.5
	451593	3 AF151879	Hs.26700		3.5 3.5
	41642	7 BE244050	Hs.7930	Rac/Cdc42 guanine exchange factor (GEF)	3.3

	427809	M26380	Hs.180878	lipoprotein lipase	3.5
	443303	U67319	Hs.9216	caspase 7, apoptosis-related cysteine pr	3.5
	422765 445936	AW409701 BE543594	Hs.1578 Hs.61478	bacutoviral IAP repeat-containing 5 (sur hypothetical protein FLJ22329	3.5 3.5
5	411537	8E073250	NS.01470	gb:MRO-BT0551-060300-102-e05 BT0551 Homo	3.5
•	432250	AA452088	Hs.274170	Opa-interacting protein 2	3.5
	458438	AJ141520	Hs.151464	ESTs, Weakly similar to ALUC_HUMAN !!!!	3.5
	407253 410507	AA411175 AA355288	Hs.141939 Hs.76064	ESTs, Moderately similar to S65657 alpha transitional epithelia response protein	3.5 3.5
10	412436	AA665089	NS.70004	gb:nu76d01.s1 NCI_CGAP_Alv1 Homo sapiens	3.5
10	416933	BE561850	Hs.80506	small nuclear ribonucleoprotein polypept	3.5
	437681	A1207958	Hs.166556	Homo sapiens, Similar to TEA domain fami	3.5 3.5
	408247 440074	AA053451 AA863045	Hs.225632 Hs.10669	leucine zipper protein 3 ESTs, Wealdy similar to T00050 hypotheti	3.5 3.5
15	422448	AW372922	Hs.116774	integrin, atpha 1	3.5
	420676	AJ434780	Hs.4248	vav 2 oncogene	3.5
	417663	R07483	Hs.180461	ESTs	3.5 3.5
	451089 451446	AA903705 AI826288	Hs.4190 Hs.171637	Homo sapiens cDNA: FLJ23269 fis, clone C hypothetical protein MGC2628	3.5
20	414727	BE466904	Hs.190162	gb:hz28f03.x1 NCI_CGAP_GC6 Homo sapiens	3.5
	421778	AA428000	Hs.283072	actin related protein 2/3 complex, subun	3.5
	427413	BE547647	Hs.177781	hypothetical protein MGC5618	3.5 3.5
	414039 456304	M83221 AI820973	Hs.858	v-rel avian reticuloendotheliosis viral gb:nc21c02.y5 NCI_CGAP_Pr1 Homo sapiens	3.5
25	449162	AI632740	Hs.10476	ESTs	3.5
	437774	AW978199	Hs.291648	ESTs, Weakly similar to I38022 hypotheti	3.5
	426827	AW067805	Hs.172665	methylenetetrahydrofolate dehydrogenase	3.4 3.4
	452203 450325	X57522 A1935962	Hs.26289	transporter 1, ATP-binding cassette, sub ESTs	3.4
30	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	3.4
••	419726	U50330	Hs.1274	bone morphogenetic protein 1	3.4
	417409	BE272506	Hs.82109	syndecan 1	3.4 3.4
	412811 430758	H06382 T91568	Hs.270616	ESTs ESTs, Moderately similar to A34087 hypol	3.4
35	425769	U72513	Hs.159486	Human RPL13-2 pseudogene mRNA, complete	3.4
•-	452682	AA456193	Hs.9071	progesterone membrane binding protein	3.4
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytolactin) cyclin-dependent kinase 2	3.4 3.4
	447674 443378	BE270640 AW392550	Hs.19192 Hs.9280	proteasome (prosome, macropain) subunit,	3.4
40	446134	AW161234	Hs.13993	TBP-like 1	3.4
	418669	U85992	Hs.87197	Human clone IMAGE:35527 unknown protein	3.4
	425006	R38685	Hs.222746	ESTs	3.4 3.4
	435256 453379	AF193766 AA035261	Hs.13872 Hs.61753	cytokine-fike protein C17 ESTs	3.4
45	448224	R48700	Hs.20733	Homo sapiens cDNA: FLJ22356 fis, clone H	3.4
	455899	BE155112		gb:PM1-HT0350-151299-003-a03 HT0350 Homo	3.4
	422017	NM_003877	Hs.110776 Hs.82084	STAT induced STAT inhibitor-2 integrin beta 3 binding protein (beta3-e	3.4 3.4
	417395 405046	BE564245	NS.02004	C3000978:gi 9280045 dbj BAB01579.1 (AB0	3.4
50	423178	A1033140	Hs.124983	Homo sapiens mRNA; cDNA DKFZp564C142 (fr	3.4
	455142	AW861840		gb:CM0-CT0337-250200-243-g01 CT0337 Homo	3.4 3.4
	418819 428289	AA228776 M26301	Hs.191721 Hs.2253	ESTs complement component 2	3.4
	412799	AI267606	N3.2230	gb:ag91h03.x1 Stanley Frontal SB pool 1	3.4
. 55	403108			ENSP00000241415*:Hypothetical 67.7 kDa p	3.4
	421637	AF035290	Hs.106300	Homo sapiens clone 23556 mRNA sequence TG-interacting factor (TALE family homeo	3.4 3.4
	419373 424408	NM_003244 AI754813	Hs.90077 Hs.146428	collagen, type V, alpha 1	3.4
	451061	AW291487	Hs.213659		3.4
60	433578	BE336886	Hs.3416	adipose differentiation-related protein	3.4 3.4
	439867	AA847510	Hs.161292 Hs.193115		3.4
	449249 420982	T52285 AW576160	Hs.100729		3.4
	440826	AW383618	Hs.345256	ESTs, Moderately similar to ALU2_HUMAN A	3.4
65	427687	AW003867	Hs.1570	histamine receptor H1	3.4 3.3
	400533 436314	A1983409	Hs.189226	ENSP00000209376*:PRED65 protein (Fragmen ESTs	3.3
	418110	R43523	Hs.217754		3.3
	448140	AF146761	Hs.20450	BCM-like membrane protein precursor	3.3
70	402229	BE262804	N- CE 43C	mitochondrial ribosomal protein S2 lysyl oxidase-like 1	3.3 3.3
	410687 424614	U24389 X54486	Hs.65436 Hs.151242		3.3
	443338	R99575	Hs.302908	ESTs	3.3
26	433062	AK001757	Hs.281348	hypothetical protein FLJ 10895	3.3
75	405303	V01003	U- CC7//	Target Exon twist (Drosophila) homolog (acrocephalos	3.3 3.3
	410889 406673	X91662 M34996	Hs.66744 Hs.198253		3.3
	431721	AB032996	Hs.268044	KIAA1170 protein	3.3
٥٨	426746	J03626	Hs.2057	uridine monophosphate synthetase (orotal	3.3 3.3
80	425262 424947	D87119 R77952	Hs.155418	GS3955 protein ESTs, Wealdy similar to afternatively sp	3.3
	437634	AW293046	Hs.25515		3.3
	437014	AA808757	Hs.22253		3.3

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		AW953440		b:EST365510 MAGE resequences, MAG8 Homo	3.3 3.3
			ts.147674 (ts.94830 1	protocadherin beta 16 ESTs, Moderately similar to T03094 A-kin	3.3
	432625 435644			ESTs	3.3
5	406060		•	Target Exon	3.3 3.3
	425018	000	Hs.154196	E4F transcription factor 1 presenitin 2 (Alzheimer disease 4)	3.3
	450728 443105		Hs.25363 Hs.9004	chondroitin sulfate proteoglycan 4 (meta	3.3
	414799		Hs.77326	insufin-like growth factor binding prote	3.3
10	435375	AI733610	Hs.187832	ESTs	3.3 3.3
	432693			ESTs	3.3
	449340		Hs.195359 Hs.118110	hypothetical protein MGC10954 bone marrow stromal cell antigen 2	3.3
	422530 448002		Hs.20149	deleted in lymphocytic leukemia, 1	3.3
15	433160	AW207002	Hs.134342	TASP for testis-specific adriamycin sens	3.3 3.3
	429125	,	Hs.271004	ESTs, Weakly similar to 138022 hypotheti	3.3
	452526	W38537 H72780	Hs.280740 Hs.20289	hypothetical protein MGC3040 ESTs	3.3
	416664 444911	U06117	Hs.250	vanthene dehydrogenase	3.3
20	453544	AA831785	Hs.171914	Homo saniens cDNA FLJ14209 fis, clone NT	3.3 3.3
	433042	AW193534	Hs.281895	Homo sapiens cDNA FLI11660 fis, clone HE	3.3
	444046	AI360834	Hs.135094 Hs.8861	ESTs ESTs	3.3
	411373 431865	BE326276 AA521106	Hs.136375	ESTs. Weakly similar to \$65824 reverse t	3.3
25	408116	AA251393	Hs.289052	Homo sapiens, Similar to RIKEN cDNA 5430	3.3 3.3
	410006	AW732308	Hs.57783	eukaryotic translation initiation factor	3.3
	442485	BE092285	Hs.29724 Hs.203933	hypothetical protein FLJ13187 ESTs	3.3
	416379 416308	N38857 AW291942	Hs.23628	3 beta-hydroxy-delta 5-C27-steroid oxido	3.3
30	427954	J03060	Hs.247551	metaxin 1	3.3 3.3
	459660	M79082		ESTs	3.3
	419829	A1924228	Hs.115185	ESTs, Moderately similar to PC4259 ferri gb:yd68c08.r1 Soares fetal liver spleen	3.3
	437945 400850	T78519		Target Exon	3.3
35	457244	AA581385	Hs.162473	FSTs. Wealdy similar to 138022 hypotheti	3.3 3.3
	430462	AI584156	Hs.105640	Homo sapiens, done IMAGE:4139775, mRNA,	3.3
	457653	AI820719	Hs.154662 Hs.271411	DnaJ (Hsp40) homolog, subfamily A, membe beta-site APP-cleaving enzyme 2	3.2
	431836 440933	AF178532 Al208217	Hs.142879	ESTs	3.2
40	418079	R40058	Hs.6911	ESTs	3.2 3.2
	414280	BE410769	Hs.75873	zyxin	3.2
	425295	AA431366	Hs.37251	ESTs ESTs	3.2
	408872 416857	AI476139 AA188775	Hs.13291 Hs.292453		3.2
45	429599	AA806106	Hs.123664	ESTs	3.2
	437437	AA226869		hypothetical protein DKFZp762L0311	3.2 3.2
	434274	AA628539	Hs.116252		3.2
	403349 449385	NM_001406 Al650471	Hs.347290	ephrin-B3 ESTs	3.2
50	431421	AW969118	Hs.108144	ESTs, Weakly similar to unnamed protein	3.2
	419865	NM_007020		U1-snRNP binding protein homolog (70kD)	3.2 3.2
	410700	AA352335	Hs.65641	hypothetical protein FLJ20073 gb:EST384819 MAGE resequences, MAGL Homo	3.2
	432044 412490	AW972727 AW803564	Hs.288850		3.2
55	408431	AI338631	Hs.43266	Homo sapiens cDNA: FLJ22536 fis, clone H	3.2
	430413		Hs.24139		3.2 3.2
	448789		Hs.22051		3.2
	439332 418030		Hs.30087 Hs.83321		3.2
60	428878		Hs.48926	FSTs	3.2 3.2
	451527		Hs.26518	transmembrane 4 superfamily member 7	3.2 3.2
	426406		Hs.16975		3.2
	448432 433894		Hs.20857 Hs.24329		3.2
65	43621		Hs.19782		3.2
-	43379		Hs.11271	8 ESTs	3.2 3.2
	45015		Hs.23510		3.2
	42751		Hs.19248 Hs.13285	t hynothetical protein FLJ11222	3.2
70	42378 45135		F13, 1020	ob:ni13a05.y5 NCI_CGAP_Co4 Homo sapiens	3.2
, 5	42906		Hs.2964	Homo sapiens cDNA FL113103 fis, clone N1	3.2 3.2
	41578	4 AA334592		4 tumican major histocompatibility complex, class	3.2
	40685				3.2
75	42803 41264			8 transmembrane protein (63kD), endoplasmi	3.2
, ,	43206		Hs.2903	protein phosphatase 4 (formerly X), cata	3.2 3.2
	41570	9 AA649850	Hs.2785		3.2
	42279		Hs.3457 Hs.1368		3.2
80	43780 42517				3.2
50	4481			85 ESTs	3.2 3.2
	4025	23		C1001173*:gi]9743439[gb]AAF79932.2[(AF2 Homo sapiens cDNA: FLJ22930 fis, clone K	3.2
	4401	46 AW01423	1 Hs.9079	U ROTTU SAPIETA CUTAL FLJ 2230 IS, CIUTE N	~ -

	429415	NM_002593		procoffagen C-endopeptidase enhancer	3.2
	422081	AW136820	Hs.196011 Hs.107125	ESTs	3.2 3.2
	436258 410886	AW867491 AW809324	ns.10/123	plasmatemma vesicle associated protein gb:MR4-ST0121-141099-010-G06_1 ST0121 Ho	3.2
5	442609	AL020996	Hs.8518	selenoprotein N	3.2
	416188	BE157260	Hs.79070	v-myc avian myelocytomatosis viral oncog	3.2
	441544 437860	AW300043 AA333063	Hs.127137 Hs.279898	ESTs Homo sapiens cDNA: FLJ23165 ffs, clone L	3.2 3.2
	419652	AL157485	Hs.91973	hypothetical protein	3.2
10	443623	AA345519	Hs.9641	complement component 1, q subcomponent,	3.2
	415198	AW009480	Hs.943	natural killer cell transcript 4	3.2 3.2
	441701 426384	AW339828 AI472078	Hs.127497 Hs.303662	ESTs hypothetical protein FLJ13189 (FLJ13189)	3.2
	420886	AA805453	115.500002	ESTs, Wealty similar to T29012 hypotheti	3.2
15	428896	AW291932	Hs.98936	ESTs	3.2
	458253	AW296952	Hs.196802	ESTs	3.2 3.2
	456895 434818	AA354771 AA650097	Hs.43047 Hs.5996	Homo sapiens cDNA FLJ13585 fis, clone PL ESTs	3.2
	424278	AK000723	Hs.144517	hypothetical protein FLJ20716	3.2
20	434131	A1858275	Hs.143659	ESTs	3.2
	447111	AI017574	Hs.17409 Hs.8904	cysteine-rich protein 1 (intestinal)	3.1 3.1
	443021 416677	AA368546 T83470	Hs.334840	Ig superfamily protein ESTs, Moderately similar to 178885 serin	3.1
	429973	AI423317	Hs.164680	ESTs	3.1
25	422545	X02761	Hs.287820	fibronectin 1	3.1 3.1
	444006 420116	8E395085 NM_013241	Hs.10086 Hs.95231	type I transmembrane protein Fn14 FH1/FH2 domain-containing protein	3.1
	401841	NW_013241	113.33231	NM_015113:Homo sapiens KIAA0399 protein	3.1
	414416	AW409985	Hs.76084	hypothetical protein MGC2721	3.1
30	431019	NM_005249	Hs.2714	forkhead box G1B	3.1 3.1
	453707 432188	AW003879 Al362952	Hs.126522 Hs.2928	Homo sapiens, ctone MGC:16722, mRNA, com solute carrier family 7 (cationic amino	3.1
	407378	AA299264	Hs.57776	ESTs, Moderately similar to 138022 hypot	3.1
25	430701	A1760833	Hs.293971	ESTs	3.1
35	429569	AA454993 H56499	Hs.138343 Hs.252692	ESTs, Weakly similar to 178885 serine/th ESTs, Weakly similar to 138022 hypotheti	3.1 3.1
	458918 439764	T26535	Hs.22744	hypothetical protein MGC13105	3.1
	452221	C21322	Hs.288057	hypothetical protein FLJ22242	3.1
40	403969			ENSP0000034663:Zinc finger protein 131	3.1 3.1
40	427359	AW020782 BE548266	Hs.79881 Hs.76057	Homo sapiens cDNA: FLJ23006 fis, clone t. galactose-4-epimerase, UDP-	3.1
	414396 444153	AK001610	Hs.10414	hypothetical protein FLJ 10748	3.1
	414403	AW969551	Hs.76064	ribosomal protein L278	3.1
45	444168	AW379879	11- 64704	gb:RC1-HT0256-081199-011-f01 HT0256 Homo	3.1 3.1
43	410595 444881	AW629223 AI623288	Hs.64794 Hs.192805	zinc finger protein 183 (RING finger, C3 ESTs	3.1
	440381	AA917808	Hs.190495	ESTs	3.1
	416207	NM_014745	Hs.79077	Homo sapiens, clone MGC:2908, mRNA, comp	3.1
50	439130	AA306090	Hs.124707 Hs.36761	ESTs HRAS-like suppressor	3.1 3.1
50	457579 406736	AB030816 AJ254733	Hs.182426	ribosomal protein S2	3.1
	420172	AA601122	Hs.95655	secreted and transmembrane 1	3.1
	428060	AA420616	Hs.249483	ESTs	3.1 3.1
55	444143 409154	AW747996 U72882	Hs.160999 Hs.50842	ESTs, Moderately similar to A56194 throm interferon-induced protein 35	3.1
55	449426	T92251	Hs.198882	ESTs	3.1
	458760	AI498631	Hs.111334	ferritin, light polypeptide	3.1 3.1
	450811 425331	A1739486 AW962128	Hs.245497	ESTs gb:EST374201 MAGE resequences, MAGG Horno	3.1
60	445211	BE045601	Hs.118248	ESTs, Wealdy similar to YC18_HUMAN HYPOT	3.1
	441318	AI078234	Hs.176130	ESTs	3.1
	450625	AW970107	14- 272455	gb:EST382188 MAGE resequences, MAGK Homo ESTs, Weakly similar to 138022 hypotheti	3.1 3.1
	437640 444672	AA764893 Z95636	Hs.272155 Hs.11669	laminin, alpha 5	3.1
65	407047	X65965	10.11000	gb:H.sapiens SOD-2 gene for manganese su	3.1
	413834	BE296896	Hs.224179		3.1 3.1
	439755	AW748482	Hs.77873 Hs.9315	87 homolog 3 HNOEL-iso protein	3.1
	435520 414598	AA297990 Al094221	Hs.135150		3.1
70	440948	AW188311	Hs.128619	ESTs	3.1
	412851	AI826502	Hs.106149		3.1 3.1
	417336 417944	R70429 AU077196	Hs.81988 Hs.82985	disabled (Drosophila) homolog 2 (mitogen collagen, type V, alpha 2	3.1
	411671	8E049094	1.0.02.000	ESTs	3.1
75	430444	AW296421	Hs.121035	ESTs	3.1
	425843	BE313280	Hs.159627	death associated protein 3 dual-specificity tyrosine-(Y)-phosphoryl	3.1 3.1
	407721 439093	Y12735 AA534163	Hs.38018 Hs.5476	Homo sapiens, clone IMAGE:3530123, mRNA,	3.1
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	3.1
80	435664	A1032087	Hs.269819		3.1 3.1
	453085 430314	AW954243 AA369601	Hs.239138	KIAA0251 protein pre-B-cell colony-enhancing factor	3.0
	447527	AI702896	Hs.42091	ESTs	3.0

	*****	41270400	Hs.159588 1	ESTs	3.0
			He 48778	nihan omtein	3.0
	455481	AW948317	4	nh:RC0-MT0015-280300-021-a09 MT0015 Homo	3.0
_	445906	N28939	Hs 13434	Homo saniens clone 24418 mRNA sequence	3.0 3.0
5	408716	AI567839	Hs.151714	Homo sapiens mRNA for KIAA1769 protein, minichromosome maintenance deficient (S.	3.0
	424308	AW975531		ESTs	3.0
	436443 425421	AW138211 L11669	Hs.157145	tetracycline transporter-like protein	3.0
	427725	U66839	Hs.180533	mitogen-activated protein kinase kinase	3.0
10	456816	AK001509	Hs.144391	hypothetical protein FLJ10647	3.0 3.0
	404632			NM_022490:Homo sapiens hypothetical prot gb:MR2-CT0222-011199-007-d06 CT0222 Homo	3.0
	411565	AW851728	Un 46000	80:MRZ-C10222-011199-007-008-C10222-1-0:10	3.0
	428917 424584	AA437337 H10692	Hs.16689 Hs.13310	ESTs	3.0
15	452483	AI903731	Hs.106357	valosin-containing protein	3.0
13	404453	, , ,		C8000963*:gi[6329915]kibj[BAA86452.1] (AB	3.0 3.0
	426931	NM_003416	Hs.2076	zinc finger protein 7 (KOX 4, clone HF.1	3.0
	455646	BE064420	Un 470976	gb:RC4-BT0311-241199-012-c08 BT0311 Homo ESTs	3.0
20	452188	AI864208 NM_006187	Hs.176275 Hs.56009	2-5'-oligoadenylate synthetase 3 (100 k	3.0
20	409703 413922	A1535895	Hs.221024	ESTs	3.0
	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	3.0
	434070	AF116652	Hs.270087	hypothetical protein PRO0813	3.0 3.0
0.5	406679	AA070786		gb:zm66b07.r1 Stratagene neuroepithelium centromere protein F (350/400kD, mitosin	3.0
25	414747	U30872	Hs.77204 Hs.283022	triggering receptor expressed on myeloid	3.0
	435472 429612	AW972330 AF062649	Hs.252587	pituitary tumor-transforming 1	3.0
	408989	AW361666	Hs.49500	KIAA0746 protein	3.0
	418365	AW014345	Hs.161690	ESTs	3.0 3.0
30	418677	S83308	Hs.87224	SRY (sex determining region Y)-box 5	3.0
	426765	AA743603	Hs.172108	nucleoporin 88kD Al905687:IL-BT095-190199-019 BT095 Homo	3.0
	400295 1 429751	W72838 M55210	Hs.214982	laminin, gamma 1 (formerly LAMB2)	3.0
	429751	W25215	113.217502	gb:zb87a09.r1 Soares_senescent_fibroblas	3.0
35	412281	AI810054	Hs.14119	ESTs	3.0 3.0
	434898	AW500458	Hs.29956	KIAA0460 protein	3.0
	424830	AW270580	Hs.189311	ESTs, Weakly similar to putative p150 (H gb:RC-BT113-060499-024 BT113 Homo sapien	3.0
	459727	A1906494 AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU S	3.0
40	453900 458729	A1364504	Hs.93967	FSTs. Wealdy similar to NBHUC8 decorn p	3.0
-10	402105			C18000230*:gi[12585552 sp Q9Y2Q1 Z257_HU	3.0 3.0
	425248	AW957442	Hs.252766		3.0
	440995	T57773	Hs.10263	ESTs Homo sapiens, Similar to RIKEN cDNA 1110	3.0
45	441360	A1091713	Hs.106597 Hs.200577		3.0
43	432692 428899	AW974944 AA744610	Hs.194431		3.0
	452811	AA937079	Hs.118983		3.0
	447183	AI554733	Hs.173182	ESTs	3.0 3.0
60	429679	NM_006290			3.0
50	416505	H66470 AA811813	Hs.16004 Hs.119421	ESTs ESTs	3.0
	420144 439184			myosin phosphatase, target subunit 1	3.0
	438033		Hs.6059	EGF-containing fibulin-like extracellula	3.0 3.0
	442476			gb:AF069475 Homo sapiens astrocytoma lib	3.0
55	441035		Hs.126450		3.0
	458810 435046		Hs.231510 Hs.17433		3.0
	414271				3.0
	450879		Hs.21034	7 ESTs	3.0 3.0
60	454036		Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	3.0
	403780			C4001759:gi]133250 sp P19474 RO52_HUMAN gb:lL3-CT0220-160200-066-F01 CT0220 Homo	3.0
	411543 440351			RAD1 (S. pombe) homolog	3.0
	452139			Homo sapiens cDNA: FLJ21482 fis, clone C	3.0
65	449433		Hs.9012	ESTs, Weakly similar to S26650 DNA-bindi	3.0 3.0
	413945			CD14 antigen	3.0
	43368		Hs.20036 Hs.11866		3.0
	422605 443500		Hs.113394	· · · · · · · · · · · · · · · · · · ·	3.0
70	41078				3.0
, ,	44942			BS ESTs	3.0 3.0
	43667	1 AW13715	9 Hs.1461	51 ESTs	3.0
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80			1 AWROQ3	262 R27868 AW811262 324 BE144977 BE144956	
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	41154			248 AW851425 AW850805 AW851021 AW850905	

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	411688	1254076_1		08189 AW857085
5	412436 412799	129439_1		A135130 AA484059 AA102419 AW877765 .121045 AA126521
,	412/99	132817_1 132943_1	MUESES AWG	x57730 AA353014 R13591 AA121201 D60420 RE263253 BE047862 Z41952 AI424991 AI693507 AI863108 AA599060 AI091148 AA598689
	412011	102540_1	R39887 AA8	13482 AW016452 H06383 R41807 AJ364268 AA620528 AJ241940 AW089149 AW090733 AW088875 Z38240 AA121202 R17734
	414372	143909_1		W753140 AA213770 AW970865 AA569075 AA492132
10	415131	1523680_1	D61119 D81	
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	419896	1888662_1	Z99362 Z993	
	420886	197344_1	AA805453 A	A281379
15	422156	212379_1	N34524 AA3	05071 AW954803 AA502335 AI433430 AI203597 AW026670 AW265323 AW850787 AA317554 AW993643 AW835572 AW385512
	423713	231290_1		32951 H62656 H53902 R88904 AW835732 NW754198 AA329983
	424009	234177_1		66570 AA33586 D30830
	424947	245247_1		48809 AW959960 AW959962 AI565552 AW070702 AA973910 R85973
20	425331	250199_1		N355353 AA427363
	429163	300543_1		W974271 AA592975 AA447312
	429940 430968	310884_1 326269_1		461079 AA461391 AA527647 AA489820 AA570362
	432044	340773_1		AA524829 AW972733
25	432363	345469_1		W970240 AW970323
	435542	407744_1	AA687376 H	174234 AW975503
	437437	43709_1	AA226869 A	A296516 AW959753 AA186390 AL359619 AA356195 AA148427 R22748 A1033624 BE548853 H95327 AW579751 BE561649 AA397533 A236444 T89946 AA247450 N55777 W38725 A1743846 A1808406 AA922229 A1051464 W04713 R11251 W19656 A1042319 AA489276
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	439566	47387_1		V77884 W72711
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35	442476 444168	593829 1	AW370870	A11262R5 H12014
55	449625	B113_1	NM 014253	x AF 100772 RE088769 AL022718 RF 161779 AW863569 RF 161640 AL039060 RF 168542 AW296554 AA323193 AA235370 AW779760
		_	N48674 AI3	75997 R45432 D59344 AI203107 F07491 R35360 R25094 AI913631 AI498402 T61382 AI016320 N45526 T61415 AA331486
	450166	82677_1	AA429504 F	R41904 AA279467 H09648 AA007236 AA131254 AA374293 AW954405 H04410 AW606284 AA151166 BE157467 BE157601 H04384 W46291 AW663674 H04021 H01532
40	450375	83327_1	AAUU96477	H03231 H59605 H01642 AAB52876 AA113758 AA626915 AA746952 A1161014 AA099554 R69067
70	450506	836_1	NM MAAR	11IN0278 LI76833 AW630055 AW471133 CD2434 W45237 AW793518 BE070112 AI587479 AI624429 AW190535 AI446661 AI478772
			AW022667	AA528235 AA599775 AW613820 AI435793 AW594230 AI051768 AI200109 AI680296 AA436611 AW609728 W42634 AI682584 AA405569
			AI685653 A	
45	450625	84032_1		AA513951 AA010406
43	451129 451350	859870_1 866945_1	A1701447 A	BE072946 AI762181 J791327 AW886809
	452203	903_2	V67633 AIA	205047 A1245107 A1204503 21205 21206 21207 21208 21204 NM 000593 F06770 F12630 X57521 R18264 T74462 AA346259
		_	AW602508	AA904076 F08426 H23432 AA313737 AA393782 M78052 AA847441 AA487637 AA135770 AA353161 AI819778 AA054458 AI346733
50	453005	04064 4	AW361447	AIA AA829930 AA412478 AA828434 AA814538 AI927418 AI192435 W52897 AA443666 AA031913 AI683306 AA918481 AI183314 D83907
50	453085	94851_1	A1206832 A	A876122 D83836 D83838 D82533 AI761290 AI191125 AI143749 AW771909 AI241436 AI767267 W56507 AA847787 AA568692 T10502
			A1247970	
	453331	96214_1	AI240665 T	53681 N77468 H51833 AA147247 R75732 C18450 R73999 AI095755 T49904 H03868 AA411580 R33395 AA410585 T48869 D63292
55			R31981 H1 R7390	2498 H02668 AA035018 R75957 AI803329 R27528 R36203 AI809932 AI808765 R78948 AA411449 AA976929 AI378760 AI378620 T48870
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	454860	1237732_1	AW835767	AW835537 BE160187
	455142	1254887_1	AW861840	AW858329 AW858192 AW858189 AW858224 AW858351
60	455481	1293182_1	AW948317	AW948322 AW948329 AW948316 AW948298 AW948330 AW948325 AW948324
00	455646 455899	1348557_1 1381547_1	BE155112	BE064435 BE064429 BE064414 BE064400 BE064517 BE155154 BE155087 BE155247 BE155499 BE155367 BE155452
	456304	176820_1		AJ734077 A1820984 AA225796 AA225060 AA225101
	457876	42814_2	AI821940 I	N57106 A1744264 AAB08846 AA643417 AA643416 Z70715
65	*****	00.		
05	TABLE 1 Pkey:		ane number cr	prresponding to an Eos probesel
	Ref:	Sec	vence source	. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA
				an chromosome 22' Dunham, et al. (1999) <u>Mature</u> 402:489-495.
70	Strand:			and from which exons were predicted. de positions of predicted exons.
70	Nt_positi	ion: ind	icates nucleoa	de positions of predicted extens.
	Pkey	Ref	Strand	Nt_position
	400533	6981826	Minus	277132-277595
75	400850	1927150	Minus	4506-4691 414660 114832
13	401454 401841	9186923 7684597	Minus Ptus	114659-114832 89868-90006,91920-92085
	402082	8117478	Minus	190046-190183
	402105	8131588	Minus	22856-24055
οΛ	402229	9965022	Minus	15739-15951,16166-16779 2017: 78704 43173 43365
80	402239 402274	7690131 2935596	Ptus Ptus	38175-38304,42133-42266 5604-6527
	402523	9798518	Minus	18729-19283
	402604	9909420	Plus	20393-20767

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	402855	9662953	Minus	59763-59909
	403011	6693597	Minus	3468-3623
	403108	8980955	Plus	93253-93667
	403267	7887182	Plus	116078-121885
5	403349	8569773	Minus	167815-168374
•	403361	8570313	Minus	112496-112687
	403481	9965004	Plus	93496-93633
	403696	3135242	Minus	143467-143634
	403780	8076989	Plus	93160-93409
10	403849	7708855	Ptus	95043-96519
	403961	7596976	Minus	110393-110603
	403969	8569909	Plus	31237-31375,32405-32506
	404209	5006246	Minus	11247-11514
	404407	7329316	Minus	48154-48499
15	404453	7657714	Plus	27768-29179
	404584	9857511	Ptus	138651-139153
	404632	9796668	Plus	45096-45229
	405046	7596829	Minus	4373-4528
	405141	8980911	Plus	99861-100054
20	405303	2078453	Minus	130607-130802
	405348	2914717	Minus	43310-43462
	405558	1621110	Plus	4502-4644,5983-6083
	405605	5836195	Minus	117070-117270
	406038	8389537	Plus	37764-37877
25	406060	6899623	Minus	20339-20746
	406478	9857502	Plus	68314-68523,68853-68950

TABLE 17A: ABOUT 1040 GENES UP-REGULATED IN GLIOBLASTOMA MULTIFORMA COMPARED TO NORMAL ADULT TISSUES
Table 17A lists about 1040 genes up-regulated in glioblastoma multiforma (G8M) compared to normal normal adult tissues. These were selected from 59680 probesets on the Affyrmetriz/Eos Hu03 GeneChip array such that the ratio of "average" globibastoma to "average" normal tissues was greater than or equal to 3.0. The "average" G8M level was set to the 85° percentile amongst various non-malignant adult tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10° percentile value amongst the various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
EXACCN: Exemplar Accession number, Genbank accession number
UniquenelD: Uniquene number 30

35

Pkey:
ExAccn:
UnigenelD:
Unigene Title:
R1:

Unigene gene title Ratio of GLIOBLASTOMA MULTIFORMA compared to NORMAL ADULT TISSUES

40	Pkey	ExAcon	UnigeneID	Unigene Title	R1
	431917	D16181	Hs.2868	peripheral myelin protein 2	57.9 50.4
	428321	A1699994	Hs.2868	peripheral myelin protein 2	50.1
	427343	AI880044	Hs.176977	protein kinase C binding protein 2	49.6
	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affi	43.9
45	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	42.9
	435147	AL133731	Hs.4774	Homo sapiens mRNA; cONA DKFZp761C1712 (f	42.5
	430838	N46664	Hs.169395	hypothetical protein FLJ12015	37.9
	418375	NM_003081	Hs.84389	synaptosomal-associated protein, 25kD	37.1
	449494	AW237014	Hs.315369	Homo sapiens cDNA: FLJ23075 fis, clone L	37.0
50	425088	AA663372	Hs.169395	hypothetical protein FLJ12015	32.7
-	425842	AI587490	Hs.159623	NK-2 (Drosophila) homolog B	32.4
	419078	M93119	Hs.89584	insulinoma-associated 1	32.1
	423849	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f	29.9
	409389	AB007979	Hs.301281	Homo sapiens mRNA, chromosome 1 specific	28.8
55	413333	M74028	Hs.75297	fibroblast growth factor 1 (acidic)	28.5
55	417183	R52089	Hs.172717	ESTs	27.6
	426325	D28114	Hs.169309	myelin-associated oligodendrocyte basic	27.6
	412733	AA984472	Hs.74554	KIAA0080 protein	25.9
	422656	AI870435	Hs.1569	LIM homeobox protein 2	25.6
60	436878	BE465204	Hs.47448	ESTs	24.9
-	437204	AL110216	Hs.22826	ESTs, Wealdy similar to I55214 salivary	24.3
	429007	D80642		gb:HUM092E09B Human fetal brain (TFujiwa	23.1
	429276	AF056085	Hs.198612	G protein-coupled receptor 51	23.1
	409395	1146745	Hs.336678	dystrobrevin, atpha	23.0
65	435708	AI362949	Hs.75169	ESTs	22.5
	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	22.2
	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone CO	22.1
	418110	R43523	Hs.217754	hypothetical protein FLJ22202	22.0
	416829	AB013805	Hs.80220	catenin (cadherin-associated protein), d	21.7
70	444513	AL120214	Hs.7117	glutamate receptor, ionotropic, AMPA 1	20.9
. •	433551	AI985544	Hs.12450	protocadherin 9	19.8
	452744	AI267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	19,1
	425057	AA826434	Hs.1619	achaete-scute complex (Drosophila) homol	19.0
	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	19.0
75	447004	AW296968	Hs.157539		18.6
	425048	H05468	Hs.164502	? ESTs	18.2
	427897	NM_017413	Hs.303084		18.0
	421264		Hs.103042	microtubule-associated protein 1B	18.0
	453642		Hs.34074	dipeptidylpeptidase VI	17.8
80	424140		Hs.141306	3 myelin oligodendrocyta głycoprotein	17.7
	444471		Hs.11217	KIAA0877 protein	17.6
	441350		Hs.7782	paraneoplastic antigen MA2	17.2
	430691		Hs.10353		16.7

	433800	AI034361	Hs.135150	tung type-I cell membrane-associated gly	16.6 16.6
	424581 408562	M62062 AI436323	Hs.150917 Hs.31141	catenin (cadherin-associated protein), a Homo sapiens mRNA for KIAA1568 protein,	16.5
_	423853	AB011537	Hs.133466	stit (Drosophila) homolog 1	16.4
5	431019	NM_005249	Hs.2714	torkhead box G18	16.4
	449539 450133	W80363 AW969769	Hs.58446 Hs.105201	ESTs ESTs	16.4 16.1
	425799	T08133	Hs.182906	Homo sapiens mRNA for KIAA1872 protein,	16.0
• •	447359	NM_012093	Hs.18268	adenylate kinase 5	15.4
10	415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	15.3 14.9
	459516 456759	AI049662 BE259150	Hs.246858 Hs.127792	EST delta (Drosophila)-like 3	14.7
	429466	M85835	Hs.12827	ESTs	14.7
1.5	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	14.7
15	443785 439415	AW449952 F05538	Hs.190125 Hs.4273	basic-helix-loop-helix-PAS protein ESTs	14.6 14.5
	408604	D51408	Hs.21925	ESTs	14.5
	444378	R41339	Hs.47860	neurotrophic tyrosine kinase, receptor,	14.3
20	428392	H10233	Hs.2265	secretory granule, neuroendocrine protei	14.0 14.0
20	418738 409799	AW388633 D11928	Hs.6682 Hs.76845	solute carrier family 7, (cationic amino phosphoserine phosphatase-like	13.9
	439239	AI031540	Hs.235331	ESTs	13.8
	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	13.7 13.6
25	448595 441285	AB014544 NM_002374	Hs.21572 Hs.167	KIAA0644 gene product microtubule-associated protein 2	13.5
23	428982	NM_005097	Hs.194704	leucine-rich, gliorna inactivated 1	13.4
	441440	AI807981	Hs.30495	ESTs	13.0
	412959	D87458	Hs.75090	KIAA0282 protein	12.8 12.8
30	413597 441016	AW302885 AW138653	Hs.117183 Hs.25845	ESTs ESTs	12.7
50	418338	NM_002522	Hs.84154	neuronal pentraxin I	12.6
	423419	R55336	Hs.23539	ESTs	12.6 12.6
	445495 441497	BE622641 R51064	Hs.38489 Hs.23172	ESTs, Weakly similar to 138022 hypotheti ESTs	12.4
35	424893	AW295112	Hs.153648	Homo sapiens cDNA FLJ13303 fis, clone OV	12.2
	453941	U39817	Hs.36820	Bloom syndrome	12.2
	427701	AA411101	Hs.243886 Hs.144006	nuclear autoantigenic sperm protein (his ESTs	12.2 12.1
	446782 437268	A1653048 A1754847	Hs.227571	regulator of G-protein signaffing 4	12.1
40	411411	AA345241	Hs.55950	ESTs, Weakly similar to KIAA1330 protein	11.9
	448302	AI480208	Hs.182906	Homo sapiens mRNA for KIAA1872 protein,	11.9 11.9
	407034 449625	U84540 NM_014253		gb:Human dystrobrevin isotorm DTN-3 (DTN odz (odd Oz/ten-m, Drosophita) homolog 1	11.7
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	11.7
45	424432	AB037821	Hs.146858	protocadherin 10	11.6
	451996	AW514021	Hs.245510		11.4 11.4
	423678 445041	AW963357 T64183	Hs.7847 Hs.282982	ESTs solute carrier	11.3
	442613	Al004002	Hs.130522		11.2
50	419721	NM_001650	Hs.288650		11.2 11.1
	446711 412986	AF169692 X81120	Hs.12450 Hs.75110	protocadherin 9 cannabinoid receptor 1 (brain)	11.0
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	10.7
<i>E E</i>	428728	NM_016625	Hs.191381		10.6 10.6
55	415849 447198	R20529 D61523	Hs.6806 Hs.283435	ESTs ESTs	10.5
	420602	AF060877	Hs.99236	regulator of G-protein signalling 20	10.3
	435793	AB037734	Hs.4993	KIAA1313 protein	10.3
60	409049	AJ423132	Hs.146343		10.2 10.2
00	449611 402604	AI970394	Hs.197075	ESTs Target Exon	10.1
	434277	X77748	Hs.3786	glutamate receptor, metabotropic 3	10.0
	440435	AL042201	Hs.21273	transcription factor NYD-sp10	10.0 10.0
65	438080 419271	AA777381 N34901	Hs.291530 Hs.238532		9.9
03	426344	H41821	Hs.322469		9.8
	449605	AW138581	Hs.198416		9.8
	408081	AW451597	Hs.167409 Hs.280740		9.8 9.8
70	452526 411305	W38537 BE241596	Hs.69547	myelin basic protein	9.8
	443455	AB001025	Hs.9349	ryanodine receptor 3	9.8
	427540	R12014	Hs.20976	ESTs ESTs, Weakly similar to 2004399A chromos	9.7 9.7
	424790 416892	AL119344 L24498	Hs.13326 Hs.80409		9.6
75	452461	N78223	Hs.108106	transcription factor	9.6
	449433	AJ672096	Hs.9012	ESTs, Wealdy similar to S26650 DNA-bindi	9.6 9.5
	454027 439199	R40192 R40373	Hs.21527 Hs.26299	Human DNA sequence from clone GS1-115M3 ESTs	9.5 9.5
	433896	AW294729	Hs.274461		9.3
80	416072	AL110370	Hs.79000	growth associated protein 43	9.3
	444119 435624		Hs.184261 Hs.24889		9.2 9.2
	412788		Hs.198410		9.2

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					9.2
				ESTs ESTs	9.2
	427304 429918			ESTs	9.1
	442910	Al365130	Hs.11307	ESTs, Weakly similar to T19326 hypotheti	9.1
5	425187	AW014486		ESTs	9.1 9.1
	436954	AA740151		ESTs ESTs	9.1
	442710 411078	AI015631 AI222020		CocoaCrisp	9.0
	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transl	9.0
10	437036	AI571514		ESTs	9.0 9.0
	448672	AI955511		ESTs ESTs	8.9
	451952 448743	AL120173 AB032962	Hs.301663 Hs.21896	KIAA1136 protein	8.9
	412068	S72043	Hs.73133	metallothionein 3 (growth inhibitory fac	8.9
15	439451	AF086270	Hs.278554	heterochromatin-like protein 1	8.8 8.8
	419088	AI538323	Hs.52620	integrin, beta 8 poly(A)-binding protein, cytoplasmic 1-l	8.8
	445873 410102	AA250970 AW248508	Hs.251946 Hs.279727	ESTs; homologue of PEM-3 [Ciona savignyi	8.8
	449571	AW016812	Hs.200266	ESTs	8.7
20	425354	U62027	Hs.155935	complement component 3a receptor 1	8.7 8.7
	452355	N54926	Hs.29202	G protein-coupled receptor 34	8.7
	410276 435501	AJ554545 AW051819	Hs.68301 Hs.129908	angiopoietin-2 KIAA0591 protein	8.6
	407728	AW071502	Hs.175931	ESTs	8.6
25	415293	R49462	Hs.106541	ESTs	8.6 8.6
	416857	AA188775	Hs.292453	ESTs ESTs, Weakly similar to 138022 hypotheti	8.5
	425234 450375	AW152225 AA009647	Hs.165909	a disintegrin and metalloproteinase doma	8.5
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	8.4
30	438380	T06430	Hs.6194	chondroitin sulfate proteoglycan BEHAB/b	8.4
	421659	NM_014459	Hs.106511	protocadherin 17	8.4 8.3
	418097	R45137	Hs.21868	ESTS	8.2
	429183	AB014604 Al221919	Hs.197955	KIAA0704 protein hypothetical protein FLJ10582	8.2
35	424945 455601	A1368680	Hs.816	SRY (sex determining region Y)-box 2	8.2
55	453884	AA355925	Hs.36232	KIAA0186 gene product	8.2 8.1
	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	8.1
	436887	AW953157	Hs.193235	hypothetical protein DKFZp547D155 KIAA1170 protein	8.1
40	431721 417160	AB032996 N76497	Hs.268044 Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	8.1
70	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	8.1
	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	8.1 8.0
	436039	AW023323	Hs.121070	ESTs solute carrier family 16 (monocarboxylic	8.0
45	449444	AW818436 AA442224	Hs.23590 Hs.97900	ESTs	8.0
43	427463 440184	AB002297	Hs.7022	dedicator of cyto-kinesis 3	7.9
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	7.8 7.7
	451621	AI879148	Hs.26770	fatty acid binding protein 7, brain	7.7 7.7
50	419929	U90268	Hs.93810	cerebral cavernous malformations 1 gb:QV-BT200-010499-007 BT200 Homo sapien	7.7
20	419544 448555	AI909154 AI536697	Hs.159863		7.7
	414372	AA143654		gb:zo65a02.r1 Stratagene pancreas (93720	7.7
	438527	AI969251	Hs.115325	RAB7, member RAS oncogene family-like 1	7.7 7.7
55	400293	N51002	Hs.306480 Hs.97206	Homo sapiens mRNA, cDNA DKFZp761E2112 (f huntingtin interacting protein 1	7.6
55	420362 430132	U79734 AA204686	Hs.234149	hypothetical protein FLJ20647	7.5
	448543	AW897741	Hs.21380		7.5
	436140		Hs.26958	7 ESTs	7.4 7.4
۲0	449340		Hs.19535		7.4
60	446372	AB020644 BE410100	Hs.14945 Hs.40368		7.4
	454117 410434		Hs.63668		7.4
	454048	H05626	Hs.6921	ESTs	7.4 7.4
15	441523				7.4
65	440074 438330		Hs.10669 Hs.25731		7.4
	433556		Hs.11146	O calcium/calmodulin-dependent protein kin	7.3
	434808		Hs.25615	O Homo sapiens, Similar to RIKEN cDNA 2810	7.3
70	445900		Hs.12503	Homo sapiens clone 24787 mRNA sequence	7.3 7.2
70	402859		7 Hs.63984	NM_001839":Homo sapiens calponin 3, acid cadherin 13, H-cadherin (heart)	7.2
	422966 439772				7.2
	43344		Hs.3281	neuronal pentraxin II	7.2
	41270	9 AL022327	Hs.74518		7.2
75	44574	5 AB007924			7.2 7.2
	44710 44893		Hs.4418 Hs.2259		7.1
	40924			5 KIAA1209 protein	7.1
	45278		Hs.2964	34 erythroid differentiation and denucleati	7.1
80	42499	8 U58515	Hs.1541		7.1 7.1
	43660		3 Hs.2110	61 ESTs gb:yh88b01.s1 Soares placenta Nb2HP Homo	7.1
	44719 41924		Hs.8976		7.1
	71024			•	

	415111	AA022012	Hs.79018	chromatin assembly factor 1, subunit A (7.1
	416111 421633	AA033813 AF121860	Hs.106260	sorting nexim 10	7.0
	428976	AL037824	Hs.194695	ras homolog gene family, member I	7.0
5	444783	AK001468	Hs.62180	anillin (Orosophila Scraps homolog), act	7.0 7.0
3	408096 426269	BE250162 H15302	Hs.83765 Hs.168950	dihydrofotate reductase Homo sapiens mRNA; cDNA DKFZp566A1046 (f	6.9
	439978	BE139460	Hs.124673	Homo sapiens cDNA FLJ11477 fis, clone HE	6.9
	439570	T79925	Hs.269165	ESTs, Weakly similar to ALU1_HUMAN ALU S	6.9
10	422980 415279	N46569 F04237	Hs.76722 Hs.1447	CCAAT/enhancer binding protein (C/EBP), glial fibrillary acidic protein	6.9 6.9
10	456965	AW131888	Hs.172792	ESTs, Weakly similar to hypothetical pro	6.9
	447773	A1423930	Hs.36790	ESTs, Weakly similar to putative p150 [H	6.9
	429927	NM_001115	Hs.2522 Hs.147674	adenylate cyclase 8 (brain)	6.9 6.8
15	447499 414696	AW262580 AF002020	Hs.76918	protocadherin beta 16 Niemann-Pick disease, type C1	6.8
	441255	R06350	Hs.171635	ESTs	6.8
	429656	X05608	Hs.211584	neurofilament, light polypeptide (68kD)	6.8 6.8
	439566 435191	AF086387 R15912	Hs.4817	gb:Homo sapiens full length insert cDNA Homo sapiens clone 24461 mRNA sequence	6.8
20	420285	AA258124	Hs.293878	ESTs, Moderately similar to ZN91_HUMAN Z	6.8
	430968	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	6.8
	458332 449048	AI000341 Z45051	Hs.220491 Hs.22920	ESTs similar to S68401 (cattle) glucose induc	6.8 6.7
	413627	BE182082	Hs.246973	ESTs	6.7
25	415079	R43179	Hs.22895	hypothetical protein FLJ23548	6.7
	418677	S83308	Hs.87224 Hs.274263	SRY (sex determining region Y)-box 5 hypothetical protein FLJ10377	6.7 6.7
	432281 425741	AK001239 AF052152	Hs.159412	Homo sapiens clone 24628 mRNA sequence	6.7
••	421141	AW117261	Hs.125914	ESTs	6.6
30	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfot	6.6 6.6
	432154 425202	A1701523 AW962282	Hs.112577 Hs.152049	ESTs ESTs, Wealdy similar to I38022 hypotheti	6.6
	434164	AW207019	Hs.148135	serine/threonine kinase 33	6.6
25	407182	AA312551	Hs.230157	ESTs	6.6
35	445034 410909	AW293376 AW898161	Hs.143659 Hs.53112	ESTs ESTs, Moderately similar to ALU8_HUMAN A	6.6 6.6
	441102	AA973905	113.33112	intermediate filament protein syncollin	6.6
	452834	A1638627	Hs.105685	KIAA1688 protein	6.6
40	429239	AA448419	Hs.45209	ESTs	6.6 6.5
40	414175 449300	AI308876 AI656959	Hs.103849 Hs.346514	hypothetical protein OKFZp761D112 ESTs	6.5
	446727	AB011095	Hs.16032	KIAA0523 protein	6.5
	429250	H56585	Hs.198308	tryptophan rich basic protein	6.5 6.5
45	420560 448321	AW207748 NM_005883	Hs.59115 Hs.20912	ESTs adenomatous polyposis cofi like	6.5
43	441390	AI692560	Hs.131175	ESTs	6.5
	407168	R45175	Hs.117183	ESTs	6.4
	447414 407235	D82343 D20569	Hs.74376 Hs.169407	neuroblastoma (nerve tissue) protein SAC2 (suppressor of actin mutations 2, y	6.4 6.4
50	433597	AA708205	Hs.100343	ESTs	6.4
	414528	AA148950	Hs.188836	ESTs	6.4
	414214 446692	D49958 Z44514	Hs.75819	gtycoprotein M6A Homo sapiens mRNA for KIAA1763 protein,	6.4 6.4
	407896	D76435	Hs.41154	Zic family member 1 (odd-paired Drosophi	6.4
55	440152	AB002376	Hs.7006	KIAA0378 protein	6.4
	453785 412530	AI368236 AA766268	Hs.283732 Hs.266273		6.3 6.3
	448902	Z45998	Hs.22543	Homo sapiens mRNA; cDNA DKFZp761I1912 (f	6.3
<i>(</i> 0	452799	AI948829	Hs.213786		6.3
60	425523	AB007948 T65213	Hs.158244	KIAA0479 protein ESTs	6.3 6.3
	422094	AF129535	Hs.4257 Hs.272027	F-box only protein 5	6.3
	420649	A1866964	Hs.124704	ESTs, Moderately similar to S65657 alpha	6.3
65	424028 447350	AF055084 AI375572	Hs.153692 Hs.172634		6.3 6.2
05	448148	NM_016578		HBV pX associated protein-8	6.2
	436936	AL134451	Hs.197478	ESTs	6.2
	448243	AW369771	Hs.52620	integrin, beta 8	6.2 6.2
70	414727 420608	BE466904 BE548277	Hs.190162 Hs.103104		6.2
. •	422949	AA319435		gb:EST21657 Adrenal gland tumor Homo sap	6.2
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	6.1 6.1
	428242 423361	H55709 AW170055	Hs.2250 Hs.47628	leukemia inhibitory factor (cholinergic ESTs	6.1
75	417417	F05745	Hs.89512	ATPase, Ca transporting, plasma membrane	6.1
	447072	D61594	Hs.17279	tyrosytprotein suffotransferase 1	6.1
	415651	AJ207162 BE207573	Hs.3815 Hs.83321	stathmin-like-protein RB3 neuromedin B	6.0 6.0
	418030 429469	BE207573 M64590	HS.83321 Hs.27	glycine dehydrogenase (decarboxylating;	6.0
80	417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cONA A430	6.0
	429900	AA460421 AA180363	Hs.30875	ESTs 9 ESTs	6.0 6.0
	416439 439845	AA180363 AL355743	Hs.118769 Hs.56663	Homo sapiens EST from clone 41214, full	6.0
				074	

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	405005	4D022050	Hs.318584 r	lovel C3HC4 type Zinc finger (ring finge	6.0
	425905 439518	A8032959 W76326	9	b:zd60d04.r1 Soares_fetal_heart_NbHH19W	6.0
	426919	AL041228		LAV (embryonic lethal, abnormal vision,	6.0 5.9
5	440492	R39127		nypothetical protein DKFZp547J036 3-phosphofructo-2-kinase/fructose-2,6-bi	5.9
3	432328 444190	Al572739 Al878918		cysteine and glycine-rich protein 2	5.9
	425984	AW836277	Hs.165636	hypothetical protein DKFZp761C07121	5.9
	425977	R15138	Hs.165570	Homo sapiens clone 25052 mRNA sequence	5.9 5.9
10	449318	AW236021 AW301344	Hs.78531 Hs.122908	Homo sapiens, Similar to RIKEN cDNA 5730 DNA replication factor	5.9
10	457465 453362	H14988		ESTs	5.9
	453924	R49295	Hs.24886	ESTs	5.9
	414825	X06370		epidermal growth factor receptor (avian	5.8 5.8
15	433701	AW445023 Al335773		ESTs	5.8
13	412777 419723	AL120193	Hs.339810	longevity assurance (LAG1, S. cerevisiae	5.8
	438054	AA776626	Hs.169309	ESTS	5.8 5.8
	416427	BE244050	Hs.79307	Rac/Cdc42 guanine exchange factor (GEF)	5.8
20	400292 407748	AA250737 AL079409	Hs.72472 Hs.38176	BMP-R1B KIAA0606 protein; SCN Circadian Oscillat	5.8
20	453313	BE005771	Hs.153746	hypothetical protein FLJ22490	5.8
	430188	AL049242	Hs.234794	Homo sapiens mRNA; cDNA DKFZp564B083 (fr	5.8 5.8
	411252	AB018549	Hs.69328	MD-2 protein hypothetical protein FLJ14627	5.7
25	448986 440052	H42169 Al633744	Hs.347310 Hs.195648	ESTs, Weakly similar to 138022 hypotheti	5.7
23	419704	AA429104	Hs.45057	ESTs	5.7
	420077	AW512260	Hs.87767	ESTs	5.7 5.7
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	5.7 5.7
30	436511 424560	AA721252 AA158727	Hs.291502 Hs.150555	ESTs protein predicted by clone 23733	5.7
50	423346	A1267677	Hs.127416	synaptojanin 1	5.7
	439249	AF086060	Hs.170053	G-protein coupled receptor 88	5.7 5.7
	428588	F12101	Hs.185701	Homo sapiens mRNA full length insert cDN TASP for testis-specific adriamycin sens	5.7 5.7
35	450927 451752	AI807804 AB032997	Hs.134342 Hs.26966	KIAA1171 protein	5.7
55	458814	AI498957	Hs.170861	ESTs, Weakly similar to Z195_HUMAN ZINC	5.6
	416406	D86961	Hs.79299	lipoma HMGIC fusion partner-like 2	5.6 5.6
	448275	BE514434	Hs.20830	kinesin-like 2 KIAA0280 protein	5.6
40	413492 444600	D87470 R41398	Hs.75400 Hs.6996	ESTs	5.6
40	421988	AW450481	Hs.161333	ESTs	5.6
	443297	AI049864	Hs.133029	ESTs	5.6 5.5
	433244	AB040943	Hs.271285	KIAA1510 protein sin3-associated polypeptide, 30kD	5.5
45	458809 448499	AW972512 BE613280	Hs.20985 Hs.77550	hypothetical protein MGC1780	5.5
73	447458	AI741082	Hs. 158961	FSTs	5.5
	436643	AA757626	Hs.10941	ESTs, Weakly similar to IPP1_HUMAN PROTE	5.5 5.5
	407886	AW969688	Hs.100826	ESTs atrophin-1 interacting protein 1; activi	5.5
50	448944 418630	AB014605 Al351311	Hs.22599 Hs.251946	poly(A)-binding protein, cytoplasmic 1-l	5.5
50	415734	NM_014747		KIAA0237 gene product	5.5
	410099	AA081630		KIAA0036 gene product	5.5 5.5
	453128	AW026516	Hs.31791	acylphosphatase 2, muscle type hypothetical protein MGC5370	5.5
55	444670 420345	H58373 AW295230	Hs.332938 Hs.25231	ESTs	5.5
55	420092	AA814043	Hs.88045	ESTs	5.5
	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity la, re	5.4 5.4
	429876 419863	AB028977 AW952691	Hs.225974 Hs.93485	KIAA1054 protein Homo sapiens mRNA; cDNA DKFZp761D191 (fr	5.4
60	429149	AW193360	Hs.197962		5.4
•	415486	H12214	Hs.13284	ESTs. Weakly similar to 2109260A B cell	5.4
	429643		Hs.167279	FYVE-finger-containing Rab5 effector pro	5.4 5.4
	446657		Hs.260702 Hs.269060		5.4
65	439662 444165		Hs.10441	hypothetical protein FLJ11236	5.4
	439192			ESTs .	5.3
	448769		Hs.38173	ESTs	5.3 5.3
	410555		Hs.64311 Hs.21711	a disintegrin and metalloproteinase doma 2 hypothetical protein MGC10825	5.3
70	424922 423905				5.3
	429433		Hs.21358	5 ESTs, Wealtly similar to KIAA1353 protein	5.3
	427359	AW020782		Homo sapiens cDNA: FLJ23006 fis, clone L	5.3 5.3
	422544				5.3
75	420547 424624				5.2
, ,	441797		Hs.21463	5 ESTs	5.2
	428832	2 AA578229			5.2 5.2
	418079		Hs.6911 Hs.13226	ESTs Homo sapiens clone 25181 mRNA sequence	5.2
80	445740 416420			3 Homo sapiens cDNA FLJ14872 fis, clone PL	5.2
	43610	9 AA922153	Hs.13276	0 hypothetical protein MGC15729	5.2
	43364	7 AA603367			5.2 5.1
	45278	6 R61362	Hs.10664	2 ES1s, Weardy Silinias in 109032 hypotheti	J. .
				775	

	436443	AW138211	Hs.128746	ESTs	5.1
	408243	Y00787	Hs.624	Interleutin 8	5.1
	404819			NM_002688*:Homo sapiens peanut (Drosophi	5.1
5	424914	AA348410	Hs.119065	ESTs	5.1 5.1
)	453331 444656	A1240665 A1277924	Hs.145199	ESTs ESTs	5.1
	437387	Al198874	Hs.28847	AD026 protein	5.1
	421027	AA761198	Hs.55254	ESTs	5.1
10	410631	AA086469	Hs.47171	ESTS	5.1 5.1
10	454293	H49739 N49776	Hs.134013 Hs.170994	ESTs, Moderately similar to HK61_HUMAN H hypothetical protein MGC10945	5.1
	416220 419498	AL036591	Hs.20887	hypothetical protein FLJ 10392	5.1
	421040	AA715026	Hs.135280	ESTs	5.1
	415170	R44386	Hs.164578	ESTs	5.1
15	412590	AL134388	Hs.135033	ESTs, Weakly similar to 138022 hypotheti	5.1 5.0
	448985 433929	AA324885 Al375499	Hs.22777 Hs.27379	carbonic anhydrase XI ESTs	5.0 5.0
	409638	AW450420	Hs.21335	ESTs	5.0
	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	5.0
20	400533			ENSP00000209376*:PRED65 protein (Fragmen	5.0
	430130	AL137311 AA323968	Hs.234074 Hs.283631	Homo sapiens mRNA; cDNA DKFZp761G02121 (hypothetical protein DKFZp547G183	5.0 5.0
	437372 414737	AI160386	Hs.125087	ESTs	5.0
	422864	AA318323	Hs.12827	gb:EST20390 Retina II Homo sapiens cDNA	5.0
25	428878	AA436884	Hs.48926	ESTs	5.0
	428841	AJ418430	Hs.104935	ESTS	5.0 5.0
	428110 444170	AI312485 AW613879	Hs.138294 Hs.102408	ESTs, Moderately similar to Z195_HUMAN Z ESTs	4.9
	448765	R15337	Hs.21958	Homo sapiens mRNA; cDNA DKFZp547D086 (fr	4.9
30	452106	AI141031	Hs.21342	ESTs	4.9
	417404	NM_007350	Hs.82101	pteckstrin homology-like domain, family	4.9
	414300	A1304870	Hs.188680	ESTs	4.9 4.9
	429399 439726	AA452244 AW449893	Hs.16727 Hs.293707	ESTs ESTs, Weakly similar to 138598 zinc fing	4.9
35	428873	AI701609	Hs.98908	ESTs	4.9
•	451516	AI800515	Hs.12024	ESTs	4.9
	407792	AI077715	Hs.39384	putative secreted ligand homologous to f	4,9 4,9
	416836 447247	D54745 AW369351	Hs.80247 Hs.287955	cholecystokinin Horno sapiens cDNA FLJ13090 fis, clone NT	4.9
40	436805	AA731533	Hs.270751	ESTs	4.9
	423175	W27595	Hs.347310	hypothetical protein FLJ14627	4.9
	415402 422263	AA164687 AA307639	Hs.177576 Hs.129908	mannosyl (alpha-1,3-)-glycoprotein beta- KIAA0591 protein	4.9 4.8
	443715	AI583187	Hs.9700	cyclin E1	4.8
45	413248	T64858	Hs.21433	hypothetical protein DKFZp547J036	4.8
	434811	AW971205	Hs.114280	ESTs	4.8 4.8
	441287 428862	AW293132 NM_000346	Hs.131373 Hs.2316	ESTs SRY (sex determining region Y)-box 9 (ca	4.8
	413834	BE296896	Hs.224179	ESTs, Weakly similar to I38022 hypotheti	4.8
50	443740	R56434	Hs.21062	ESTs	4.8
	416871	H98716	11- 120075	gb:yx13d08.s1 Soares melanocyte 2NbHM Ho	4.8 4.8
	441916 413530	AA993571 AA130158	Hs.129075 Hs.19977	ESTs ESTs, Moderately similar to ALUB_HUMAN A	4.8
	424240	AB023185	Hs.143535	calcium/calmodulin-dependent protein kin	4.8
55	414998	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin	4.8
	448425	A1500359	Hs.346112 Hs.310359		4.8 4.8
	423600 424687	AI633559 J05070	Hs.151738		4.8
	423869	BE409301	Hs.134012	C1g-related factor	4.8
60	425402	AI215881	Hs.24970	ESTs, Weakly similar to B34323 GTP-bindi	4,7
	422809	AK001379	Hs.121028		4.7 4.7
	407808 428748	AA663559 AW593206	Hs.279789 Hs.98785	histone deacetylase 3 Ksp37 protein	4.7
	434859	BE255080	Hs.299315		4.7
65	431820	AW410408	Hs.271167		4.7
	409100	H98216	Hs.42245	ESTs, Moderately similar to 138022 hypot	4.7 4.7
	420133 420297	AA426117 AI628272	Hs.155543 Hs.88323	ESTs ESTs, Weakly similar to ALU1_HUMAN ALU S	4.7
	443462	AI064690	Hs.171176		4.7
70	424481	R19453	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	4.7
	431454	AW975980	Hs.292918		4.7 4.7
	432682 434933	Al376400 R91095	Hs.159588 Hs.4276	ESTs KIAA1701 protein	4.7
	421247	BE391727	Hs.102910		4.7
75	435538	AB011540	Hs.4930	low density lipoprotein receptor-related	4.7
	441703	AW390054	Hs.192843		4.7 4.7
	418661 412266	NM_001949 N59006	Hs.1189 Hs.26133	E2F transcription factor 3 ESTs	4.7 4.7
	417675	A1808607	Hs.3781	similar to murine leucine-rich repeat pr	4.6
80	422564	A1148006	Hs.222120	ESTs .	4.6
	427250	R35941 R88483	Hs.25418 Hs.172862	ESTs PESTs	4.6 4.6
	427695 434269	AK001991	Hs.3781	similar to murine leucine-rich repeat pr	4.6
			'	•	

	407603	AW955705	Hs.62604 H	lomo sapiens, clone IMAGE:4299322, mRNA,	4.6 4.6
	427687		Hs.1570 h	istamine receptor H1	4.6
	427194			ESTs cholinergic receptor, muscarinic 3	4.6
5	440286 427099		Hs.173560 (odd Oz/ten-m hornolog 2 (Drosophila, mous	4.6
_	458760	AI498631	Hs.111334 1	erritin, light polypeptide	4.6 4.6
	433675	AW977653		ibonucleotide reductase M2 polypeptide	4.6
	429170 427712	NM_001394 Al368024	He 283696	dual specificity phosphatase 4 ESTs	4.6
10	437834	AA769294	Hs.283854	gb:nz36g03.s1 NCI_CGAP_GCB1 Homo sapiens	4.6
	408947	AL080093	Hs.49117	Homo sapians mRNA; cDNA DKFZp564N1662 (f	4.6 4.6
	424458	M29273		myelin associated glycoprotein Homo sapiens cDNA FLJ10784 fis, clone NT	4.6
	450568 424635	AL050078 AA420687	Hs.25159 Hs.115455	Homo sapiens cDNA FLJ14259 fis, clone PL	4.6
15	440491	R35252	Hs.130558	ESTs, Wealty similar to 2109260A B cell	4.6
	428409	AW117207	Hs.98523	ESTs	4.5 4.5
	423476	AL035633	Hs.110165	Hurnan DNA sequence from clone RP5-1046G1 ribosomal protein L26 homolog	4.5
	421977 440105	W94197 AA694010	Hs.6932	Homo sapiens clone 23809 mRNA sequence	4.5
20	422411	AW749443	Hs.22511	ESTs	4.5
	443361	AI792628	Hs.133273	ESTs	4.5 4.5
	453857	AL080235	Hs.35861	DKFZP586E1621 protein gb:::n67b05.x1 NCI_CGAP_CML1 Homo saplens	4.5
	408432 444127	AW195262 N63620	Hs.13281	ESTs	4.5
25	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	4.5 4.5
	422661	NM_014700	Hs.119004	KIAA0665 gene product	4.5
	440684	AI253123	Hs.127356 Hs.272072	ESTs, Highty similar to S21424 nestin [H ESTs, Weakly similar to 138022 hypotheti	4.5
	407385 425256	AA610150 BE297611	Hs.155392	collapsin response mediator protein 1	4.5
30	441364	AW450466	Hs.126830	ESTs, Weakly similar to YD38_YEAST HYPOT	4.5 4.5
	430471	AF064845	Hs.241523	hypothetical protein FLJ10142	4.5
	412043	BE156622 AA380153	Hs.333371	Horno sapiens clone TA40 untranslated mRN gb:EST93093 Skin turnor I Horno sapiens cD	4.5
	426503 418771	AA807881	Hs.25329	ESTs	4.4
35	414706	AW340125	Hs.76989	KIAA0097 gene product	4.4 4.4
	424800	AL035588	Hs.153203	MyoD family inhibitor	4.4
	441217	AI922183 AA325138	Hs.213246 Hs.235873	ESTs hypothetical protein FLJ22672	4.4
	422421 446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	4.4
40	444153	AK001610	Hs.10414	hypothetical protein FLJ10748	4.4 4.4
	435542	AA687376		ESTs	4.4
	443912	R37257	Hs.184780 Hs.77631	ESTs glycine cleavage system protein H (amino	4.4
	414922 432527	D00723 AW975028	Hs.102754	ESTs	4.4
45	410082	AA081594	Hs.158311	Musashi (Drosophila) homolog 1	4.4 4.4
	446936	H10207	Hs.47314	ESTs	4.4 4.4
	425212	AW962253 NM_001196	Hs.171618 Hs.315689	ESTs Homo sapiens cDNA: FLJ22373 fis, clone H	4.4
	426925 427221	L15409	Hs.174007	von Hippel-Lindau syndrome	4.4
50	439274	AF086092	Hs.48372	ESTs	4.4 4.4
	412799	AI267606		gb:aq91h03.x1 Stanley Frontal SB pool 1 gb:Homo sapiens envelope protein RiC-3 (4.4
	430676	AF084866		C7001664:gi]12698061]dbj[BAB21849.1] (AB	4.4
	405348 419412	AW161058	Hs.90297	synuclein, beta	4.3
55	447397	BE247676	Hs.18442	E-1 enzyme	4.3 4.3
	409125		Hs.343567 Hs.159142		4.3
	433323 450530			cytochrome P450, subfamily 46 (cholester	4.3
	428227	T	Hs.2248	small inducible cytokine subfamily B (Cy	4.3
60	408622	AA056060	Hs.202577		4.3 4.3
	433610		Hs.112547 Hs.29808	ESTs Homo sapiens cDNA: FLJ21122 fis, clone C	4.3
	429281 451320			diacylglycerol kinase, zeta (104kD)	4.3
	430979		Hs.129010		4.3
65	452092	BE245374	Hs.27842		4.3 4.3
	438456		Hs.20594	ESTs regulator of G-protein signalling 6	4.3
	433236 445133				4.3
	412125		Hs.73393	eyes absent (Drosophila) homolog 4	4.2
70	432882	2 NM_01325			4.2 4.2
	40784				4.2
	417918 42448		Hs.16375 Hs.27447		4.2
	45368		10.21 441	gb:yd71e08.r1 Soares fetal liver spleen	4.2
75	44556	8 H00918	Hs.26874		4.2 4.2
	44852	6 AB028946			4.2
	42645		7 Hs.16996 Hs.78854		4.2
	41579 43887				4.2
80	42800	1 H97428	Hs.21990)7 ESTs, Moderately similar to Transforming	4.2 4.2
	41036	1 BE391804			4.2 4.2
	44592		1 Hs.14614 Hs.2744		4.2
	41219	M MIDIOU	10.41	y,v	

	445666	R59960	Hs.282386	ESTs	4.2
	439538	AA837323	Hs.56407	ESTs	4.2
	437814	AX088192 AX001853	Hs.135474 Hs.61508	ESTs, Weakly similar to DDX9_HUMAN ATP-D Homo sapiens cDNA FLJ10991 fis, clone PL	4.2 4.2
5	410264 409091	AW970386	Hs.269423	ESTs	4.2
•	459527	AW977556	Hs.291735	ESTs, Wealthy similar to 178885 serine/th	4.2
	426271	AF026547	Hs.169047	chondroitin sulfate proteoglycan 3 (neur	4.2
	432731	R31178	Hs.287820	Shronectin 1 ESTs	4.2 4.2
10	423135 446131	N67655 NM_000929	Hs.26411 Hs.290	phospholipase A2, group V	4.2
10	424736	AF230877	Hs.152701	microtubule-interacting protein that ass	4.2
	408298	AI745325	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	4.2
	452234	AW084176	Hs.223295	ESTs, Wealdy similar to 138022 hypotheti	4.2
15	451468	AW503398 AL031658	Hs.293663	ESTs, Moderately similar to I38022 hypot Human DNA sequence from clone RP1-310013	4.2 4.2
13	429421 422374	AW732869	Hs.1519	protein kinase, cAMP-dependent, regulato	4.1
	402145	AIIII	10.1515	Target Exon	4.1
	440483	AI200836	Hs.150386	ESTs	4.1
20	425018	BE245277	Hs.154196	E4F transcription factor 1	4.1 4.1
20	448048 445868	BE281291 BE169357	Hs.170408 Hs.207428	ESTs, Moderately similar to A47582 B-cel ESTs	4.1
	431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	4.1
	435575	AF213457	Hs.44234	triggering receptor expressed on myeloid	4.1
25	424726	AK001007	Hs.138760	Homo sepiens cDNA FLJ10145 ffs, clone HE	4.1
25	450325	AJ935962	Hs.26289 Hs.277174	ESTs ESTs	4,1 4,1
	450639 445102	AI703186 AW204610	Hs.22270	ESTS	4.1
	416547	H62914	Hs.268946	ESTs, Weakly similar to PC4259 ferritin	4.1
	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	4.1
30	408296	AL117452	Hs.44155	DKFZP586G1517 protein	4.1 4.1
	439519 442326	AA837118 H92962	Hs.118366 Hs.124813	ESTs hypothetical protein MGC14817	4.1
	404150	1152502	113.124013	Target Exon	4.1
	420805	L10333	Hs.99947	reticulon 1	4.1
35	429125	AA446854	Hs.271004	ESTs, Wealthy similar to 138022 hypotheti	4.1 4.1
	427302	AA400540 AW271626	Hs.135282 Hs.42294	Horno sapiens cDNA FLJ11554 fis, ctone HE ESTs	4.1
	444534 437414	AW894071	Hs.48448	hypothetical protein DKFZp547C176	4.1
	418512	AW498974		diacytglycerol kinase, zeta (104kD)	4.1
40	414217	Al309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fls, clone L	4.1
	449328	A1962493	Hs.345303	ESTs	4.1 4.1
	432683 435312	AW995441 AJ243396	Hs.10475 Hs.4865	ESTs voltage-gated sodium channel beta-3 subu	4.1
	429163	AA884766	113.4003	gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	4.1
45	453096	AW294631	Hs.11325	ESTs	4.1
	414683	\$78296	Hs.76888	hypothetical protein MGC12702	4.0 4.0
	433523 422170	H29882 Al791949	Hs.112432	ESTs anti-Multerian hormone	4.0
	424120	T80579	Hs.290270		4.0
50	448548	R13209	Hs.21413	solute carrier family 12, (potassium-chl	4.0
	433009	AA761668	LL 224020	gb:nz24c08.s1 NCI_CGAP_GC81 Homo sapiens 1-acytglycerol-3-phosphate O-acytransfe	4.0 4.0
	434834 439099	AF156774 AB037800	Hs.324020 Hs.6462	protein kinase C and casein kinase subst	4.0
	444001	AI095087	Hs.152299		4.0
55	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	4.0
	423279	AW959861	Hs.290943		4.0 4.0
	457211 450581	AW972565 AF081513	Hs.32399 Hs.25195	ESTs, Wealdy similar to SS1797 vasodilat TGF-beta 4	4.0
	435854	AJ278120	Hs.4996	putative ankyrin-repeat containing prote	4.0
60	433615	AA732982	Hs.269607	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.0
	424001	W67883	Hs.137476		4.0 4.0
	432058 423713	AW665996 AW754182	Hs.130729	ESTs, Wealdy similar to ALU1_HUMAN ALU S gb:RC2-CT0321-131199-011-c01 CT0321 Homo	4.0
	419629	AB020695	Hs.91662	KIAA0888 protein	4.0
65	439108	AW163034	Hs.6467	synaptogyrin 3	4.0
	440866	AI703103	Hs.271360		4.0
	422887	AI751848	Hs.49215	ESTs NM_024560:Homo sapiens hypothetical prot	4.0 4.0
	405331 457005	AJ007421	Hs.172597		4.0
70	437948	AA772920	Hs.303527		4.0
	440471	AA886146	Hs.307944		4.0
	432149	AW614326			4.0 4.0
	449655 448299	AI021987 AA497044	Hs.59970 Hs.20887	ESTs hypothetical protein FLJ10392	4.0
75	435743		Hs.12962	ESTs	4.0
	412659	AW753865	Hs.74376	offactomedin related ER localized protei	4.0
	430694		Hs.30936	ESTs, Weakly similar to H2BH_HUMAN HISTO	3.9 3.9
	437807 440085	AI017875 BE270761	Hs.136829 Hs.23158	ESTs ESTs	3.9
80	449722		Hs.23960	cyclin B1	3.9
	445523	Z30118	Hs.293788		3.9
	420948		Hs.100469		3.9 3.9
	407198	H91679		gb:yv04a07.s1 Soares fetal liver spleen	5.5

			U- 220000 F		3.9
	447519 429038			ESTs eizure related gene 6 (mouse)-like	3.9
	414761		Hs.77256 e	enhancer of zeste (Drosophila) homolog 2	3.9
_	404584		1	Farget Exon	3.9 3.9
5	449670	F07693 W88559	Hs.85603 I	Horno sapiens mRNA; cDNA DKFZp434K2172 (f proteolipid protein 1 (Pelizaeus-Merzbac	3.9
	414117 433290	R20077	Hs.302185	Homo sapiens clone 23618 mRNA sequence	3.9
	441707	R42637	Hs.21963	hypothetical protein DKFZp761B0514	3.9
10	431789	H19500		mitogen-activated protein kinase 4	3.9 3.9
10	434149 446896	Z43829 T15767		hypothetical protein MGC5469 Homo sapiens mRNA for KIAA1737 protein,	3.9
	411555	AF113537		HMP19 protein	3.9
	426646	AA382787		ESTs	3.9 3.9
15	450297	AW901347		hypothetical protein FLJ23342 ESTs	3.9
13	429228 451433	AI553633 AA021140		ESTs, Weakly similar to A46010 X-linked	3.9
	447937	AL109716	Hs.20034	Homo sapiens mRNA full length insert cDN	3.9
	436734	Al937612		hypothetical protein FLJ23112	3.9 3.9
20	417576	AA339449		phosphoribosylglycinamide formyltransfer glycoprotein M6B	3.9
20	417632 414245	R20855 BE148072	Hs.75850	WAS protein family, member 1	3.9
	418203	X54942	Hs.83758	CDC28 protein kinase 2	3.9
	453438	AJ469935	Hs.22792	ESTs	3.9 3.8
25	408449 411048	NM_004408 AK001742	Hs.166161 Hs.67991	dynamin 1 hypothetical protein DKFZp434G0522	3.8
23	405819	A1001142	110.01001	NM_002578:Homo sapiens p21 (CDKN1A)-acti	3.8
	445255	NM_014841	Hs.12477	synaptosomal-associated protein, 91 kDa	3.8 3.8
	432715	AA247152	Hs.200483 Hs.281462	ESTs, Weakly similar to KIAA1074 protein hypothetical protein FLJ14251	3.8
30	457292 432593	AJ921270 AW301003	Hs.51483	ESTs, Weakly similar to hypothetical pro	3.8
20	413589	AW452631	Hs.313803	ESTs, Highly similar to AF157833 1 noncl	3.8
	426847	S78723	Hs.298623	5-hydroxytryptamine (serotonin) receptor	3.8 3.8
	410768	AF038185 AW965339	Hs.66187 Hs.111471	Homo sapiens clone 23700 mRNA sequence ESTs	3.8
35	417791 454120	A8032990	Hs.40719	hypothetical protein KIAA1164	3.8
20	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	3.8
	449145	AI632122	Hs.198408	ESTs	3.8 3.8
	446997	AA383439 AA565832	Hs.16758 Hs.271649	Spir-1 protein gb:nj32b03.s1 NCI_CGAP_AA1 Homo sapiens	3.8
40	407304 437269	AA334384	Hs.149420	ESTs	3.8
	443539	AI076182	Hs.134074	ESTs, Moderately similar to ALU6_HUMAN A	3,8 3.8
	426855	AL117427	Hs.172778	Homo sapiens mRNA; cDNA DKFZp566P013 (fr	3.6 3.8
	418821 408875	AA436002 NM_015434	Hs.183161 Hs.48604	ESTs DKFZP434B168 protein	3.8
45	422175	N79885	Hs.6382	ESTs, Highly similar to T00391 hypotheti	3.8
	432488	AA551010	Hs.216640	ESTs	3.8 3.8
	450582	AJ339732	Hs.149990	G-rich RNA sequence binding factor 1 ESTs	3.8
	426380 451407	AI291267 AA131376	Hs.343809	fibroblast growth factor 128	3.8
50	451778	AJ826131	Hs.62954	ESTs, Wealdy similar to zinc finger prot	3.8
	425652	AB021742	Hs.322431	neurogenic differentiation 2 gb:CM3-BN0075-240200-101-d11 BN0075 Homo	3.8 3.8
	412820 412193	BE001236 AI684467	Hs.144057	gs:CM3-BN0073-240200-101-011 BN0073-10110	3.8
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	3.8
55	433042	AW193534	Hs.281895	Homo sapiens cDNA FLJ11660 fis, clone HE	3.8 3.8
	437756	AA767537 AA923729	Hs.197096 Hs.26322	ESTs cell cycle related kinase	3.8
	451367 425390	AI092634	Hs.156114		3.8
	445292	AV653264	Hs.13982	Homo sapiens cDNA FLJ14666 fis, clone NT	3.8
60	425843	BE313280	Hs.159627	death associated protein 3 ESTs, Moderately similar to ALU5_HUMAN A	3.8 3.7
	443301 440210	AI733614 AW674562	Hs.220587 Hs.125296	ESTs Moderately similar to ALOS_HOWARD A	3.7
	430287		Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	3.7
	437252	AI433833	Hs.164159		3.7 3.7
65	409327		Hs.53563 Hs.195614	cottagen, type IX, alpha 3 splicing factor 3b, subunit 3, 130kD	3.7
	429084 457183		Hs.118569	and a common of the common of	3.7
	403696			C4001100":gi 5852342 gb AAD54015.1 (AF0	3.7
70	408670		Hs.46784	potassium large conductance calcium-acti	3.7 3.7
70	416677 422253		Hs.334840 Hs.118329		3.7
	450154		Hs.281587	Human (clone CTG-A4) mRNA sequence	3.7
	408453	AI369838	Hs.45127	chondroitin sulfate proteoglycan 5 (neur	3.7 3.7
75	440553		Hs.34404	Homo sapiens cDNA FLJ14459 fis, clone HE visinin-like 1	3.7 3.7
13	428538 426413		Hs.2288	gb:EST90805 Synovial sarcoma Horno sapien	3.7
	40917		Hs.12259	3 ESTs	3.7
	44162	7 AA947552			3.7 3.7
80	41821				3.7
30	40879 43744			9 Homo sapiens mRNA; cDNA DKFZp762G113 (fr	3.7
	43603	5 AA703679	Hs.10699	9 ESTs, Weakly similar to SYT5_HUMAN SYNAP	3.7
	45169	7 AW44977	4 Hs.29638	0 POM (POM121 rat homolog) and ZP3 fusion	3.7

	420001	AW375974	Un 156704	FOY-	3.7
	436961 409953	AN373974 AA332277	Hs.156704 Hs.57691	ESTs cadherin 18, type 2	3.7
	435832	AA425688	Hs.41641	Bruno (Drosophita) -like 4, RNA binding	3.7
	424343	AW956360	Hs.4748	adenytate cyclase activating polypeptide	3.6
5	437470	AL390147	Hs.134742	hypothetical protein DKFZpS47D065	3.6
•	440168	AA868507	Hs.126141	ESTs	3.6
	427624	AA406245	Hs.24895	·ESTs	3.6
	418293	AI224483	Hs.16063	hypothetical protein FLJ21877	3.6
10	445888	AF070564	Hs.13415	Homo sapiens clone 24571 mRNA sequence	3.6
10	458912	AI911066		ESTs	3.6
	419390	A1701162	Hs.90207	hypothetical protein MGC11138	3.6
	449256 425010	AA059050 T16837	Hs.59847 Hs.4241	ESTs ESTs	3.6 3.6
	412754	AW160375	Hs.74565	amyloid beta (A4) precursor-like protein	3.6
15	400777		10.1700	NM_007325*:Homo sapiens glutamate recept	3.6
	438831	BE263273	Hs.6439	synapsin II	3.6
	419235	AW470411	Hs.288433	neurotrimin	3.6
	424947	R77952		ESTs, Wealthy similar to alternatively sp	3.6
~~	407624	AW157431	Hs.248941	ESTs	3.6
20	440351	AF030933	Hs.7179	RAD1 (S. pombe) homolog	3.6
	440404	AI015881	Hs.324527	mitochondrial ribosomal protein S5	3.6
	439267	AA287747	Hs.173012	ESTs, Weakly similar to A46010 X-linked	3.6
	424340 423178	AA339036 AI033140	Hs.7033 Hs.124983	ESTs Homo sapiens mRNA; cDNA DKFZp564C142 (fr	3.6 3.6
25	418064	BE387287	Hs.83384	S100 calcium-binding protein, beta (neur	3.6
23	428483	AI908539	Hs.184592	KIAA0344 gene product	3.6
	453875	AW001783	Hs.232711	ESTs	3.6
	430183	BE010038		gb:PM3-BN0176-100400-001-g04 BN0176 Homo	3.6
	431552	AI815863	Hs.259873	axonal transport of synaptic vesicles	3.6
30	424278	AK000723	Hs.144517	hypothetical protein FLJ20716	3.6
	434131	AI858275	Hs.143659	ESTs	3.6
	435923	BE301930	Hs.5010	Homo sapiens clone 24672 mRNA sequence	3.6
	415709	AA649850	Hs.278558	ESTs	3.6
25	437640	AA764893	Hs.272155	ESTs, Weakly similar to 138022 hypotheti	3.6
35	419586	AI088485	Hs.144759	ESTs, Weakly similar to 138022 hypotheti	3.6 3.6
	414040 427315	N58513 AA179949	Hs.32171 Hs.175563	ESTs Homo sapiens mRNA; cDNA DXFZp564N0763 (f	3.6
	410711	AB002318	Hs.65746	KIAA0318 protein	3.6
	445953	AI612775	Hs.145710	ESTs	3.6
40	444794	AJ419991	Hs.145225	ESTs	3.6
	411968	AI207410	Hs.69280	Homo sapiens, clone IMAGE:3636299, mRNA,	3.6
	428180	AJ129767	Hs.182874	guanine nucleotide binding protein (G pr	3.6
	415283	R40504	Hs.21245	ESTs	3.6
4.5	433160	AW207002	Hs.134342	TASP for testis-specific adriamycin sens	3.5
45	410386	W26187	Hs.3327	Homo sapiens cDNA: FLJ22219 fis, clone H	3.5
	430818	Al311928	Hs.348156	gb:qo89h04.x1 NCI_CGAP_Kid5 Homo sapiens	3.5
	433932	AW954599	Hs.169330	neuronal protein	3.5 3.5
	420578 456723	AA813546 Z43902	Hs.99034 Hs.4748	GTP-binding protein Rho7	3.5
50	416340	N31772	Hs.79226	adenylate cyclase activating polypeptide fasciculation and elongation protein zet	3.5
50	451455	AI937227	Hs.8821	hepcidin antimicrobial peptide	3.5
	412719	AW016610	Hs.816	ESTs	3.5
	435910	AI084152	Hs.21782	ESTs, Weakly similar to ALU7_HUMAN ALU S	3.5
	439340	AB032436	Hs.6535	brain-specific Na-dependent inorganic ph	3.5
55	458072	AI890347	Hs.271923	Horno sapiens cDNA: FLJ22785 fis, clone K	3.5
	439710	AF086543		gb:Homo sapiens full length insert cDNA	3.5
	453896	AW293483	Hs.255205	KIAA1853 protein	3.5
	407253	AA411175	Hs.141939	ESTs, Moderately similar to \$65657 alpha	3.5 3.5
60	449969 439231	AW295142 AW581935	Hs.180187 Hs.141480	Homo sapiens cDNA FLJ14337 fis, clone PL Homo sapiens mRNA; cDNA DKFZp434N079 (fr	3.5 3.5
v	424332	AA338919	Hs.101615	ESTs	3.5
	456497	AW967956	Hs.123648	ESTs, Weakly similar to AF108460 1 ubinu	3.5
	442264	AI278777	Hs.263455	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.5
	404295			Target Exon	3.5
65	427209	H06509	Hs.92423	KIAA1566 protein	3.5
	439627	BE621702	Hs.29076	hypothetical protein FLJ21841	3.5
	427513	AI476318	Hs.192480	ESTs	3.5
	458435	AI418718	Hs.144121	ESTs, Weakly similar to T46916 hypotheti	3.5
70	435545	AA687415	Hs.28107	ESTS	3.5
70	413199	M82843	Hs.75236	ELAV (embryonic lethal, abnormal vision,	3.5 3.5
	441607 452449	NM_005010 AW068658	Hs.7912 Hs.20943	neuronal cell adhesion molecule ESTs	3.5
	443257	A1334040	Hs.11614	HSPC065 protein	3.5
	423641	AL137256	Hs.130489	ATPase, aminophospholipid transporter-li	3.5
75	427581	NM_014788	Hs.179703		3.5
	424090	X99699	Hs.139262		3.5
	422906	U80773	Hs. 121580	Human EST clone 42944 mariner transposon	3.5
	429698	A1685086	Hs.26339	ESTs, Weakly similar to S21348 probable	3.5
οΛ	439920	H05430	Hs.288433		3.5
80	436899	AA764852	Hs.291567		3.5
	414178	AW957372	Hs.46791	ESTs, Weakly similar to 138022 hypotheti ESTs	3.5 3.4
	418365 414598	AW014345 Al094221	Hs.161690 Hs.135150		3.4
	414030	~~~~~	19.133130	and the comment and an and the	4.4

					3.4
	452571		Hs.34665 (ESTs similar to pregnancy-associated plasma p	3.4
	443633 408955			Target CAT	3.4
	443206		Hs.9075	serine/threonine kinase 17a (apoptosis-i	3.4
5	419617	AL008583	He 91622	neumo al nentrazio (BCEDIDI	3.4
	454171	AW854832		gb:QV2-CT0261-201099-011-f05 CT0261 Homo	3.4 3.4
	426529	AF090100		Homo sapiens clone IMAGE 23915	3.4
	440652	AI216751		ESTs ESTs	3.4
10	450813 429323	A1739625 NM_001649		apical protein, Xenopus laevis-like	3.4
10	439774	AL360257	Hs 213493	Homo sapiens mRNA full length insert cDN	3.4
	409892	AW956113	Hs.7149	gb:EST368183 MAGE resequences, MAGD Horno	3.4
	439963	AW247529		platelet-activating factor acetylhydrola	3.4
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	3.4 3.4
15	453740	AL120295	Hs.311809	ESTs, Moderately similar to PC4259 femi cytokine-like protein C17	3.4
	435256 453305	AF193766	Hs.13872 Hs.267997	EHM2 gene	3.4
	425287	R39224 R88249	Hs.155524	peanut (Drosophila)-like 2	3.4
	417663	R07483	Hs.180461	ESTs	3.4
20	448533	AL119710	Hs.21365	nucleosome assembly protein 1-like 3	3.4
	441834	AL138034	Hs.7979	KIAA0736 gene product	3.4 3.4
	457876	A1821940		ESTs, Moderately similar to ALUS_HUMAN A	3.4
	407842	BE410100	Hs.40368 Hs.1570	adaptor-related protein complex 1, sigma histarnine receptor H1	3.4
25	422676 408926	D28481 AF217525	Hs.49002	Down syndrome cell adhesion molecule	3.4
23	430762	A1343652	Hs.105667	ESTs	3.4
	430890	X54232	Hs.2699	glypican 1	3.4
	445078	A1869975	Hs.4775	junctophilin 3	3.4
	423257	AW161039	Hs.125878	synapsin III	3.4 3.4
30	417402	BE503227	Hs.134759	ESTS	3.4
	410011	AB020641	Hs.57856	PFTAIRE protein kinase 1 NM_030795:Homo sapiens stathmin-like 4 (3.4
	404541 436291	BE568452	Hs.344037	protein regulator of cytokinesis 1	3.4
	443672	AA323362	Hs.9667	butyrobetaine (gamma), 2-oxoglutarate di	3.4
35	432140	AK000404	Hs.272688	hypothetical protein FLJ20397	3.4
	451061	AW291487	Hs.213659	ESTs, Weakly similar to KIAA1357 protein	3.4 3.4
	425782	U66468	Hs.159525	cell growth regulatory with EF-hand doma gb:EST388454 MAGE resequences, MAGN Homo	3.4
	420692	AW976345	Un 76064	transitional epithelia response protein	3.4
40	410507	AA355288 AA665089	Hs.76064	gb:nu76d01.s1 NCI_CGAP_Alv1 Homo sapiens	3.4
40	412436 448112	AW245919	Hs.34969	hypothetical protein OKFZp566N034	3.4
	429269	AA449013	Hs.99203	ESTs	3.4
	408037	AW271720	Hs.42233	hypothetical protein FLJ 10300	3.3
	418858	AW961605	Hs.21145	hypothetical protein RG083M05.2	3.3 3.3
45	420050	AL118615	Hs.94653	neurochondrin	3.3
	436277	R88520	Hs.120917	ESTs ESTs	3.3
	430412 408554	AW341754 AA836381	Hs.189305 Hs.315111	nuclear receptor co-repressor/HDAC3 comp	3.3
	432663	A1984317	Hs.122589	ESTs	3.3
50	449919	AI674685	Hs.200141	ESTs	3.3
	438509	R45367	Hs.101191	ESTs	3.3
	429037	X81895	Hs.194765	H.sapiens GENX-5624 mRNA, 3' UTR	3.3 3.3
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6 KIAA0444 protein	3.3
55	425537 408369	AB007913 R38438	Hs.158291 Hs.182575		3.3
,,,	449686	AW072813	Hs.270868		3.3
	417333	AL157545	Hs.173179		3.3
	410592	R94088	Hs.43569	ESTs	3.3
	439444	A1277652	Hs.54578	ESTs, Wealdy similar to 138022 hypotheti	3.3 3.3
60	435375	A1733610	Hs.187832	ESTS PARTIE PAS PROPERTY	3.3
	409746	NM_004794		RAB33A, member RAS oncogene family ESTs	3.3
	425588 412155	F07396 R38167	Hs.46627 Hs.12449	Homo sapiens transmembrane protein HTMP1	3.3
	425242	D13635	Hs.155287		3.3
65	417280				3.3
	423748		Hs.30211	hypothetical protein FLJ22313	3.3
	452856		Hs.30881	protein tyrosine phosphalase, receptor I	3.3 3.3
	419103		Hs.96423		3.3
70	435718		Hs.26953 Hs.19311		3.3
70	449249 423770				3.3
	409557			3 ESTs	3.3
	439285			hypothetical protein FLJ20093	3.3
	421183	AL135740	Hs.10244		3.3
75	433894	AI907682	Hs.24329		3.3 3.3
	445225		Hs.20239		3.3
	411379		Hs.12554 Hs.12845		3.3
	436207 436870				3.3
80	441791				3.3
	408547			ESTs	3.3
	42098	2 AW576160			3.3 3.3
	45162	5 R56793	Hs.10657	6 alanine-glyoxylate aminotransferase 2-li	3.3

	44.0000		11. 00.00	n to A come & D and basis Instincts	3.3
	418932 453496	L34059 AA442103	Hs.89484 Hs.33084	cacherin 4, type 1, R-cacherin (retinal) sotute carrier family 2 (facilitated glu	3.3
	423169	BE047009	Hs.21837	ESTs, Weakly similar to KIAA0927 protein	3.3
_	418049	AA211467	Hs.190488	Homo sapiens, Similar to nuclear localiz	3.3
5	441243	AI767056	Hs.193002	ESTs	3.3
	444427	H25094	Hs.293663	ESTs, Moderately similar to I38022 hypot	3.3 3.3
	449115 446416	AW959952 AV658299	Hs.37528 Hs.163959	ESTs, Weakly similar to AF090944 1 PRO06 ESTs	3.3
	437762	T78028	Hs.154679	synaptotagmin I	3.3
10	450336	AA046B14	Hs.288928	Homo sapiens cONA: FLJ23296 fis, clone H	3.3
	433842	AI652156	Hs.26346	ESTs	3.3
	444124	R43097	Hs.6818	ESTs Homo sapiens mRNA; cDNA DXFZp434B0650 (f	3.3 3.3
	423858 454792	AL137326 AW820794	Hs.133483 Hs.252406	hypothetical protein FLJ12296 similar to	3.3
15	412775	AA709046	Hs.27552	Homo sapiens mRNA; cONA DKFZp586N2424 (f	3.3
	429609	AF002246	Hs.210863	cell adhesion molecute with homology to	3.2
	413951	AW051200	Hs.75640	natriuretic peptide precursor A	3.2
	433325	AW206986	Hs.143905	ESTs atoha2,8-siatyttransferase	3.2 3.2
20	449092 422390	U91641 AW450893	Hs.22985 Hs.121830	ESTs, Wealdy similar to T42682 hypotheti	3.2
20	424899	AL119387	Hs.119062	ESTs	3.2
	454253	AV660717	Hs.47144	DKFZP586N0819 protein	3.2
	410126	BE169274		KIAA0036 gene product	3.2
25	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	3.2 3.2
23	405303 420871	AA702972	Hs.65300	Target Exon ESTs	3.2
	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	3.2
	425769	U72513	Hs.159486	Human RPL13-2 pseudogene mRNA, complete	3.2
20	442320	AI287817	Hs.129636	ESTs	3.2 3.2
30	407378	AA299264	Hs.57776 Hs.22744	ESTs, Moderately similar to 138022 hypot hypothetical protein MGC13105	3.2
	439764 410425	T26535 BE278367	Hs.63510	KIAA0141 gene product	3.2
	422156	N34524	110.00010	gb:yy56d10.s1 Soares_multiple_sclerosis_	3.2
~~	451489	NM_005503	Hs.26468	armyloid beta (A4) precursor protein-bind	3.2
35	457358	AI479755	Hs.129010	ESTs	3.2 3.2
	407721	Y12735 AI885742	Hs.38018 Hs.228474	dual-specificity tyrosine-(Y)-phosphoryl ESTs	3.2
	452372 459660	M79082	113.220474	ESTs	3.2
	437085	AA743935	Hs.202329	ESTs	3.2
40	419852	AW503756	Hs.286184	hypothetical protein dJ551D2.5	3.2
	440080	AW051597	Hs.143707	ESTs	3.2 3.2
	449714 450407	AB033015 NM_000810	Hs.23941 Hs.24969	KIAA1189 protein gamma-aminobutyric acid (GABA) A recepto	3.2
	423165	AI937547	Hs.124915	hypothetical protein MGC2601	3.2
45	449961	AW265634	Hs.133100	ESTs	3.2
	454036	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	3.2
	419865	NM_007020	Hs.93502	U1-snRNP binding protein homolog (70kD) Homo sapiens mRNA; cDNA DKFZp761l1224 (f	3.2 3.2
	423420 420352	AI571364 BE258835	Hs.128382	gb:601117374F1 NIH_MGC_16 Homo sapiens c	3.2
50	424641	AB001106	Hs.151413	glia maturation factor, beta	3.2
	453544	AA831785	Hs.171914	Homo sapiens cDNA FLJ14209 fis, clone NT	3.2
	447877	AJ435184	Hs.164252		3.2 3.2
	419683	AA248897 AA013218	Hs.48784 Hs.157492	ESTs cer-d4 (mouse) homolog	3.2
55	451026 422709	AA315331	Hs.153485	ESTs	3.2
55	432809	AA565509	Hs.131703		3.2
	446593	W79572	Hs.13277	hypothetical protein FLJ22054	3.2
	457728	AW974811		gb:EST386916 MAGE resequences, MAGN Homo NM_001334*:Homo sapiens cathepsin O (CTS	3.2 3.2
60	403790 445413	AA151342	Hs.12677	CGI-147 protein	3.2
v	438703	AI803373	Hs.31599	ESTs	3.1
	434577	R37316	Hs.179769	Homo sapiens cDNA: FLJ22487 fis, clone H	3.1
	422772	AL119585	Hs.120228		3.1 3.1
65	433434 427961	AA588429 AW293165	Hs.143134	gb:no22b03.s1 NCI_CGAP_Pr22 Homo sapiens ESTs	3.1
05	414430	A1346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	3.1
	420552	AK000492	Hs.98806	hypothetical protein	3.1
	456209	W60633	Hs.297792		3.1
70	418819	AA228776	Hs.191721	ESTs KIAA1444 protein	3.1 3.1
70	438944 439086	AA302517 AF085947	Hs.92732	gb:Homo sapiens full length insert cDNA	31
	451734	NM_006176	Hs.26944	neurogranin (protein kinase C substrate,	3.1
	415257	F03016	Hs.27513	ESTS	3.1
75	442789	AW904361	Hs.131191		3.1 3.1
75	432675	AJ791855	Hs.105884 Hs.171014		31
	426600 435092		Hs.4749	Homo sapiens mRNA; cDNA DKFZp761E13121 (3.1
	439039		Hs.48713	ESTs	3.1
00	450358	AB010098	Hs.24907	coronin, actin-binding protein, 28	31
80	400850		No 10131	Target Exon ? ESTs	3.1 3.1
	417636 425790		Hs.191212 Hs.288446		3.1
	415314		Hs.5422	glycoprotein M68	3.1

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					3.1
	436456			3 protein-coupled receptor 24 protein A	3.1
	408601 420886	U47928 AA805453		ESTs, Wealdy similar to T29012 hypotheti	3.1
_	437162		Hs.5464	hyroid hormone receptor coactivating pr	3.1
5	445704			ESTs, Moderately similar to 138022 hypot guanine nucleotide binding protein (G pr	3.1 3.1
	440700 414747	AW952281 U30872		centromere protein F (350/400kD, mitosin	3.1
	431553	X78075	Hs 2799	cartilage linking protein 1	3.1
10	405605			C2001342:gi 127814 sp P26434 NAH4_RAT SO	3.1 3.1
10	431467	N71831 AA331517		Homo sapiens mRNA; cDNA DKFZp434E0528 (f chimerin (chimaerin) 2	3.1
	457561 412507	L36645	Hs.73964	EphA4	3.1
	413448	AL134467	Hs.25307	Homo sapiens clone 24812 mRNA sequence	3.1
15	444168	AW379879		gb:RC1-HT0256-081199-011-f01 HT0256 Homo	3.1 3.1
15	400090 433642	BE466341	Hs.189746	Eos Control ESTs, Weakly similar to 138022 hypotheti	3.1
	422938	NM_001809	Hs. 1594	centromere protein A (17kD)	3.1
	426318	AA375125		Homo sapiens cDNA: FLJ22322 fis, clone H	3.1 3.1
20	428896	AW291932	Hs.98936 Hs.43670	ESTs ESTs	3.1
20	449277 426509	AA001064 M31166	Hs.2050	pentaxin-related gene, rapidly induced b	3.1
	412216	AW901517		gb:RC5-NN1013-310300-021-C03 NN1013 Homo	3.1 3.1
	428845	AL157579	Hs.153610	KIAA0751 gene product	3.1 3.1
25	431512 418113	BE270734 AI272141	Hs.2795 Hs.83484	tactate dehydrogenase A SRY (sex determining region Y)-box 4	3.0
23	450661	AW952160	Hs.83849	ESTs	3.0
	448448	NM_014954	Hs.21239	KIAA0985 protein	3.0 3.0
	422631	BE218919	Hs.118793 Hs.227699	hypothetical protein FLJ10688 ESTs, Weakly similar to T2D3_HUMAN TRANS	3.0
30	419687 450963	A1638859 A1864668	Hs.48832	ESTs	3.0
50	435060	Al422719	Hs.120873	ESTs, Weakly similar to fork head like p	3.0
	440274	R24595	Hs.7122	scrapie responsive protein 1	3.0 3.0
	437438 435401	AL359620 R44477	Hs.14217 Hs.10056	hypothetical protein DKFZp762P2111 hypothetical protein FLJ14621	3.0
35	416737	AF154335	Hs.79691	LIM domain protein	3.0
	445314	A1689948	Hs.65489	Homo sapiens cDNA: FLJ21517 fis, clone C	3.0 3.0
	425870	R13406	Hs.56782	ESTs HNK-1 sulfotransferase	3.0
	425294 416404	AF033827 AA180138	Hs.155553 Hs.107924	ESTs	3.0
40	413995	BE048146	Hs.75671	syntaxin 1A (brain)	3.0
	422798	R92347	Hs.34574	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.0 3.0
	426384 430147	AI472078 R60704	Hs.303662 Hs.234434	hypothetical protein FLJ13189 (FLJ13189) hairy/enhancer-of-split related with YRP	3.0
	425264	AA353953	Hs.20369	ESTs, Wealdy similar to gonadotropin ind	3.0
45	406917	X65964		gb:H.sapiens nestin gene.	3.0 3.0
	425262	D87119	Hs.155418	GS3955 protein ENSP0000220478*:SECRETOGRANIN III.	3.0
	401558 439345	AW444759	Hs.146171	ESTs	3.0
	414865	AA157155	Hs.274414	hypothetical protein FLJ14457	3.0 3.0
50	453976	BE463830	Hs.163714	ESTs ENSP00000244751*:Copine-like protein KIA	3.0
	404283 432890	NM_014442	Hs.279751	sialic acid binding Ig-like lectin 8	3.0
	451491	A1972094	Hs.286221	Homo sapiens cDNA FLJ13741 fis, clone PL	3.0
55	442573	H93366	Hs.7567	branched chain aminotransferase 1, cytos	3.0 3.0
55	428361 443753	NM_015905 AW367578	Hs.183858 Hs.134749		3.0
	417868	AI078534	Hs.122592		3.0
	443898	AW804296	Hs.9950	Sec61 gamma gb:Homo sapiens full length insert cDNA	3.0 3.0
60	438869 453900	AF075009 AW003582	Hs.226414		3.0
00	447714	AW296313	Hs.255537		3.0
	426581		Hs.135890		3.0 3.0
	421126		Hs.102122 Hs.66170	insufin-like growth factor binding prote HSKM-B protein	3.0
65	410762 431462				3.0
	452221	C21322	Hs.288057	hypothetical protein FLJ22242	3.0 3.0
	412326		Hs.73817		3.0
	428600 426501				3.0
70	405558			Target Exon	3.0
	421483			7 hypothetical protein MGC11333	3.0 3.0
	448681 452108		Hs.21754 Hs.20301		3.0
	429569				3.0
75	450728	AW162923	Hs.25363	presenilin 2 (Alzheimer disease 4)	3.0 3.0
	429371				3.0
	437435 432188		Hs.27027 Hs.2928	solute carrier family 7 (cationic amino	3.0
	40463	2		NM_022490:Homo sapiens hypothetical prot	3.0
80	452619				3.0 3.0
	421450 419030				3.0
	45356				3.0

	405239	U89281	oxidative 3 alpha hydroxysteroid dehydro 3.0
	TABLE 17B		
_	Pkey:		ue Eos probeset identifier number
5	CAT number		e duster number
	Accession:	Gen	bank accession numbers
	Pkey	CAT Number	Accession
	408432	1058567_1	AW195262 R27R6R AWR11262
10	410099	117647_1	AA081630 T08671 A1174254 D83874 AW959843 AA364503 AA693467 AW993370 BE327037 AA167714 N79906 AW901977 AW901980 W52882
			T07735 AA484549 W60090 D52685 T23811 BE327043 AW901768 BE551237 AA917004 AA716027 Al439658 AA283724 Al805992 Al457096 AA084618 BE467736 Al092635 Al887863 Al697593 AA436618 Al167419 Al418634 T31586 AA436630 AA706191 Al041169 Al422304 T03534
			AA211402 AI204899 AI366472 AW827081 AA788593 T32736 AI767935 AA167791 AA747914 AA663870 AI865504
	410126	117761_1	BE169274 AW893230 AA210998 H24222 AA081774 BE000935 BE000834 AA334880
15	412216	1283670_1	AW901517 AW901523 AW901521 AW901547
	412436	129439_1	AA665089 AA135130 AA484059 AA102419 AW877765
	412799 412820	132817_1 1330039_1	A1267605 AA121045 AA126521 BE001236 BE001177 BE001180 BE001234
	414372	143909_1	AA143654 AW753140 AA213770 AW970865 AA569075 AA492132
20	416871	1626761_1	H98716 N90792 N24283
	418512	176394_1	AW498974 T09332 R58460 AA350990 T33786 T30936 AA350905 T08592 T09274 AA224297 D54678 T08951 R15346 AW953188 AA350074
	419544	185760 2	AW890649 AI909154 AA526337 AA244193 AI909153
	420352	192979_1	BE258835 AV958316 AA258918 AW843305 R14744 AI580388 BE071923 R36280
25	420692	195649_1	AW976345 AA279423 AA761070
	420886	197344_1	AA805453 AA281379 N34524 AA305071 AW954803 AA502335 AI433430 AI203597 AW026670 AW265323 AW850787 AA317554 AW993643 AW835572 AW385512
	422156	212379_1	N34524 AA308071 AM954803 AA502335 AA50430 M203357 AM020070 AM203325 AM030707 AA517356 AM350540 AM030707 AA517356 AM030707 AM50707 AM50
	422949	223184_1	AA 319435 N56456 AA 319377 AW961532 T48452 AA894424
30	423476	22861_1	AL035633 F11794 F11783 H18042 T66089 H29379 R19493 AW134660 Al299437 AL133995 AA057405 N78357 AA917450 Al002692 T09262 T65008
			H29290 AI200874 AA894415 AI732887 AI791768 AI733447 AA988785 N62128 T09261 AW956936
	423713 424945	231290_1 245223_1	AW754182 AW754198 AA329983 AI221919 Z19967 AA348780 AW964077 AW166028 BE540193 N94800 AA452368 N99604 AI341345 AW298800 AA724961 AA931158 AI741227
	424343	243223_1	AI805660 AI982626 D81263 D53937 D52496 AA974487 AW043854 N50483 Z39997 AI492961 AI361526 F04002 AA452141 T23551 AI472655
35			A1193667 A1341984 N92658 T32870 R52664 N50428 AW089291 A1934175 A1423737 D60665
	424947	245247_1	R77952 AA348809 AW959960 AW959962 AI565552 AW070702 AA973910 R85973
	426413 426503	266650_1 268283_1	AA377823 AW954494 Al022688 AA380153 AA380233 AW963529
	426919	273507_1	AL 041228 D82004 D61361 AL203314 AL990307 AW900295 AL018308 AW087473 AW183530 AA393346 H50055 AA935601
40	428342	290035_2	A1739168 AA426249 A1199636 AW505198 AW977291 AA824583 AA883419 AA724079 A1015524 A1377728 AW293682 A1928140 AA731438 A1092404
		******	A1085630 AA731340
	429007 429163	298301_1 300543_1	D80642 AA443145 AL119015 AW904500 AA884766 AW974271 AA592975 AA447312
	429421	30431_1	AL 031658 ALGO3758 AL 040619 AW977914 AAR11957 AL352198 AW104364 AA648367 AA897604 AW341668 AL201382 AL040620
45	430183	31412_2	REGIGGS AAG76833 AI311783 TR6895 W68032 REG64393 REG64394 BE157228 BE183282 AI936370 AA552514 T67280 AAU39909
	430676	32168_1	AF084866 AF084870 AF084864 AF084867 AF084869 AF084865 AF084868 AW818206 AW812038 BE144813 BE144812 AW812041 AW812040 AW812067 BE061583 BE061604 T05808 A352469 AA580921 BE141783 BE141782 BE061601 AW814393 AW885029
	430968	326269_1	AW972830 AA527647 AA489820 AA570362
	433009	357371_1	AA761668 AA573621 R92814 R09670
50	433434	366095_1	AAS88429 AI972567 AW504832 AI299694
	433523 435542	368873_1 407744_1	H29882 AW665533 AW149901 AI572917 AA598500 AI686466 AI336390 AW864390 AW864320 AA687376 H74234 AW975503
	438869	46651_1	AF075009 R63109 R63068
	439086	46852_1	A FORSOAT HTTIGER 1 HTTIGER 1
55	439285	47065_1	AL 133916 N79113 AF086101 N76721 AW950828 AA364013 AW955684 AI346341 AI867454 N54784 AI655270 AI421279 AW014882 AA775552
	439518	47334_1	N62351 N59253 AA626243 A1341407 BE175639 AA456968 A1358918 AA457077 W76326 AF086341 W72300
	439566	47387_1	AF085387 W77884 W72711
	439710	47550_1	AF086543 W96291 W96225
60	441102	509604_1	AA973905 AI299888 AA917019 H63235 T90771
	444168	593829_1 689623_1	AW379879 A126285 H12014 Z44514 A1352097 A1803984 AW235923 AW196558 A1954637 A1336983
	446692 447197	711623_1	DREATS AIRESAS BREIST
	449625	8113_1	NM_014253 AF100772 BF088769 AL022718 BE161779 AW863569 BE161640 AL039060 BE168542 AW296554 AA323193 AA235370 AW779760
65			N48674 A1375997 R45432 D59344 A1203107 F07491 R35360 R25094 A1913631 A1498402 T61382 A1016320 N45526 T61415 AA331486
	450375	83327_1	AA009647 AA131254 AA374293 AW954405 H04410 AW606284 AA151166 BE157467 BE157601 H04384 W46291 AW663674 H04021 H01532 AA190993 H03231 H59605 H01642 AA852876 AA113758 AA626915 AA746952 A1161014 AA099554 R69067
	450582	83933_1	A1339732 AAN10300 AWK15041 AA758334 N29860 AA425874 AA425118 AA865829 AW936878
	451320	86576_1	AWI 18072 AIG31982 T 15734 AA224196 AI701458 W20198 F26326 AA890570 N90552 AW071907 AIG71352 AI375892 T03517 R88265 AI124088
70			AA224388 AI084316 AI354686 T33652 AI140719 AI720211 T03490 AI372637 T15415 AW205836 AA630384 T03515 T33230 AA017131 AA443303
	453331	00214 1	T33623 AI222556 T33511 T33785 AI419606 D55612 AI240665 T53681 N77468 H51833 AA147247 R75732 C18450 R73999 AI095755 T49904 H03868 AA411580 R33395 AA410586 T48869 D63292
	433331	96214_1	PRINT H1240R H0266R AACISCUR R75057 AIRCLID PRINTS R36203 AIRO9932 AIRO8765 R78948 AA411449 AA976929 AI378760 AIJ78020 140070
			R73906 R75632 H03612 AA909684 N50695 H02580 H12839 N58781 AA742532 A1360919 H03502 BE208298 R68588 A1350463 K31935 AW069127
75			AA411621 R25671 R36105 H12451 H03869 H51263 AA035486 R25109 R25110 AA147933
	453682 454171	977454_1 1049240_1	T79703 T96307 AL079725 I AW854832 AW854798 AW854857 AW854816 AW854834 AW854817
	457728	393853_1	
	457876	42814_2	AI821940 N57106 AI744264 AA808846 AA643417 AA543416 Z70715
80	458912	823104_1	A)911066 A)933734 A)680889 A)003599
	TABLE 1	7C:	
	Pkey:		inique number corresponding to an Eos probeset
			224

PCT/US02/29560 WO 03/025138

	Ref:	Secu	jence of huma	The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication emitted "The DNA in chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
	Strand:		CALLES LINA SUZ	nd from which exons were predicted. le positions of predicted exons.
5	Nt_position	: Inon	Lates HUCHEOUG	o positions of production and the control of the co
,	Pkey	Ref	Strand	NL position
	400533	6981826	Minus	277132-277595
	400777	8131663	Plus	70745-71121
	400850	1927150	Minus	4506-4691
10	401558	7139678	Plus	103510-104090
. •	402145	8018280	Plus	113086-114800
	402604	9909420	Plus	20393-20767
	402855	9662953	Minus	59763-59909
	403696	3135242	Minus	143467-143634
15	403790	8084957	Minus	87826-87947,89835-90002
• •	404150	7534008	Plus	165811-165943
	404283	2276311	Minus	99460-99564
	404295	9856663	Minus	75747-75947
	404541	8318559	Plus	103456-103664
20	404584	9857511	Ptus	138651-139153
	404632	9796668	Plus	45096-45229
•	404819	4678240	Plus	45096-45229 16223-16319,16427-16513,16736-16859,16941-17075,17170-17287,17389-17529,18261-18357,18443-18578
	405239	7249119	Plus	144345-144464,144690-144836,151750-151883,152407-152484
	405303	2078453	Minus	130607-130802
25	405331	3236226	Minus	32502-32690
	405348	2914717	Minus	43310-43462
	405558	1621110	Plus	4502-4644,5983-6083
	405605	5836195	Minus	117070-117270
	405819	4007557	Plus	2830-2967
30	4000.0			

IABLE 18A: ABOUT 445 CNS-ENRICHED GENES SIGNIFICANTLY DOWN-REGULATED IN GUOBLASTOMA MULTIFORMA COMPARED TO NORMAL ADULT CNS
Table 18A lists about 446 CNS-enriched genes significantly down-regulated in glioblastoma multiforma (GBM) compared to normal adult CNS tissues. These were selected from
59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" normal CNS to "average" GBM was greater than or equal to 2. The "average" normal
CNS level was set to the 85th percentile amongst various tumor samples. To enrich for
CNS specific genes, the ratio of "average" CNS to "average" non-CNS normal adult tissues was calculated to be greater than or equal to 3. The "average" CNS level was set to the
85th percentile amongst various CNS tissues. The "average" normal non-CNS adult tissue level was set to the 95th percentile amongst various non-CNS normal tissues. In order to
85th percentile amongst various CNS tissues. The "average" normal non-CNS adult tissue level was set to the 95th percentile amongst various non-CNS normal tissues. In order to
85th percentile amongst various horn-cns normal tissues was subtracted from both the numerator and
remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and 35

the denominator before the ratios were evaluated.

Pkey: Unique Eos probeset identifier number 40 Pkey:

UnigenelD:

Unigene Title: R1:

Unique Eos proceset Mentmer number Exemplar Accession number, Genbank accession number Unigene number Unigene gene title Ratio of CNS to GLIOBLASTOMA MULTIFORMA Ratio of CNS to NON-CNS NORMAL ADULT TISSUES 45

			_		R1	R2
	Pkey	ExAcon	UnigenelD	Unigene Title	38.8	10.5
	425489	M58594	Hs.1905	prolactin	23.4	23.4
	410330	AW023630	Hs.159425	ESTs	22.6	22.6
50	430538	AB032435	Hs.242821	differentiation-associated Na-dependent	22.4	6.0
	417275	X63578	Hs.295449	parvalbumin	22.3	22.3
	453590	AF150278	Hs.33578	KIAA0820 protein	21.8	21.8
	428505	AL035461	Hs.2281	chromogranin 8 (secretogranin 1)	19.9	19.9
	453220	AB033089	Hs.32452	Homo sapiens mRNA for KIAA1263 protein,	19.4	19.4
55	411498	NM_014210	Hs.70499	ecotropic viral integration site 2A	19.4	19.4
	408040	AJ266496	Hs.22905	ESTs, Wealty similar to RHG6_HUMAN RHO-G	18.5	3.8
	435145	A1277259	Hs.116631	ESTs	18.1	18.1
	407039	X00368	_	gb:Human prolactin gene 5' region.	16.8	16.8
	409263	AA069573	Hs.50319	ESTs	16.1	16.1
60	449078	AK001256	Hs.22975	KIAA1576 protein	15.3	15.3
	426968	U07616	Hs.173034	amphiphysin (Stiff-Mann syndrome with br	15.1	15.1
	432298	AL118812	Hs.274293		15.1	15.1
	424645	NM_014682	Hs.151449		14.9	3.8
	450590	A1701507	Hs.273740		14.6	8.9
65	417175	R44558	Hs.94002	ESTs	14.5	14.5
-	423449	A1497900	Hs.33067	ESTs	14.4	14.9
	441869	NM_003947	Hs.8004	huntingtin-associated protein interactin	14.0	8.0
	405560	AW887701		hypothetical protein FLJ20628	13.9	18.7
	440209	H05049	Hs.247837		13.9	5.3
70	439238	N47305	Hs.302161		13.8	13.8
	452022	AW072330	Hs.293875		13.5	13.5
	459080	AW192083	Hs.290855	ESTs	13.4	38.6
	425649	U30930	Hs.158540	UDP glycosyltransferase 8 (UDP-galactose	13.2	13.2
	413324	V00571	Hs.75294	corticotropin releasing hormone	13.1	13.1
75	443992	AW022228	Hs.322922		12.9	6.6
	410635	D58863	Hs.334372		12.5	12.5
	420156	AW449258	Hs.6187	ESTs	12.5	12.5
	416490	AF090116	Hs.79348	regulator of G-protein signalling 7	12.2	3.2
	450757	BE081050	Hs.31570	ESTs, Wealdy similar to KIAA1324 protein	12.2	12.2
80	410037	AB020725	Hs.58009	KIAA0918 protein	12.0	12.0
	433940	H05129		cyclic AMP-regulated phosphoprotein, 21	11.6	5.6
	434367	AB020700	Hs.3830	KIAA0893 protein	11.5	11.5
	410657	AF063228	Hs.65248	dynein, cytoplasmic, intermediate polype	11.5	71.0

	431988	AC002302	Hs.77202	protein kinase C, beta 1	11.2	10.5
	451783	R42554	Hs.210862	T-box, brain, 1	11.2	11.2
	453165 452238	S74727 F01811	Hs.32042 Hs.345757	aspartoacytase (aminoacytase 2, Cenavan ESTs	10.7 10.6	10.7 3.8
5	417167	AW206437	Hs.4290	ESTs	10,4	10.4
_	420033	059502	Hs.292590	ESTs	10.4	10.4
	427224	AL135554	Hs.101937	sine oculis homeobox (Drosophila) homolo	10.4	3.9
	424153	AAA51737	Hs.141496	MAGE-like 2	10.3 10.0	5.1 10.0
10	413293 400438	AL047483 AF185611	Hs.302498 Hs.115352	GTP-binding protein homologous to Saccha Target	9.9	5.1
	447750	AJ422234	Hs.143434	contactin 1	9.8	9.8
	419347	C15944	Hs.90005	superiorcervical ganglia, neural specifi	9.8	22.2
	418207	C14685	Hs.34772	ESTS	9.8 9.4	9.8 9.4
15	413409 447746	AI638418 AW015920	Hs.1440 Hs.161359	DEAD/H (Asp-Gtu-Ala-Asp/His) box polypep ESTs	9.2	9.9
1.5	406311	A11013320	16.101333	NM_021979°:Homo sapiens heat shock 70kD	9.1	11.5
	444330	AI597655	Hs.49265	ESTs	9.1	9.1
	426365	AA376667	Hs.10283	RNA binding motif protein 88	9.0	4.1
20	427322 439450	AK002017 R51613	Hs.176227 Hs.125304	hypothetical protein FLJ11155 ESTs	8.9 8.7	8.9 8.3
20	439430 429096	AB011106	Hs.196012	KIAA0534 protein	8.6	8.6
	428652	AA584272	Hs.336224	transmembrane protein with EGF-like and	8.6	8.6
	408814	N62499	Hs.176227	hypothetical protein FLJ11155	8.6	8.6
25	410309 408950	BE043077 AA707814	Hs.278153 Hs.14945	ESTs long fatty acyl-CoA synthetase 2 gene	8.5 8.5	8.5 8.5
23	426814	AF036943	Hs.172619	myelin transcription factor 1-like	8.5	14.2
	416851	AW963951	Hs.85618	ESTs	8.5	8.5
	430004	U27768	Hs.227571	regulator of G-protein signalling 4	8.4	15.7
30	412155	R38167	Hs.12449	Homo sapiens transmembrane protein HTMP1	8.4 8.4	27.9 8.4
20	427061 412049	AB032971 N53437	Hs.173392 Hs.18268	KIAA1145 protein adenylate kinase 5	8.3	10.7
	452752	AW044058	Hs.33578	KIAA0820 protein	8.2	13.4
	414699	AI815523	Hs.76930	synuclein, alpha (non A4 component of am	8.2	4.5
25	422756	AA441787	Hs.119689	glycoprotein hormones, alpha polypeptide	8.1 8.1	5.8 8.1
35	435648 429470	H24347 A1878901	Hs.27524 Hs.203862	ESTs guanine nucleotide binding protein (G pr	8.0	8.0
	416133	NM_001683	Hs.89512	ATPase, Ca transporting, plasma membrane	8.0	8.0
	438208	AL041224	Hs.65379	ESTs	7.9	5.8
40	436427	AI344378	Hs.143399	ESTs	7.8	7.8
40	441005 442023	Z41305 Al187878	Hs.303172 Hs.144549	Homo sapiens mRNA; cDNA DKFZp547G133 (fr ESTs	7.7 7.7	7.7 5.6
	444458	BE041526	Hs.31746	hypothetical protein DKFZpS47F072	7.7	7.7
	429033	NM_007374	Hs.194756	sine oculis homeobox (Drosophita) homolo	7.6	5.5
45	450642	R39773	Hs.7130	copine IV	7.6	5.6
45	446544	AI631932	Hs.7047	ESTs, Weakly similar to Unknown [H.sapie	7.5 7.5	12.4 7.5
	438283 437073	AI458931 AI885608	Hs.37282 Hs.94122	ESTs ESTs	7.5	7.5
	408577	H50572	Hs.19515	ESTs, Highly similar to NRG3_HUMAN PRO-N	7.4	7.4
50	424264	D80400	Hs.239388	Human DNA sequence from clone RP1-304B14	7.3	7.3
50	441264	AA927170	Hs.23290	ESTs	7.3 7.2	7.3 7.2
	450474 425352	AW872844 NM_000939	Hs.117494 Hs.1897	ESTs proopiomelanocortin (adrenocorticotropin	7.2	6.1
	450715	AI266484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	7.2	7.2
	450181	H05254	Hs.201198	ESTS	7.2	7.2
55	415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	7.1	4.8
	419318 423003	AW969742 AL120077	Hs.291005 Hs.122967	ESTs kelch (Drosophila)-like 2 (Mayven)	7.1 7.0	3.1 7.0
	434460	AA478486	Hs.3852	KIAA0368 protein	7.0	4.8
	433921	AA618174		gb:nq14f01.s1 NCI_CGAP_Thy1 Homo sapiens	7.0	7.0
60	418940	H17739	Hs.288513	Human DNA sequence from clone RP5-899C14	7.0	7.0
	410765 457012	Al694972 R41480	Hs.66180	nucleosome assembly protein 1-like 2	7.0 6.9	8.0 6.9
	416018	AW138239	Hs.302754 Hs.78977	ESTs proprotein convertase subtilisin/kexin t	6.9	14.0
	445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	6.9	6.9
65	415669	NM_005025		serine (or cysteine) proteinase inhibito	6.9	10.2
	433558	AA833757	Hs.201769		6.9 6.8	6.9 6.8
	409031 409339	AA376836 AB020686	Hs.288856 Hs.54037	ESTs ectonucleotide pyrophosphatase/phosphodi	6.8	3.6
	436568	H12049	Hs.91564	ESTs	6.8	6.8
70	442593	R39804	Hs.31961	ESTs	6.7	6.7
	437948	AA772920	Hs.303527		6.7	24.8
	412266	N59006 N46569	Hs.26133 Hs.76722	ESTs CCAAT/enhancer binding protein (C/EBP),	6.6 6.6	30.9 45.2
	422980 442026	AI243749	Hs.8074	brain-specific angiogenesis inhibitor 3	6.5	6.5
75	429946	R49390	Hs.254129		6.4	4.5
	445279	R41900	Hs.22245	ESTs	6.4	6.4
	428414	AL049980	Hs.184216		6.4 5.4	6.4 3.3
	407868	NM_000950		profine-rich Gla (G-carboxyglutarnic acid hypothetical protein PRO2198	6.4 6.4	3.3 4.0
80	434104 443244	AF116691 AI457235	Hs.116459 Hs.166479		6.3	3.0
	442042	AI990506	Hs.8077	Homo sapiens mRNA; cDNA DKFZp547E184 (fr	6.2	6.2
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homotog), act	6.2	43.2
	428536	AI143139	Hs.2288	visinin-like 1	6.0	22.1
				20		

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				ISTs	6.0 5.9	6.0 5.9
	448958 431467		Hs.256398 1	(IAA0844 protein tomo sapiens mRNA; cDNA DKFZp434E0528 (f	5.9	6.0
_	447138	Al439112	Hs.93828	STs, Weakly similar to 2109260A B cell	5.8 5.8	5.8 3.6
5	414545	AA149287		STs	5.8	5.8
	418202 410389	N48521 AW954049	Hs.26549 Hs.8177	(IAA1708 protein ESTs, Weakly similar to PIHUB6 salivary	5.7	9.6
	444124	R43097	He SR1R	SSTs.	5.7	9.3
10	408065	AW954272	1	b:EST366342 MAGE resequences, MAGC Homo	5.6 5.6	5.6 9.6
10	448533	AL119710		nucleosome assembly protein 1-like 3 KIAA0479 protein	5.6	35.0
	425523 459697	AB007948 AA406062	Hs 98002	ESTs	5.6	5.4
	408428	NM_014787	He AARGE	DnaJ (Hsp40) homolog, subfamily B, membe	5.6 5.5	5.6 3.2
1.5	420111	AA255652		gb:zs21h11.r1 NCI_CGAP_GCB1 Homo sapiens Zic family member 2 (odd-paired Drosophi	5.4	5.4
15	450149 424918	AW969781 R13982	Hs.132863 Hs.169309	myelin-associated oligodendrocyte basic	5.3	5.3
	438202	AW169287	Hs.22588	EŠTs .	5.3	5.3 5.3
	448605	AL109678		Homo sapiens mRNA full length insert cON	5.3 5.3	3.5
20	425580	L11144 T65754	Hs.1907	gatanin gb:yc11c07.s1 Stratagene lung (937210) H	5.3	3.8
20	418866 430091	AB032958	Hs.233023	KIAA1132 protein	5.3	4.9
	448786	BE048842	Hs.179075	Homo sapiens cDNA FLJ11881 fis, clone HE	5.2 5.2	5.2 3.0
	427283	AL119796	Hs.174185	ectonucleotide pyrophosphatase/phosphodi gb:yu03c11.r1 Soares fetal liver spleen	5.2	5.2
25	415666 410240	H72693 AL157424	Hs.61289	synaptoianin 2	5.2	4.6
23	428784	Y12851	Hs.193470	nurinergic recentor P2X, ligand-gated to	5.2	7.7
	446692	Z44514		Homo sapiens mRNA for KIAA1763 protein,	5.2 5.2	33.0 4.1
	428508	BE252383	Hs.184668	SBBI31 protein ESTs	5.1	5.1
30	446353 423135	AI290919 N67655	Hs.153661 Hs.26411	ESTs	5.1	8.2
50	437331	AL353933	Hs.21710	hypothetical protein DKFZp761G0313	5.1	5.1
	413988	M81883	Hs.324784	glutamate decarboxylase 1 (brain, 67kD)	5.1 5.1	5.1 5.1
	429859	NM_007050	Hs.225952	protein tyrosine phosphatase, receptor t ESTs, Wealdy similar to NPL4_HUMAN NUCLE	5.0	11.2
35	411379 408068	AI816344 AW148652	Hs.12554 Hs.167398	ESTs. Weavy similar to the E4_ roots at the	5.0	5.0
33	415734	NM_014747	Hs.78748	KIAA0237 gene product	5.0	27.4
	439607	BE540565	Hs.159460	ESTs	5.0 4.9	5.6 29.3
	425984	AWB36277	Hs.165636	hypothetical protein DKFZp761C07121	4.9	4.9
40	414631	AW970130 AL049256	Hs.65406 Hs.122593	ESTs ESTs	4.9	3.8
40	437117 418527	AA450386	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	4.9	4.9
	425073	W39609	Hs.22003	solute carrier family 6 (neurotransmitte	4.9 4.9	4.9 4.9
	455364	H72176	Hs.4273	hypothetical protein FLJ13159	4.9	7.6
45	443150	AJ034467	Hs.34650 Hs.22511	ESTs ESTs	4.9	12.0
43	422411 414931	AW749443 AK000342	Hs.77646	Homo sapiens mRNA; cDNA DKFZp761M0223 (f	4.9	3.4
	430456	AA314998	Hs.241503	hypothetical protein	4.8 4.8	4.7 3.9
	428186	AW504300	Hs.295605	mannosidase, alpha, class 2A, member 2	4.0 4.8	4.8
50	433516	AA595802 NM_014903	Hs.33410 Hs.174188	ESTs, Weakly similar to T17279 hypotheti KIAA0938 protein	4.8	4.8
30	427287 416101	R24854	Hs.268806	ESTs	. 4.8	3.3
	447252	R90916	Hs.12449	Homo sapiens transmembrane protein HTMP1	4.8 4.7	3.2 3.9
	458268	AA428403	Hs.106131	ESTs Homo sapiens clone 23809 mRNA sequence	4.7	8.2
55	440105 445102	AA694010 AW204610	Hs.6932 Hs.22270	ESTs	4.7	19.2
33	419643	F06066	Hs.91791	chromosome 11 open reading frame 25	4.7	4.7
	414949	C15314	Hs.323349		4.7 4.7	3.8 4.7
	453534	NM_01479	6 Hs.33187 Hs.13223	KtAA0748 gene product Homo sapiens mRNA full tength insert cDN	4.7	4.0
60	445729 451032	H21066 W03692	Hs.323079		4.7	4.9
•••	434792		Hs.132458	ESTs	4.7 4.7	3.8 3.0
	447104		Hs.210706	Homo sapiens cDNA FLJ13182 fis, clone NT	4.6	4.6
	430537		Hs.2593 Hs.32973	phosphodiesterase 68, cGMP-specific, rod glycine receptor, beta	4.6	4.6
65	453431 453302			glutamate receptor, metabotropic 1	4.6	4.6
03	429876		Hs.225974	KIAA1054 protein	4.6 4.6	16.8 6.3
	451516		Hs.12024	ESTs gb:no87h09.s1 NCI_CGAP_AA1 Horno sapiens	4.6	3.9
	433670		Hs.11219		4.5	3.8
70	437380 410366		Hs.30268	hypothetical protein	4.5	10.4
. •	419191		Hs.89666	A kinase (PRKA) anchor protein 6	4.5	4.5 3.3
	429290				4.5 4.5	10.2
	424932		Hs.31536 Hs.17990		4.4	4.0
75	432736 421952			ESTs, Moderately similar to AF161511 1 H	4.4	3.2
	42896	3 AW38268	2 Hs.25820	8 Homo sapiens, clone MGC:15606, mRNA, com	4.3 4.3	3.3 4.7
	43504				4.3 4.3	4.3
	45130		Hs.20989 Hs.29088		4.3	4.3
80	45238 41030				4.3	7.8
	43310	9 N58907	Hs.16243	O EST	4.3 4.3	3.9 8.0
	43134) ESTs DnaJ (Hsp40) homolog, subfamily C, membe	4.3	3.4
	44716	3 AW29277	0 Hs.5542	• • •		
				28	37	

					4.2	5.3
	422414	AW875237	Hs.13701	ESTs	4.2 4.2	18.3
	439274	AF085092	Hs.48372 Hs.209569	ESTS	4.2	4.2
	423589 429956	AA328082 AI374651	Hs.22542	ESTs ESTs	4.2	3.2
5	427317	AB028955	Hs.175780	KIAA1032 protein	4.2	5.3
,	426847	S78723	Hs.298623	5-hydroxytryptamine (serotonin) receptor	4,1	7.9
	408206	AF041853	Hs.43670	kinesin family member 3A	4.1	4.1
	433803	AI823593	Hs.27688	ESTs	4.1	4.1
	413024	AF036268	Hs.75149	SH3-domain GRB2-like 2	4.1	4.0
10	448117	H49129	Hs.172982	ESTs	4.1	4.1
	450600	BE079478	Hs.24880	ESTs	4.1	3.9
	429550	AW293055	Hs.119357	ESTs	4.1	6.4
	448681	AL109781	Hs.21754	Homo sapiens mRNA tull length insert cDN	4.0	7.2
	458694	F12832	Hs.3610	ESTs	4.0	4.0
15	452197	AW023595	Hs.232048	ESTs	4.0	4.0
	423728	AW891294	Hs.132136	solute carrier family 4, sodium bicarbon	4.0	7.9
	429656	X05608	Hs.211584	neurofitament, light polypeptide (68kD)	4.0	13.1
	448583	NM_015239	Hs.21542	KIAA 1035 protein	4.0	4.0
20	419863	AW952691	Hs.93485	Homo sapiens mRNA; cDNA DKFZp761D191 (fr	3.9	21.4
20	442412	R77677	Hs.346644	ESTs	3.9	3.9
	424001	W67883	Hs.137476	paternally expressed 10	3.9 3.9	5.4 3.9
	440293	Al004193	Hs.22123	ESTs	3.9	3.6
	422890	243784	41 400400	ankyrin 3, node of Ranvier (ankyrin G)	3.9	3.9
25	426054	U12431	Hs.166109	ELAV (embryonic lethal, abnormal vision,	3.8	3.7
23	412949	AI471639	Hs.71913	ESTS	3.8	11.1
	427457	AW779105	Hs.164682	ESTs	3.8	4.4
	416530	U62801 A1733585	Hs.79361	kallikrein 6 (neurosin, zyme) ESTs	3.8	3.8
	442676	AW975157	Hs.130897	ESTs	3.7	3.7
30	434998 424945	AV1975157 AI221919	Hs.26037	hypothetical protein FLJ 10582	3.7	30.5
50	415257	F03016	Hs.27513	ESTs	3.7	8.6
	407886	AW969688	Hs.100826	ESTs	3.7	20.2
	400844	A11303000	113.100040	NM_003105*:Horno sapiens sortilin-related	3.7	3.1
	456765	A1497900	Hs.33067	ESTs	3.7	3.7
35	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	3.6	7.6
33	452667	T87219	Hs.13219	ESTs	3.6	3.6
	436773	AW078629		PC4 and SFRS1 interacting protein 1	3.6	3.6
	424120	T80579	Hs.290270	ESTs	3.6	14.7
	446574	Al310135	Hs.335933	ESTs	3.6	3.5
40	432453	AI885537	Hs.27172	ESTs, Moderately similar to PC4259 ferri	3.6	3.9
. •	408119	W26213	Hs.101672	ESTs, Wealthy similar to T00331 hypotheti	3.6	3.6
	449093	AB035356	Hs.22998	neurexin 1	3.6	3.6
	439239	AI031540	Hs.235331	ESTs	3.6	49.5
	451625	R56793	Hs.106576	alanine-glyoxylate aminotransferase 2-li	3.6	4.1
45	435059	Z45270	Hs.235873	hypothetical protein FLJ22672	3.6	4.8
	423346	Al267677	Hs.127416	synaplojanin 1	3.6	20.1
	442738	AW002370	Hs.131055	ESTs, Weakly similar to NPM_HUMAN NUCLEO	3.5	3.5
	442106	AW205881	Hs.326728	ESTs	3.5	3.2
60	449117	AW449310	Hs.210262	ESTs, Weakly similar to HSS2_HUMAN HEPAR	3.5	3.5
50	405819			NM_002578:Homo sapiens p21 (CDKN1A)-acti	3.5	13.5
	452311	AW304029	Hs.252744	ESTs Pure But	3.5	3.5
	448902	Z45998	Hs.22543	Homo sapiens mRNA; cDNA DKFZp76111912 (f	3.5	21.8
	410224	M55513	Hs.150208	potassium voltage-gated channel, shaker-	3.4 3.4	3.4 3.4
55	400098		11- 040007	Eos Control	3.4	5.9
22	428001	H97428	Hs.219907	ESTs, Moderately similar to Transforming	3.4	14.0
	437268	A1754847	Hs.227571 Hs.47248	regulator of G-protein signalling 4 ESTs, Highly similar to similar to Cdc14	3.4	3.3
	443682	AI383061	Hs.89512	ATPase, Ca transporting, plasma membrane	3.3	17.1
	417417 419629	F05745 AB020695	Hs.91662	KIAA0888 protein	3.3	13.4
60	419852	AW503756	Hs.286184		3.3	4.1
00	417063	N50515	Hs.45061	ESTs	3.3	3.3
	435071	D60683	Hs.35495	ESTs	3.3	3.3
	446377	AW014022	Hs.170953		3.3	3.3
	412453	R20205	Hs.75236	ESTs	3.3	3.3
65	450561	R49674	Hs.25909	ESTs	3.3	3.3
	423829	R44107	Hs.240905	ESTs	3.3	4.4
	415527	F11624		gb:HSC2ZD101 normalized infant brain cDN	3.3	3.3
	427386	AW836261	Hs.6727	ESTs	3.3	3.3
	425121	AJ797511	Hs.154679	synaptotagmin I	3.2	3.9
70	452856	AF034799	Hs.30881	protein tyrosine phosphatase, receptor t	3.2	10.7
	442879	AF032922	Hs.8813	syntaxin binding protein 3	3.2	3.2
	417284	N62889	Hs.107242		3.2	3.2
	416805	F13271	Hs.79981	Human clone 23560 mRNA sequence	3.2	6.7
70	429477	AI275514	Hs.6658	ESTs	32	3.2
75	453169	AB037815	Hs.32156	KIAA1394 protein	3.2	5.7 3.2
	408039	AA131424	Hs.336636		3.2	3.2 22.1
	426269		Hs.168950		3.2 3.2	10.6
	409746			RAB33A, member RAS oncogene family	3.2	6.0
80	416874		Hs.42568 Hs.7076	ESTs KIAA1705 protein	3.2	3.2
οv	453919	AW959912 R46789	Hs.76118	ubiquitin carboxyl-terminal esterase L1	3.2	3.2
	444861 433315		Hs.239706		3.2	3.1
	433315 419103		Hs.96423	hypothetical protein FLI23033	3.2	8.4
	413103	r40163				

						EC 0
	424140		Hs.141308	myelin oligodendrocyte glycoprotein	3.2 3.2	56.0 4.1
	421790	AW896201		sodium channel, voltage-gated, type I, a	3.1	9.9
	432809	AA565509		ESTs	3.1	5.5
5	445225	AI216555		ESTs contactin 1	3.1	3.1
,	424087 437924	N69333 A1935 34 4	Hs.164118	ESTs, Wealthy similar to SL51_HUMAN SODIU	3.1	3.2
	419683	AA248897	Hs.48784	ESTs	3.1	5.9
	420173	AA256151		ESTs	3.1	4.1
	411666	AF106564	Hs.71346	neurofitament 3 (150kD medium)	3.1	6.6
10	416220	N49776	Hs.170994	hypothetical protein MGC10946	3.1	4.5
	425138	H08849	Hs.167464	glutamate receptor, ionotropic, N-methyl	3.1 3.1	4.2 3.1
	422234	AF119818	Hs.113287	discs, targe (Drosophila) homolog-associ	3.1	3:1
	445194	AI215667	Hs.175044	ESTS	3.1	10.2
15	438054	AA776626	Hs.169309 Hs.133483	ESTs ESTs, Weakly similar to T34549 probable	3.1	12.2
13	432149	AW614326 AK000956	Hs.13209	hypothetical protein FLJ 10094	3.0	3.0
	445725 414245	BE148072	Hs.75850	WAS protein family, member 1	3.0	11.7
	447673	AI823987	Hs.182285	ESTs	3.0	3.0
	428392	H10233	Hs.2265	secretory granule, neuroendocrine protei	3.0	42.3
20	418410	AA811441	Hs.107393	chromosome 3 open reading frame 4	3.0	3.9
	429024	AI652297	Hs.119302	complement-c1q tumor necrosis factor-rel	3.0 3.0	3.7 9.0
	426919	AL041228		ELAV (embryonic lethal, abnormal vision,	3.0	3.0
	424724	T06532	Hs.287709	Homo sapiens cDNA: FLJ22674 fis, clone H PFTAIRE protein kinase 1	3.0	10.0
25	410011	AB020641	Hs.57856 Hs.49117	Homo sapiens mRNA; cDNA DKFZp564N1662 (f	3.0	13.5
23	408947 426325	AL080093 D28114	Hs.169309	myelin-associated oligodendrocyte basic	2.9	81.1
	429006	AA443143	Hs.50929	hypothetical protein FLJ13842	2.9	6.6
	410711	AB002316	Hs.65746	KIAA0318 protein	2.9	6.1
	415486	H12214	Hs.13284	ESTs, Weakly similar to 2109260A B cell	2.9	15.7
30	424474	AA308883	Hs.148680	catcyon; D1 dopamine receptor-interactin	2.9	3.6
	448299	AA497044	Hs.20887	hypothetical protein FLJ10392	2.9 2.9	11.5 3.6
	419518	U79289	Hs.90798	Human clone 23695 mRNA sequence	2.9	5.1
	426529	AF090100	Hs.170241	Homo sapiens clone IMAGE 23915	2.9	3.2
35	430347	NM_002039	Hs.239706 Hs.99272	GRB2-associated binding protein 1 ESTs, Wealdy similar to S32567 A4 protei	2.9	6.1
22	429401	AW296102 R15891	Hs.281587	Human (clone CTG-A4) mRNA sequence	2.9	5.9
	450154 434277	X77748	Hs.3786	glutarnate receptor, metabotropic 3	2.8	28.5
	424790	AL119344	Hs.13326	ESTs, Wealdy similar to 2004399A chromos	28	23.1
	416836	D54745	Hs.80247	cholecystokinin	2.8	6.8
40	449277	AA001064	Hs.43670	ESTs	2.8	8.5
	451952	AL120173	Hs.301663	ESTs	2.7 2.7	19.2 3.7
	408554	AAB36381	Hs.315111	nuclear receptor co-repressor/HDAC3 comp	2.7	3.0
	413408	R51793	Hs.1440	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	2.7	3.2
15	410343	AA084273	Hs.76561	ESTs, Weakly similar to S47072 finger pr	2.7	4.1
45	420489	AA815089	Hs.193513 Hs.18268	ESTs adenylate kinase 5	2.7	17.2
	447359 423731	NM_012093 T08814	rs.10200	gb:EST06706 Infant Brain, Bento Soares H	2.7	4.0
	409953	AA332277	Hs.57691	cadherin 18, type 2	2.7	5.5
	424481	R19453	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	2.7	11.5
50	449714	AB033015	Hs.23941	KIAA1189 protein	2.7	7.5 3.7
	424922	BE386547	Hs.217112		2.7 2.7	3.7 4.1
	432447	X92681	Hs.2998	contactin 2 (axonal)	2.7	5.1
	420071	AB028985	Hs.94806	ATP-binding cassette, sub-family A (ABC1 Homo sapiens cDNA: FLJ23133 fis, clone L	2.6	5.1
55	438068 418512	AI927209 AW498974	Hs.306210	diacylglycerol kinase, zeta (104kD)	2.6	7.9
33	447761	AF061573	Hs.19492	protocadherin 8	2.6	6.3
	448743	AB032962	Hs.21896	KIAA1136 protein	2.6	23.2
	408547	AA574291	Hs.57837	ESTs	2.6	4.0
	426380	Al291267	Hs.149990		2.6	6.9 3.7
60	420898	AB002379	Hs.100113	KIAA0381 protein	2.6 2.6	3.7
	440357		Hs.20950	phospholysine phospholistidine inorganic	2.6	5.9
	424572) U= 04454	2,3-cyclic nucleotide 3 phosphodieste	2.5	6.1
	418338		2 Hs.84154 Hs.30868	neuronal pentraxin i nogo receptor	2.5	3.0
65	427658 410359		Hs.10631		2.5	6.3
05	449717		Hs.23954	cerebral cell adhesion molecule	2.5	4.5
	424458		Hs.1780	myelin associated glycoprotein	2.5	10.1
	450133				2.5	40.5
	428976	AL037824	Hs.19469		2.5	17.4
70	454293		Hs.13401		2.5 2.5	9.5 3.9
	408447		Hs.45080		2.5	7.1
	414683		Hs.76888		2.5	3.0
	422927		Hs.30142 Hs.23740		2.5	3.6
75	449568 454053				2.5	3.6
, ,	428495			0 hypothetical protein MGC10781	2.5	3.2
	431096				2.4	3.6
	45237	1 R40990	Hs.21658	ESTs	24	3.3
00	42499	7 AL138167			2.4 2.4	6.2 3.6
80	450310		Hs.94116		24	3.9
	45289				2.4	4.7
	43673 42193		Hs.27375 14 Hs.1440	gamma-aminobutyric acid (GABA) A recepto	24	3.1
	42133			9		

	439428 445255	AA835825 NM_014841	Hs.190490 Hs.12477	ESTs synaptosomal-associated protein, 91 kDa	24 24	3.0 8.1
	436420	AA443966	Hs.31595	ESTs	2.4	3.7
_	408822	AW500715	Hs.57079	Homo sapiens cDNA FLJ13267 fis, clone OV	24	3.0
5	451407	AA131376	Hs.343809	fibroblast growth factor 128	2.4 2.4	7.2 3.3
	419757 446100	AA773820 AW967109	Hs.63970 Hs.13804	ESTs hypothetical protein dJ462O23.2	24	3.6
	439199	R40373	Hs.26299	ESTs	2.3	9.5
	427627	R87582	Hs.179915	guanine nucleotide binding protein (G pr	2.3	5.6
10	45404B	H05626	Hs.6921	ESTs	2.3	9.9
	412675	AA460716	Hs.9788 Hs.114280	hypothetical protein MGC10924 similar to	2.3 2.3	3.3 6.7
	434811 431677	AW971205 AK000496	Hs.306989	ESTs hypothetical protein FLJ20489	2.3	3.1
	451386	AB029006	Hs.26334	spastic paraplegia 4 (autosomal dominant	2.3	3.1
15	447028	AJ973128	Hs.167257	brain link protein-1	2.3	5.6
	451050	AW937420	Hs.69662	ESTs	2.3 2.3	4,4 4.8
	437397 408838	AA349847 AI669535	Hs.4221 Hs.40369	hypothetical protein DKFZp761H039 ESTs	2.3	3.0
	408777	U71204	Hs.47626	Ric (Drosophila)-like, expressed in neur	2.3	3.8
20	453924	R49295	Hs.24886	ESTs	2.3	13.4
	422709	AA315331	Hs.153485	ESTs	2.3 2.3	4.4 3.3
	438911 439108	AF085841 AW163034	Hs.301920 Hs.6467	ESTs synaptogyrin 3	2.2	6.9
	420297	AI628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.2	4.1
25	404819			NM_002688*:Homo sapiens peanul (Drosophi	2.2	5.8
•	422544	AB018259	Hs.118140	KIAA0716 gene product	2.2 2.2	11.8 11.0
	433597 440152	AA708205 AB002376	Hs.100343 Hs.7006	ESTs KIAA0378 protein	2.2	14.2
	418375	NM_003081	Hs.84389	synaptosomal-associated protein, 25kD	2.2	82.9
30	409892	AW956113	Hs.7149	gb:EST368183 MAGE resequences, MAGD Homo	2.2	4.2
	425287	R88249	Hs.155524	peanut (Drosophila)-like 2	2.2 2.2	6.0 5.0
	433657 438703	A1244368 A1803373	Hs.8124 Hs.31599	PH domain containing protein in retina 1 ESTs	2.2	5.0 6.2
	428845	AL157579	Hs.153610	KIAA0751 gene product	2.2	6.7
35	417865	AW086059	Hs.6529	ESTs, Weakly similar to 178885 serine/th	2.2	3.5
	425897	AA935315	Hs.48965	Homo sapiens cDNA: FLJ21693 fis, clone C	2.2	3.2
	419271	N34901 R13209	Hs.238532 Hs.21413	ESTs solute carrier family 12, (potassium-chl	2.2 2.2	7.5 7.3
	448548 439415	F05538	Hs.4273	ESTs	2.2	31.3
40	415170	R44386	Hs.164578	ESTs	2.2	10.9
	423641	AL137256	Hs.130489	ATPase, aminophospholipid transporter-li	2.1	6.2
	443728	AI083876	Hs.148383	ESTs	2.1 2.1	4.1 5.7
	452108 429037	AW135982 X81895	Hs.203013 Hs.194765	hypothetical protein FLJ12748 H.sapiens GENX-5624 mRNA, 3' UTR	2.1	7.1
45	418900	8E207357	Hs.3454	KIAA1821 protein	2.1	4.3
	421268	AI126821	Hs.30514	ESTs	2.1	4.2
	446372	A8020644	Hs.14945	long fatty acyl-CoA synthetase 2 gene	2.1 2.1	15.6 6.5
	425741 450214	AF052152 BE439763	Hs.159412 Hs.227571	Homo sapiens clone 24628 mRNA sequence regulator of G-protein signalling 4	2.1	3.3
50	452738	AL133800	Hs.7086	hypothetical protein MGC12435	2.1	3.5
	447877	AI435184	Hs.164252	ESTs	2.1	5.1
	422421	AA325138	Hs.235873	hypothetical protein FLJ22672	2.1 2.1	8.3 4.2
	432882 410631	NM_013257 AA086469	Hs.279696 Hs.47171	serum/glucocorticoid regulated kinase-li ESTs	2.1	5.8
55	407808	AA663559	Hs.279789	histone deacetylase 3	2.1	5.7
-	424379	Z42034	Hs.93597	cyclin-dependent kinase 5, regulatory su	2.1	3.2
	448410	AK000227	Hs.21126	hypothetical protein FLJ20220	2.1 2.1	3.0 6.9
	433932 425130	AW954599 AA448208	Hs.169330 Hs.99163	neuronal protein ESTs	2.1	3.1
60	402027	77770200	113.33100	Target Exon	2.0	3.5
	435191	R15912	Hs.4817	Homo sapiens clone 24461 mRNA sequence	2.0	7.5
	420547	AF155140	Hs.98738	gonadotropin-regulated testicular RNA he	2.0 2.0	10.7 6.0
	404541 420050	AL118615	Hs.94653	NM_030795:Homo sapiens stathmin-like 4 (neurochondrin	2.0	6.5
65	417868	AI078534	Hs.122592		2.0	5.6
	416602	NM_006159	Hs.79389	nel (chicken)-like 2	2.0	3.2
	436315	BE390513	Hs.27935	hypothetical protein MGC4837	2.0	4.2
	439340	AB032436	Hs.6535 Hs.30875	brain-specific Na-dependent inorganic ph ESTs	2.0 2.0	6.3 4.2
70	429900 437762	AA460421 T78028	Hs.154679		2.0	4.6
. •	425172	AA447729	Hs.12714	ESTs	2.0	3.1
	419587	\$62907	Hs.91343	gamma-aminobutyric acid (GABA) A recepto	20	3.1
	451734	NM_006176		neurogranin (protein kinase C substrate, Homo sapiens KIAA0420 mRNA, complete cds	2.0 2.0	4.9 4.3
75	423603 438277	AB007880 AL022326	Hs.129883 Hs.6139	synaptogyrin 1	2.0	3.4
	423767	H18283	Hs.132753	F-box only protein 2	2.0	3.2
	434933	R91095	Hs.4276	KIAA1701 protein	2.0	6.1 4.6
	426575	M74826	Hs.170808	glutamate decarboxylase 2 (pancreatic is	2.0	4.0
80	TABLE	188:				

TABLE 188: Pkey: CAT number: Accession:

Unique Eos probeset identifier number Gene cluster number Genbant accession numbers

	Pikey		Accession	045 4 4 4 050000 A 4 045044											
	408065 415527	103646_1 1539393_1	AW954272 AUU E11624 743212	3154 AA059300 AA046911 H08936 R56332 H09256 R52303 R13075											
5	415666	1543492 1					T00054 D4	45746 AMMERION A ARENOTA							
•	418512	176394_1	AW498974 T093	1 H72694 F20990 R08580 332 R58460 AA350990 T33786 T30936 AA35090	5 T08592 T09274 AAZ	24297 D54	9/8 (0832) KI	15340 A44533 100 AA330074							
	440000	470700 4	AW890649 165754 AA2298	E7 AA 220668											
	418866 420111	179788_1 190755_1							40						
10	422890	222707_1			5 AW004030 BE50253	0 Z25032	AA805324 AA44	49241 Al651825 Al264863 AW1969 5646 D01142 H17038 AW162343	118						
		-	AA948267 AI95	1 AW572911 AA449369 H17037 K19003 A163230 3735 A1263703 AA319159 AW964436 A1903440 /	AVV5941/1 AIB6/44/ A	WYZU4U7 1	AW950110 C15	3010 001142 1111 030 711 102040							
		******	T87230 AI3	AL120536 AA330218 AW961552 N47159											
	423731 424572	231466_1 24097_1			76814 F12085 BE2552	64 BE251	393 T65248 AA	380585 AA380465 BE408684							
15	424372	24007_1	AA459037 AW4	0 R18721 AW896146 AW869320 AR192302 AR1 198869 AA776107 BE274289 D45269 M61958 AA	.378818 AW663180 AV	N672958 H	108611 M78164	(BE393721 AA348660 K36303							
			AW498662 AAG	019090 AA001	104800 AA452368 N90	2604 A1341	345 AW298800	0 AA724961 AA931158 AI741227							
	424945	245223_1	AI221919 Z199	67 AA348780 AW964077 AW 166028 BES401551 2626 D81263 D53937 D52496 AA974487 AW043	854 N50483 Z39997 A	492961 A	361526 F04002	2 AA452141 T23551 A1472655							
			**********	•											
20	426919	273507_1	AL041228 D82	1 004 D61361 Al203314 Al990307 AW900295 Al01	8308 AW087473 AW1	83530 AA3	193346 H50U55	AA935601							
	433670	372721_1	AA604405 BEC	405 BE062234 AW748386 174 A1114549 R36464 R36465											
	433921 433940	377350_1 37787_1	H05129 N6343	3 A1651350 AA984734 A1368716 N40915 A19897	05 F09042 T03905 R8	8588 AF 11	2220								
	436773	426857_1	AWN78629 AIR	57375 N64357 AA731069											
25	446692	689623_1	Z44514 AI3520	997 AI803984 AW235923 AW196558 AI954637 A	1336983										
	TABLE 18	^.													
	Pkey:		ue number corre:	sponding to an Eos probeset		Nb a	i al " aufoan les éh	he subsection entitled The DNA							
••	Ref:	Coni	ionco emirra Th	e 7 digit numbers in this column are Genbank Ide	ntifier (GI) numbers.	Dunnam, e	(a). Telefs to ut	ie publication entraco into prov							
30	Od-	sequ	ence of human c	teromosome 22° Dunham, et al. (1999) Nature 402 from which exons were predicted.	400-455.										
	Strand: Nt. positio	o. Indic	ates nucleotide (ositions of predicted exons.											
		•••													
25	Pkey	Ref 9188605		Nt_position 24746-24872.25035-25204											
35	400844 402027	7622350		51645-51888,52917-53006											
	404541	8318559		100150 100001	PAYE 4717A 17707 17	200 17520	18261-18367 1	18443.18578							
	404819	4678240		103456-103664 16223-16319,16427-16513,16736-16859,16941- 5495-5655,6077-6241,6495-6692	1/0/3,1/1/0-1/20/,1/	303-17323	,10201-10007,	19710 10010							
40	405560 405819	183148 4007557	Plus Plus	2830-2967											
70	406311	9211559	Minus	137114-139033											
	=======================================	AL ADOLIT 25	CONG ENDICUE	D GENES SIGNIFICANTLY DOWN-REGULATED	IN GLIOBLASTOMA	COMPARE	D TO NORMA	L ADULT CNS							
	Table 19	A lists about 356	CNS-enriched	enes significantly down-regulated in glioblastoma	compared to normal a	dult CNS ti	ssues. These v	were selected from 59680 probesets	iON Alwas						
45	the Affyrr	netrix/Eos Hu03	GeneChip array	such that the ratio of "average" normal CNS to av	terage groundstorner w	& namanti	e amoonst vario	ous tumor samples. To enrich for C	NS						
	set to the	85" percentile	amongst various	normal CNS tissues. The "average" global stoma to "average" non-CNS normal adult tissues was to	calculated to be greater	r than or ea	qual to 3. The	'average" CNS level was set to the 8	35 h						
	specinc g nercentil	genes, une rauo i e amonost vario	us CNS tissues.	to "average" non-CNS normal adult tissues was the "average" normal non-CNS adult tissue level	was set to the 95th per	centile am	ongst various no	on-CNS normal tissues. In order to							
	remove (gene-specific ba	ckground levels	of non-specific hydricization, the 10" percentile va	lue amongst non-malig	nant tissue	s was subtracte	ed trom both the numerator and me							
50		ator before the	ratios were evalu	ated. et identifier number											
	Pkey: ExAccn:		ique cos procese emolar Accessior	n number, Genbank accession number											
	Unigene		igene number	•											
	Unigene	Title: Un	igene gene title	N-t				•							
55	R1: R2:	Ra Da	tio of CNS to Glid	N-CNS NORMAL ADULT TISSUES											
	ru.	100				04	R2								
	Pkey	ExAcon	UnigenelD	Unigene Title		R1 24.8	10.5								
60	425489 410330		Hs.1905 Hs.159425	profactin ESTs		23.4	23.4								
00	430538		Hs.242821	differentiation-associated Na-dependent		22.6	22.6 6.0								
	417275		Hs.295449	parvalbumin		22.4 21.8	21.8								
	428505 408040		Hs.2281 Hs.22905	chromogranin B (secretogranin 1) ESTs, Wealdy similar to RHG6_HUMAN RHO-0	3	19.4	19.4								
65	435145		Hs.116631	ESTs		18.5	3.8								
	407039	X00368		gb:Human prolactin gene 5' region.		18.1 16.8	18.1 16.8								
	409263			ESTs Homo sapiens mRNA; cDNA DKFZp761G1111	tf.	15.1	15.1								
	432298 424645			KIAA0535 gene product	•	15.1	15.1								
70	416018			proprotein convertase subtilisin/kexin t		14.0 13.9	14.0 8.0								
	405560			hypothetical protein FLJ20628		13.8	13.8								
	452022 413324		0 Hs.293875 Hs.75294	ESTs corticotropin releasing hormone		13.2	13.2								
	411498			ecotropic viral integration site 2A		12.9	19.4								
75	423449	A1497900		ESTs cyclic AMP-regulated phosphoprotein, 21		12.4 12.0	14.5 12.0								
	43394		Hs.65248	dynein, cyloplasmic, intermediate polype		11.5	11.5								
	41065 44907			KIAA1576 protein		11.0	16.1								
00	41063	5 D58863	Hs.334372			11.0 10.7	6.6 10.7								
80	45316		Hs.32042 7 Hs.4290	æpartoacytæe (aminoacytæe 2, Canavan ESTs		10.4	10.4								
	41716 42003		Hs.292590	ESTs .		10.4	10.4								
	41329					10.0	10.0								
				•	201										

					0.0	9.8
	418207	C14685	Hs.34772	ESTs ESTs	9.8 9.6	9.0 8.9
	417175 444330	R44558 Al597655	Hs.94002 Hs.49265	ESTs	9.1	9.1
	427322	AK002017	Hs.176227	hypothetical protein FLJ11155	8.9	8.9
5	429096	AB011106	Hs.196012	KIAA0534 protein	8.6	8.6
	428652	AA584272	Hs.335224	transmembrane protein with EGF-like and	8.6	8.6
	419347	C15944	Hs.90005	superiorcervical ganglia, neural specifi	8.6	22.2
	410309	BE043077	Hs.278153	ESTs	8.5	8.5
	416851	AW963951	Hs.85618	ESTs	8.5	8.5
10	427061	AB032971	Hs.173392	KIAA1145 protein	8.4	8.4
	400438	AF185611	Hs.115352	Target	8.3	5.1
	440209	H05049	Hs.247837	neurexin 3	8.2	18.7
	422756	AA441787	Hs.119689	glycoprotein hormones, alpha polypeptide	8.1 8.1	5.8 8.1
15	435648	H24347	Hs.27524	ESTs	8.0	8.0
15	429470	AI878901	Hs.203862	guanine nucleotide binding protein (G pr ATPase, Ca transporting, plasma membrane	8.0	8.0
	416133 408814	NM_001683 N62499	Hs.89512 Hs.176227	hypothetical protein FLJ11155	7.9	8.6
	430004	U27768	Hs.227571	regulator of G-protein signalling 4	7.9	15.7
	436427	AI344378	Hs.143399	ESTs	7.8	7.8
20	434367	AB020700	Hs.3830	KIAA0893 protein	7.8	5.6
	429876	AB028977	Hs.225974	KIAA1054 protein	7.8	16.8
	441005	Z41305	Hs.303172	Homo sapiens mRNA; cDNA DKFZp547G133 (fr	7.7	7.7
	442023	AI187878	Hs.144549	ESTs	7.7	5.6
	429033	NM_007374	Hs.194756	sine oculis homeobox (Drosophila) homolo	7.6	5.5
25	450642	R39773	Hs.7130	copine IV	7.6	5.6
	437073	A1885608	Hs.94122	ESTs	7.5	7.5
	441264	AA927170	Hs.23290	ESTs	7.3	7.3
	424153	AA451737	Hs.141496	MAGE-like 2	7.3	5.1 7.2
20	450474	AW872844	Hs.117494	ESTs	7.2 7.2	7.2 7.2
30	450715	AI266484	Hs.31570	ESTs, Wealdy similar to KIAA1324 protein	7.1	4.8
	415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	7.0	7.0
	423003 433921	AL120077 AA618174	Hs.122967	kelch (Drosophila)-like 2 (Mayven) ab:no14f01.s1 NCI_CGAP_Thy1 Homo sapiens	7.0	7.0
	435321	NM_000939	Hs.1897	prooplomelanocortin (adrenocorticotropin	6.9	6.1
35	457012	R41480	Hs.302754	ESTs	6.9	6.9
55	445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	6.9	6.9
	433558	AA833757	Hs.201769	ESTs, Weakly similar to T24435 hypotheti	6.9	6.9
	409031	AA376836	Hs.288856	ESTs	6.8	6.8
	453590	AF150278	Hs.33578	KIAA0820 protein	6.6	22.3
40	450181	H05254	Hs.201198	ESTs	6.6	7.2
	425580	L11144	Hs.1907	galanin	6.5	3.5
	445279	R41900	Hs.22245	ESTs	6.4	6.4
	428414	AL049980	Hs.184216	DKFZP564C152 protein	6.4	6.4
45	434104	AF116691	Hs.116459	hypothetical protein PRO2198	6.4	4.0 3.0
45	443244	AI457235	Hs.166479	ESTs	6.3 6.2	9.8
	447750	AI422234	Hs.143434	contactin 1	6.0	6.0
	415114	D60468	Hs.94181	ESTs	5.9	3.9
	450600	BE079478 BE041526	Hs.24880 Hs.31746	hypothetical protein DKFZp547F072	5.9	7.7
50	444458 448958	AB020651	Hs.22653	KIAA0844 protein	5.9	5.9
30	447138	AJ439112	Hs.93828	ESTs, Weakly similar to 2109260A 8 cell	5.8	5.8
	414545	AA149287	Hs.76605	ESTs	5.8	3.6
	410389	AW954049	Hs.8177	ESTs. Weakly similar to PIHU86 salivary	5.6	9.6
	450590	AI701507	Hs.273740	ESTs	5.6	3.8
55	408428	NM_014787	Hs.44896	DnaJ (Hsp40) homotog, subfamily B, membe	5.6	5.6
	442026	AI243749	Hs.8074	brain-specific angiogenesis inhibitor 3	5.5	6.5
	450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophi	5.4	5.4
	414699	AI815523	Hs.76930	synuclein, alpha (non A4 component of am	5.3	4.5
۲0	438202	AW169287	Hs.22588	ESTs	5.3	5.3 5.3
60	448605	AL109678	Hs.21597	Homo sapiens mRNA full length insert cDN	5.3 5.3	3.8
	418866	T65754	41- 470075	gb:yc11c07.s1 Stratagene lung (937210) H	5.2	5.2
	448786	BE048842	Hs.179075		5.2	11.5
	406311	A12020C4	Un 47249	NM_021979*:Homo sapiens heat shock 70kD ESTs, Highly similar to similar to Cdc14	5.2	3.3
65	443682 415666	AI383061 H72693	Hs.47248	gb:yu03c11.r1 Soares fetal liver spleen	5.2	5.2
UJ	416101	R24854	Hs.268806	ESTs	5.2	3.3
	428508	BE252383	Hs.184668		5.2	4.1
	419318	AW969742	Hs.291005		5.2	3.1
	439238	N47305	Hs.302161	ESTs	5.1	5.3
70	446353	AI290919	Hs.153661		5.1	5.1
	412049	N53437	Hs.18268	adenylate kinase 5	5.1	10.7
	437331	AL353933	Hs.21710	hypothetical protein DKFZp761G0313	5.1	5.1
	413988	M81883	Hs.324784		5.1	5.1
75	408068	AW148652	Hs.167398		5.0	5.0
75	414631	AW970130	Hs.65406	ESTs	4.9	4.9 4.9
	418527	AA450386	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	4.9 4.9	4.9 4.9
	425073	W39609	Hs.22003	solute carrier family 6 (neurotransmitte	4.9	3.9
	427224	AL135554 AA595802	Hs.101937 Hs.33410	sine ocutis homeobox (Drosophila) homolo ESTs, Weakly similar to T17279 hypotheti	4.8	4.8
80	433516 427287	NM_014903			4.8	4.8
30	447252	R90916	Hs.12449	Homo sapiens transmembrane protein HTMP1	4.8	3.2
	424932	R14070	Hs.315369		4.7	10.2
	419643	F06066	Hs.91791	chromosome 11 open reading frame 25	4.7	4.7

					4,7	3.8
	414949	C15314 NM_014796		ESTs KIAA0748 gene product	4.7	4.7
	453534 430537	X62692	Hs.2593	phosphodiesterase 68, cGMP-specific, rod	4.6	4.6
_	453431	AF094754	Hs.32973	glycine receptor, beta	4.6	4.6 4.6
5	453302	NM_000838	Hs.32945	glutarnate receptor, metabotropic 1 Homo sapiens cDNA FLJ13182 fis, clone NT	4.6 4.6	4.6 3.0
	447104 418202	R19085 N48521		KIAA1708 protein	4.6	5.8
	419191	U17195		A kinase (PRKA) anchor protein 6	4.5	4.5
10	459080	AW192083		ESTs	4.5 4.4	13.5 11.2
10	451783	R42554	Hs.210862 Hs.98849	T-box, brain, 1 ESTs, Moderately similar to AF161511 1 H	4.4	3.2
	421952 451050	AA300900 AW937420		ESTs	4.4	4.4
	423728	AW891294		solute carrier family 4, sodium bicarbon	4.4	7.9
1.5	447746	AW015920		ESTs	4.3 4.3	9.9 4.3
15	451301 452381	A1769514 H23329	Hs.209890 Hs.290880	ESTs, Wealdy similar to ALU1_HUMAN ALU S	4.3	4.3
	433109	N58907	Hs.162430	EST	4.3	3.9
	412155	R38167	Hs.12449	Homo sapiens transmembrane protein HTMP1	4.3	27.9 4.1
20	426365	AA376667	Hs.10283	RNA binding motif protein 88	4.3 4.2	4.2
20	423589	AA328082 Al885537	Hs.209569 Hs.27172	ESTs Moderately similar to PC4259 ferri	4.2	3.9
	432453 420489	AA815089	Hs.193513	ESTs	4.1	4.1
	427457	AW779105	Hs.164682	ESTs	4.1	11.1 4.1
25	408206	AF041853	Hs.43670	kinesin family member 3A	4.1 4.1	4.1
25	433803 407868	A1823593 NM_000950	Hs.27688 Hs.40637	ESTs proline-rich Gta (G-carboxyglutamic acid	4.1	3.3
	448117	H49129	Hs.172982	ESTs	4.1	4.1
	442106	AW205881	Hs.326728	ESTS	4.1	3.2 3.2
20	450757	BE081050	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	4.0 4.0	6.2
30	442042	Al990506 F12832	Hs.8077 Hs.3610	Homo sapiens mRNA; cDNA DKFZp547E184 (fr ESTs	4.0	4.0
	458694 452197	AW023595	Hs.232048	ESTs	4.0	4.0
	448583	NM_015239	Hs.21542	KIAA1035 protein	4.0	4.0 7.0
25	418940	H17739	Hs.288513	Human DNA sequence from clone RP5-899C14	3.9 3.9	3.9
35	442412 440293	R77677 AI004193	Hs.346644 Hs.22123	ESTs ESTs	3.9	3.9
	433670	AA604405	113.22120	gb:no87h09.s1 NCI_CGAP_AA1 Homo sapiens	3.9	3.9
	459697	AA406062	Hs.98002	ESTs	3.9	5.4
40	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	3.9 3.9	3.3 3.9
40	426054	U12431 W67883	Hs.166109 Hs.137476	ELAV (embryonic lethal, abnormal vision, paternally expressed 10	3.8	5.4
	424001 442676	A1733585	Hs.130897	ESTs	3.8	3.8
	410240	AL157424	Hs.61289	synaptojanin 2	3.8	4.6
45	409339	AB020686	Hs.54037	ectonucleotide pyrophosphatase/phosphodi	3.7 3.7	3.6 3.7
45	434998	AW975157	Hs.26037 Hs.125304	ESTs ESTs	3.7	8.3
	439450 455364	R51613 H72176	Hs.4273	hypothetical protein FLJ13159	3.7	4.9
	400844		1.0.1.0	NM_003105":Homo sapiens sortilin-related	3.7	3.1
50	456765	AI497900	Hs.33067	ESTs	3.7 3.6	3.7 3.6
50	452667	T87219	Hs.13219	ESTs PC4 and SFRS1 interacting protein 1	3.6	3.6
	436773 453220	AW078629 AB033089	Hs.32452	Homo sapiens mRNA for KIAA1263 protein,	3.6	19.9
	432149	AW614326	Hs.133483	ESTs, Weakly similar to T34549 probable	3.6	12.2
66	408119	W26213	Hs.101672		3.6 3.6	3.6 3.6
55	449093	AB035356 U07616	Hs.22998 Hs.173034	neurexin 1 amphiphysin (Stiff-Mann syndrome with br	3.6	15.3
	426968 410011	AB020641	Hs.57856	PFTAIRE protein kinase 1	3.6	10.0
	442738	AW002370	Hs.131055		3.5	3.5 4.9
۲۸	451032	W03692	Hs.323079		3.5 3.5	3.5
60	449117	AW449310 AF090116	Hs.210262 Hs.79348		3.5	12.5
	416490 412266		Hs.26133	ESTs	3.5	30.9
	452311	AW304029			3.5 3.5	3.5 38.6
65	425649		Hs.158540		3.5 3.4	3.4
05	410224 451516		Hs.150208 Hs.12024	ESTs	3.4	6.3
	400098		10.12021	Eos Control	3.4	3.4
	424918	R13982	Hs.169309		3.4 3.3	5.3 3.8
70	452238		Hs.345757		. 3.3	3.3
70	417063 443992		Hs.45061 3 Hs.32292		3.3	13.1
	412453		Hs.75236	ESTs	3.3	3.3
	450561		Hs.25909	ESTs	3.3	3.3
75	415527	F11624	t the enter	gb:HSC2ZD101 normalized infant brain cDN	3.3 3.3	3.3 3.3
75	427386 427346		1 Hs.6727 Hs.12741	ESTs 6 synaptojanin 1	3.2	20.1
	423346 431342			ESTs	3.2	8.0
	448533	3 AL119710	Hs.21365	nucleosome assembly protein 1-like 3	3.2 3.2	9.6 3.2
80	442879			syntaxin binding protein 3 Homo sapiens cDNA FLJ12965 fis, clone NT	3.2 3.2	3.2
٥٥	417284 429477		Hs.10724 Hs.6658	ESTs	3.2	3.2
	41034			ESTs, Weakly similar to \$47072 finger pr	3.2	3.2
	427317		5 Hs.17578	0 KIAA1032 protein	3.2	5.3

	400020	A A 131434	Un 220020	ECT-	3.2	3.2
	408039 428976	AA131424 AL037824	Hs.336636 Hs.194695	ESTs res homolog gene family, member I	3.2	17.4
	420297	AI628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.2	4.1
_	453919	AW959912	Hs.7076	KIAA1705 protein	3.2	3.2
5	428963	AW382682	Hs.258208	Homo sepiens, clone MGC:15606, mRNA, com	3.2	3.3
	423829	R44107	Hs.240905	ESTs	3.1 3.1	4.4 3.1
	424087 419852	N69333 AW503756	Hs.143434 Hs.286184	contactin 1 hypothetical protein dJ551D2.5	3.1	4.1
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	3.1	43.2
10	422234	AF119818	Hs.113287	discs, large (Drosophila) homolog-associ	31	3.1
	446692	Z44514		Homo sapiens mRNA for KIAA1763 protein,	3.1	33.0
	437117	AL049256	Hs.122593	ESTs	3.1	3.8
	405819	AW044058	No 22570	NM_002578:Homo sapiens p21 (CDKN1A)-acti	3.1 3.1	13.5 13.4
15	452752 416220	N49776	Hs.33578 Hs.170994	KIAA0820 protein hypothetical protein MGC10946	3.1	4.5
1.5	437380	AL359577	Hs.112198	Homo saplens mRNA; cDNA DKFZp547M073 (fr	3.0	3.8
	428001	H97428	Hs.219907	ESTs, Moderately similar to Transforming	3.0	5.9
	445725	AK000956	Hs.13209	hypothetical protein FLJ10094	3.0	3.0
20	447673	AI823987	Hs.182285	ESTs	3.0 3.0	3.0 3.0
20	427283	AL119796 T06532	Hs.174185 Hs.287709	ectonucleotide pyrophosphatase/phosphodi Homo sepiens cDNA: FLJ/22674 fis, clone H	3.0	3.0
	424724 408547	AA574291	Hs.57837	ESTs	3.0	4.0
	433315	R96754	Hs.239706	GRB2-associated binding protein 1	3.0	3.1
	439274	AF086092	Hs.48372	ESTs	3.0	18.3
25	410765	AI694972	Hs.66180	nucleosome assembly protein 1-like 2	3.0	8.0
	458268	AA428403	Hs.106131	ESTs	3.0 3.0	3.9 5.6
	424641 441869	AB001106 NM_003947	Hs.151413 Hs.8004	glia maturation factor, beta huntingtin-associated protein interactin	3.0	14.9
	442593	R39804	Hs.31961	ESTs	2.9	6.7
30	426380	AI291267	Hs.149990	ESTs	2.9	6.9
	428536	Al143139	Hs.2288	visinin-like 1	2.9	22.1
	417417	F05745	Hs.89512	ATPase, Ca transporting, plasma membrane	29	17.1
	411379	AI816344	Hs.12554	ESTs, Weakly similar to NPL4_HUMAN NUCLE	2.9 2.9	11.2 5.3
35	422414	AW875237	Hs.13701 Hs.295605	ESTs	2.9	3.9
33	428186 419518	AW504300 U79289	Hs.90798	mannosidase, alpha, class 2A, member 2 Human clone 23695 mRNA sequence	2.9	3.6
	426919	AL041228	113.507.50	ELAV (embryonic lethal, abnormal vision,	2.9	9.0
	446544	AI631932	Hs.7047	ESTs, Weakly similar to Unknown [H.sapie	2.8	12.4
40	422411	AW749443	Hs.22511	ESTs	2.8	12.0
40	416874	H98752	Hs.42568	ESTs	2.8	6.0
	448902	Z45998	Hs.22543	Homo sepiens mRNA; cDNA DKFZp761I1912 (f	2.8 2.8	21.8 4.7
	430456 429859	AA314998 NM_007050	Hs.241503 Hs.225952	hypothetical protein protein tyrosine phosphatase, receptor t	2.8	5.1
	429656	X05608	Hs.211584	neurofilament, light polypeptide (68kD)	2.8	13.1
45	437948	AA772920	Hs.303527	ESTs	2.8	24.8
	440105	AA694010	Hs.6932	Homo sapiens clone 23809 mRNA sequence	2.8	8.2
	414931	AK000342	Hs.77646	Homo sapiens mRNA; cDNA DKFZp761M0223 (f	2.8 2.8	3.4 4.4
	416530	U62801	Hs.79361 Hs.335933	kallikrein 6 (neurosin, zyme) ESTs	2.8	3.5
50	446574 422890	AI310135 Z43784	ns.333333	ankyrin 3, node of Ranvier (ankyrin G)	2.8	3.6
-	410711	AB002316	Hs.65746	KIAA0318 protein	2.7	6.1
	422980	N46569	Hs.76722	CCAAT/enhancer binding protein (C/EBP).	2.7	45.2
	408554	AA836381	Hs.315111	nuclear receptor co-repressor/HDAC3 comp	2.7	3.7
55	434460	AA478486	Hs.3852	KIAA0368 protein	2.7 2.7	4.8 10.5
33	431988 447163	AC002302 AW292770	Hs.77202 Hs.5542	protein kinase C, beta 1 OnaJ (Hsp40) homolog, subfamily C, membe	2.7	3.4
	437924	A1935344	Hs.164118		2.6	3.2
	424945	AJ221919	,	hypothetical protein FLJ10582	2.6	30.5
	425984	AW836277	Hs.165636	hypothetical protein DKFZp761C07121	2.6	29.3
60	447761	AF061573	Hs.19492	protocadherin 8	2.6	6.3 4.2
	425138	H08849	Hs.167464	glutamate receptor, ionotropic, N-methyl ESTs	26 26	6.8
	436568 408065	H12049 AW954272	Hs.91564	gb:EST366342 MAGE resequences, MAGC Homo	26	5.6
	430287	AW182459	Hs.125759		2.6	7.6
65	408777	U71204	Hs.47626	Ric (Drosophila)-like, expressed in neur	2.6	3.8
	420173	AA256151	Hs.22999	ESTs	2.6	4.1
	429550	AW293055	Hs.119357		2.6	6.4
	438068	AI927209	Hs.306210		2.6 2.6	5.1 7.3
70	424264 432809	D80400 AA565509	Hs.239388 Hs.131703		2.6	9.9
, ,	407886	AW969688	Hs.100826		2.5	20.2
	445225	AI216555	Hs.202398		2.5	5.5
	415257	F03016	Hs.27513	ESTs	2.5	8.6
75	423135	N67655	Hs.26411	ESTs	2.5	8.2 7.5
75	438283	AI458931	Hs.37282	ESTs ESTs Moderately similar to PCA259 ferri	2.5 2.4	7.5 3.6
	454053	AW023006 Al034467	Hs.27172 Hs.34650	ESTs, Moderately similar to PC4259 ferri ESTs	2.4	7.6
	443150 429956	AJ374651	Hs.22542	ESTs	24	3.2
	428392	H10233	Hs.2265	secretory granule, neuroendocrine protei	2.4	42.3
80	437268	A1754847	Hs.227571		2.4	14.0
	426529	AF090100	Hs.170241		2.4 2.4	5.1 3.2
	430347 422949	NM_002039 AA319435	Hs.239706	GRB2-associated binding protein 1 gb:EST21657 Adrenal gland tumor Horno sap	2.4 2.4	7.4
	442349			ATTENDED TO THE PROPERTY OF THE PARTY OF THE	•	

					•	40.0
	451952	AL120173		ESTs 2	2.4 2.4	19.2 28.5
	434277	X77748	Hs.3786	glutamate receptor, metabotropic 3	2.4	3.0
	422927 425121	AW247388 AI797511		calcium binding protein 1 (calbrain) synaptotagmin I	2.4	3.9
5	435059	Z45270		hypothetical protein FLJ22672	2.4	4.8
•	446377	AW014022		ESTs	2.4	3.3
	452371	R40990		ESTs	2.4	3.3
	419103	Z40229		hypothetical protein FLJ23033	2.4 2.4	8.4 3.0
10	427658 446100	H61387 AW967109		nogo receptor hypothetical protein dJ462O23.2	2.3	3.6
10	439607	BE540565		ESTs	2.3	5.6
	412949	Al471639		ESTs	2.3	3.7
	419757	AA773820	Hs.63970	ESTs	2.3	3.3 12.2
1.5	410037	AB020725	Hs.58009	KIAA0918 protein	2.3 2.3	3.1
15	451386	A8029006 AA332277	Hs.26334 Hs.57691	spastic paraplegia 4 (autosomal dominant cadherin 18, type 2	23	5.5
	409953 419629	AB020695	Hs.91662	KIAA0888 protein	2.3	13.4
	434792	AA649253	Hs.132458	ESTs	2.3	3.8
	429006	AA443143	Hs.50929	hypothetical protein FLJ13842	2.3	6.6
20	445194	AI215667	Hs.175044	ESTs	23 23	3.1 3.6
	422491	AA338548	Hs.117546	neuronatin KIAA0237 gene product	2.3	27.4
	415734 434933	NM_014747 R91095	Hs.78748 Hs.4276	KIAA1701 protein	2.2	6.1
	424922	BE386547	Hs.217112	hypothetical protein MGC10825	2.2	3.7
25	426325	D28114	Hs.169309	myelin-associated oligodendrocyte basic	2.2	81.1
	424140	Z48051	Hs.141308	myelin oligodendrocyte glycoprotein	2.2 2.2	56.0 3.9
	418410	AA811441	Hs.107393	chromosome 3 open reading frame 4 RAB33A, member RAS oncogene family	2.2	10.6
	409746 439239	NM_004794 Al031540	Hs.56294 Hs.235331	ESTs	2.2	49.5
30	450310	N62341	Hs.94116	ESTs	2.2	3.6
20	453924	R49295	Hs.24886	ESTs	2.2	13.4
	411666	AF106564	Hs.71346	neurofilament 3 (150kD medium)	2.2 2.2	6.6 5.8
	404819		11- 027/0	NM_002688*:Homo sapiens peanut (Drosophi	2.2	3.6
35	449568	AL157479 N34901	Hs.23740 Hs.238532	KIAA1598 protein ESTs	2.2	7.5
55	419271 424474	AA308883	Hs.148680	calcyon; D1 dopamine receptor-interactin	2.2	3.6
	438208	AL041224	Hs.65379	ESTs	2.2	5.8
	424458	M29273	Hs.1780	myelin associated glycoprotein	2.2	10.1
40	421790	AW896201	Hs.22654	sodium channel, voltage-gated, type I, a	2.2 2.1	4.1 4.2
40	432882	NM_013257	Hs.279696 Hs.93485	serum/glucocorticoid regulated kinase-li Homo sapiens mRNA; cDNA DKFZp761D191 (fr	2.1	21.4
	419863 449277	AW952691 AA001064	Hs.43670	ESTs	2.1	8.5
	420156	AW449258	Hs.6187	ESTs	2.1	12.5
	452738	AL133800	Hs.7086	hypothetical protein MGC12435	2.1	3.5
45	410366	AI267589	Hs.302689	hypothetical protein	2.1 2.1	10.4 3.4
	452106	AI141031	Hs.21342	ESTs DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	21	9.4
	413409 423641	AI638418 AL137256	Hs.1440 Hs.130489	ATPase, aminophospholipid transporter-li	2.1	6.2
	410909	AW898161	Hs.53112	ESTs, Moderately similar to ALU8_HUMAN A	2.1	12.5
50	410631	AA086469	Hs.47171	ESTs	2.1	5.8
	412675	AA460716	Hs.9788	hypothetical protein MGC10924 similar to	2.1 2.1	3.3 11.5
	448299	AA497044	Hs.20887 Hs.6818	hypothetical protein FLJ10392 ESTs	2.1	9.3
	444124 408950	R43097 AA707814	Hs.14945	long fatty acyl-CoA synthetase 2 gene	2.1	8.5
55	432736	AA788898	Hs.179902		2.1	4.0
-	429024	A1652297	Hs.119302		21	3.7
	420071	AB028985	Hs.94806	ATP-binding cassette, sub-family A (ABC1	2.1 2.1	5.1 3.0
	408822 424790	AW500715 AL119344	Hs.57079 Hs.13326	Homo sapiens cDNA FLJ 13267 fis, clone OV ESTs, Weakly similar to 2004399A chromos	2.1	23.1
60	426814	AF036943	Hs.172619		2.1	14.2
•	425130		Hs.99163	ESTs	2.1	3.1
	449714	AB033015	Hs.23941	KIAA1189 protein	20	7.5 6.9
	439108		Hs.6467	synaptogyrin 3	2.0 2.0	10.2
65	415669 435040		5 Hs.78589 Hs.152825	serine (or cysteine) proteinase inhibito ESTs	2.0 ·	4.7
05	440152		Hs.7006	KIAA0378 protein	2.0	14.2
	445102			ESTs	2.0	19.2
	436734		Hs.273758		2.0	4.7
70	437414			hypothetical protein DKFZp547C176	2.0 2.0	6.4 7.9
70	418512		Hs.32156	diacytglycerol kinase, zeta (104k0) KIAA1394 protein	2.0	5.7
	453169 420050		Hs.94653		2.0	6.5
	429900		Hs.30875	ESTs	2.0	4.2
	432447	X92681	Hs.2998	contactin 2 (axonal)	2.0	4.1
75	431677		Hs.306989		2.0 2.0	3.1 10.7
	452856		Hs.30881 Hs.21754		2.0	7.2
	448681 453754				2.0	3.4
	422544			0 KIAA0716 gene product	2.0	11.8
80	416836	D54745	Hs.80247	cholecystokinin	2.0	6.8
	454048		Hs.6921	ESTs 2. Homo senions clone 24628 mRNA sequence	2.0 2.0	9.9 6.5
	425741	AF052152	Hs.15941	2 Homo sapiens clone 24628 mRNA sequence	2.0	0.0

	74DLC 100.								
	TABLE 198: Pkey:		ue Eos probeset	identifier number					
	CAT number		e cluster number						
_	Accession:		bank accession r	umbers					
5									
		CAT Number		207454 4 4050700 4 4045044					
	408065	103646_1 1539393_1		003154 AA059300 AA046911 12 H08936 R56332 H09256 R52303 R13075					
	415527 415666	1543492_1	H72693 R086	73 H72694 F20990 R08580					
10	418512	176394_1	AW498974 TO	9332 R58460 AA350990 T33786 T30936 AA350905 T	08592 T09274 AA	224297 C	X54678 T08951 F	R15346 AW953188 AA350074	
••	410012		AW890649						
	418866	179788_1	T65754 AA22	9857 AA229658					
	422890	222707_1	Z43784 R133	82 AW572911 AA449369 H17037 R19603 AI632565 A	W004030 BE5025	30 Z2503	12 AA805324 AA	449241 Albo1825 Al264863 AV	W196918
1.5				953735 AI263703 AA319159 AW964436 AI903440 AW	594171 AB67447	AWZUGU	VI WARAZOLIO CI	13010 D01142 H1/U30 ATT 102	343
15			T87230 AI3	CAFC AADAODT ANIOCAEDD TADAED AADOAADA					
	422949	223184_1	AA319435 NO	6456 AA319377 AW961532 T48452 AA894424 1967 AA348780 AW964077 AW166028 BE540193 N94	IRNO AA45236R NG	9604 AI3	41345 AW29880	00 AA724961 AA931158 AI741	227
	424945	245223_1	AIROSSSO AIG	82626 D81263 D53937 D52496 AA974487 AW043854	N50483 Z39997 A	U492961	Al361526 F0400)2 AA452141 T23551 AI472655	5
			AI193667 AI3	41					
20	426919	273507_1	AL041228 D8	2004 D61361 AI203314 AI990307 AW900295 AI01830	08 AW087473 AW1	183530 A	A393346 H5005!	5 AA935601	
	433670	372721_1		062234 AW748386					
	433921	377350_1	AA518174 AI	114549 R36464 R36465		0600 AE	112220		
	433940	37787_1 426857_1		33 AI651350 AA984734 AI368716 N40915 AI989705 1 857375 N64357 AA731069	rusu42 100505 No	10300 A	112220		
25	436773 446692	689623_1		2097 AI803984 AW235923 AW196558 AI954637 AI33	6983				
23	440032		240147400						
	TABLE 190	:							
	Pkey:	Uni	que number corre	esponding to an Eos probeset				4 400 04-4 6The Phi	
20	Ref:	Sec	juence source. T	he 7 digit numbers in this column are Genbank Identifi	er (GI) numbers. "	Dunham,	et all." reters to t	ve broncadou eutited . The run	A
30				chromosome 22' Dunham, et al. (1999) Nature 402:48	9-490.				
	Strand:			d from which exons were predicted. positions of predicted exons.					
	Nt_position	. 1110	icales mucieude	positions of producted exons.					
	Pkey	Ref	Strand	Nt_position					
35	400844	9188605	Plus	24746-24872,25035-25204					
	404819	4678240	Ptus	16223-16319,16427-16513,16736-16859,16941-1707	75,17170-17287,17	389-1752	29,18261-18357,	18443-18578	
	405560	183148	Plus	5495-5655,6077-6241,6495-6692					
	405819	4007557	Plus	2830-2967					
40	406311	9211559	Minus	137114-139033					
40									
	TABLE 20	A: ABOUT 3	8 CNS-ENRICH	ED GENES SIGNIFICANTLY DOWN-REGULATED IN	LOWER GRADE (SLIOBLA	STOMA COMPA	RED TO NORMAL ADULT CN	S
	Table 204	liete about 32	hadring 2M7 B	nonce elanificantly down-regulated in lawer grade, glick	hlasioma (LGG) co	moared t	o normal adult Ci	INS tissues. I hese were select	ed from
4.5	E0000		ASS		ymal CNS in "aver	aon IGG	• was dreater in	ian or equal to 2. The "average	noma
45	CNS level	was set to the	85 th percentile a	unongst various normal CNS tissues. The "average" L " CNS to "average" non-CNS normal adult tissues was	GG level was set it	mater the	beceause surous	The "average" CNS level was	el to the
	CNS speci	nc genes, the	ratio of "average	ues. The "average" normal non-CNS adult tissue level	was set to the 95°	oercenti	le amonost vario	us non-CNS normal tissues. In	order to
	competes	na snacific h	various CNS uss arknmund levels	of non-specific hybridization, the 10th percentile value a	emonast various no	n-malign	ant tissues was s	subtracted from both the numer	ator and
			the ratios were e			•			
50	Pkey:	Ur	ique Eos probes	et identifier number					
	ExAcon:			n number, Genbank accession number					
	UnigenelC		igene number						
	Unigene T		igene gene title	ared to LOWER GRADE GLIOBLASTOMA					
55	R1; R2;			ared to NON-CNS NORMAL ADULT TISSUE					
33	IVZ.	14	mo or caro comp	200 20 11007-0110 1100 1100 1100 1100 1100 11					
	Pkay	ExAcon	UnigenelD	Unigene Title		R1	R2		
	425580	L11144	Hs.1907	galanin		33.1	3.5		
C 0	425489	M58594	Hs.1905	protactin		24.7 22.6	10.5 22.6		
60	430538	AB032435	Hs.242821	differentiation-associated Na-dependent		22.0 22.4	6.0		
	417275	X63578 AL035461	Hs.295449 Hs.2281	parvalbumin chromogranin B (secretogranin 1)		21.8	21.8		
	428505 408040	AL035461 Al266496	Hs.22905	ESTs, Weakly similar to RHG6_HUMAN RHO-G		19.4	19.4		
	435145	A1277259	Hs.116631	ESTs		18.5	3.8		
65	407039	X00368		gb:Human prolactin gene 5' region.		18.1	18.1		
	428976	AL037824	Hs.194695	ras homolog gene family, member t		17.4	17.4		
	409263	AA069573		ESTs		16.8	16.8		
	424645	NM_01468		KIAA0535 gene product		15.1 14.0	15.1 14.0		
70	416018	AW138239		proprotein convertase subtilisin/kexin t hypothetical protein FLJ20628		13.9	8.0		
70	405560 452022	AW88770* AW072336		ESTs		13.8	13.8		
	433940	H05129	16.23000	cyclic AMP-regulated phosphoprotein, 21		12.0	12.0		
	413324	V00571	Hs.75294	corticotropin releasing hormone		12.0	13.2		
	410657	AF063228	Hs.65248	dynein, cytoplasmic, intermediate polype		11.5	11.5		
75	410330	AW02363		ESTs		11.1	23.4		
	453165	S74727	Hs.32042	aspartoacylase (aminoacylase 2, Canavan		10.7 10.5	10.7 4.1		
	420297 417167	AI628272 AW20643	Hs.88323 7 Hs.4290	ESTs, Weakly similar to ALU1_HUMAN ALU S ESTs		10.4	10.4		
	420033	D59502	/ NS.4230 Hs.292590			10.4	10.4		
80	413293	AL047483				10.0	10.0		
	426380	AJ291267	Hs. 149990	ESTs		9.8	6.9		
	410635	D58863	Hs.334372			9.5	6.6 5.8		
	422756	AA441787	Hs.119689			9.1	5.8		
				204	-				

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	444330			ESTs	9.1 8.9	9.1 8.9
				nypothetical protein FLJ11155 sorting nexin 10	8.6	6.7
	421633 429096		Hs 196012	KIAA0534 protein	8.6	8.6
5	428652	AA584272	Hs.336224	transmembrane protein with EGF-like and	8.6 8.5	8.6 8.5
	410309		Hs.278153	ESTs Homo sapiens cDNA: FLJ23075 fis, clone L	8.5	10.2
	424932			ESTs	8.4	8.9
	417175 427061		Hs.173392	KIAA1145 protein	8.4	8.4 5.1
10	400438	AF185611	Hs.115352	Target	8.3 8.2	9.8
	418207	C14685	Hs.34772 Hs.247837	ESTs neurexin 3	8.1	18.7
	440209 429876	H05049 AB028977	Hs.225974	KIAA1054 protein	8.1	16.8
	429470	AI878901	Hs.203862	guanine nucleotide binding protein (G pr	8.0 7.9	8.0 15.7
15	430004	U27768	Hs.227571	regulator of G-protein signalling 4	7.8	7.8
	436427 408814	A1344378 N62499	Hs.143399 Hs.176227	ESTs hypothetical protein FLJ11155	7.8	8.6
	434367	AB020700	Hs.3830	KIAA0893 protein	7.7	5.6 7.7
••	441005	Z41305	Hs.303172	Homo sapiens mRNA; cDNA DKFZp547G133 (fr	7.7 7.7	8.5
20	416851	AW963951	Hs:85618 Hs:194756	ESTs sine oculis homeobox (Drosophila) homolo	7.6	5.5
	429033 437073	NM_007374 A1885608	Hs.94122	ESTs	7.5	7.5
	441264	AA927170	Hs.23290	ESTs	7.3 7.2	7.3 7.2
25	450715	A1266484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein guanylate cyclase 1, soluble, beta 3	7.1	4.8
25	415076 410011	NM_000857 AB020641	Hs.77890 Hs.57856	PFTAIRE protein kinase 1	7.1	10.0
	423003	AL120077	Hs.122967	kelch (Drosophila)-like 2 (Mayven)	7.0 7.0	7.0 7.0
	433921	AA518174		gb:nq14f01.s1 NCI_CGAP_Thy1 Homo sapiens	6.9	6.9
20	457012	R41480	Hs.302754 Hs.13423	ESTs Homo sapiens clone 24468 mRNA sequence	6.9	6.9
30	445898 425352	AF070623 NM_000939	Hs. 1897	proopiomelanocortin (adrenocorticotropin	6.9	6.1
	433558	AA833757	Hs.201769	ESTs, Wealdy similar to T24435 hypotheti	6.9 6.8	6.9 6.8
	409031	AA376836	Hs.288856	ESTs superiorcervical ganglia, neural specifi	6.5	22.2
35	419347 445279	C15944 R41900	Hs.90005 Hs.22245	ESTs	6.4	6.4
55	437414	AW894071	Hs.48448	hypothetical protein DKFZp547C176	6.4	6.4 6.4
	428414	AL049980	Hs.184216	DKFZP564C152 protein	6.4 6.4	4.0
	434104	AF116691	Hs.116459 Hs.166479	hypothetical protein PRO2198 ESTs	6.3	3.0
40	443244 447761	AI457235 AF061573	Hs.19492	protocadherin 8	6.3	6.3
-10	450600	BE079478	Hs.24880	ESTs	6.2 6.2	3.9 11.1
	427457	AW779105	Hs.164682	ESTs ATPase, Ca transporting, plasma membrane	6.1	8.0
	416133	NM_001683 AI885537	Hs.89512 Hs.27172	ESTs, Moderately similar to PC4259 ferri	6.0	3.9
45	432453 432298	AL118812	Hs.274293	Homo sapiens mRNA; cDNA DKFZp761G1111 (f	6.0	15.1 6.0
	415114	D6046B	Hs.94181	ESTs	6.0 5.9	3.3
	416101	R24854	Hs.268806 Hs.22653	ESTs KIAA0844 protein	5.9	5.9
	448958 447138	AB020651 AI439112	Hs.93828	ESTs, Weakly similar to 2109260A B cell	5.8	5.8
50	414545	AA149287	Hs.76605	ESTs	5.8 5.7	3.6 5.1
	424153	AA451737	Hs.141496		5.6	5.6
	424641 410389	AB001106 AW954049	Hs.151413 Hs.8177	ESTs, Weakly similar to PIHUB6 salivary	5.6	9.6
	432149		Hs.133483	ESTs. Wealdy similar to T34549 probable	5.6 5.6	12.2 5.6
55	408428			DnaJ (Hsp40) homolog, subfamily B, membe	5.5 5.5	6.1
	443912 442023		Hs.184784 Hs.144549		5.5	5.6
	450642		Hs.7130	copine IV	5.4 5.4	5.6 9.8
60	439772	AL365406	Hs.10268	Homo sapiens mRNA full length insert cDN	5.4 5.4	5.4
60	450149 438202				5.3	5.3
	448605		Hs.21597	Homo sapiens mRNA full length insert cDN	5.3	5.3
	418866	T65754		ob:vc11c07.s1 Stratagene lung (937210) H	5.3 5.2	3.8 5.2
65	448786		Hs.17907 Hs.47248		5.2	3.3
03	443682 415666		FIS.47 240	gb:yu03c11.r1 Soares fetal liver spleen	5.2	5.2
	428508			8 S88131 protein	5.2 5.1	4.1 5.1
	44635		Hs.15366		5.1	3.2
70	44210 43733				5.1	5.1
,0	43733			05 ESTs	5.0	3.1 6.0
	40806	8 AW148652	2 Hs.1673	98 ESTs	5.0 5.0	5.0 5.0
	43414		Hs.2446 Hs.3021		4.9	5.3
75	43923 41463			5 ESTs	4.9	4.9
	44710	4 R19085	Hs.2107	06 Homo sapiens cDNA FLJ13182 fis, clone NT	4.9 4.9	3.0 4.9
	41852	7 AA450386	5 Hs.7149 Hs.2200		4.9	4.9
	42507 43351				4.8	4.8
80	43331		103 Hs.1741	88 KIAA0938 protein	4.8 4.8	4.8 3.2
	44725	2 R90916	Hs.1244		4.0	4.7
	41964 4149		Hs.9179 Hs.3233	* *	4.7	3.8
	41494	· · · · · · · · ·	1 10.020			

	429900	AA460421	Hs.30875	ESTs	4.7 4.7	4.2 7.4
	422949	AA319435 X62692	Hs.2593	gb:EST21657 Adrenal gland tumor Homo sap phosphodiesterase 6B, cGMP-specific, rod	4.6	4.6
	430537 419191	U17195	Hs.89666	A kinase (PRKA) anchor protein 6	4.5	4.5
5	421952	AA300900	Hs.98849	ESTs, Moderately similar to AF161511 1 H	4.4	3.2
•	406311			NM_021979":Homo sapiens heat shock 70kO	4.4	11.5
	451050	AW937420	Hs.69662	ESTs	4.4	4.4
	423728	AW891294	Hs.132136	solute carrier family 4, sodium bicarbon	4.4	7.9
10	411498	NM_014210	Hs.70499	ecotropic viral integration site 2A	4.3 4.3	19.4 4.3
10	451301 452381	A1769514 H23329	Hs.209890 Hs.290880	EST ESTs, Wealdy similar to ALU1_HUMAN ALU S	4.3	4.3
	433109	N58907	Hs.162430	EST STORY	4.3	3.9
	423589	AA328082	Hs.209569	ESTs	4.2	4.2
	427224	AL135554	Hs.101937	sine oculis homeobox (Drosophila) homolo	4.2	3.9
15	420489	AA815089	Hs.193513	EST8	4.1	4.1
	408206	AF041853 N48521	Hs.43670	kinesin tamily member 3A KIAA1708 protein	4.1 4.1	4,1 5.8
	418202 448117	H49129	Hs.26549 Hs.172982	ESTs	4.1	4.1
	412155	R38167	Hs.12449	Homo sapiens transmembrane protein HTMP1	4.0	27.9
20	458694	F12832	Hs.3610	ESTs	4.0	4.0
	452197	AW023595	Hs.232048	ESTs	4.0	4.0
	408547	AA574291	Hs.57837	ESTs .	4.0 4.0	4.0 3.7
	433447 448583	U29195 NM_015239	Hs.3281 Hs.21542	neuronal pentraxin II KIAA1035 protein	4.0	4.0
25	442412	R77677	Hs.346644	ESTs	3.9	3.9
	440293	At004193	Hs.22123	ESTs	3.9	3.9
	426365	AA376667	Hs.10283	RNA binding motif protein 88	3.9	4.1
	400844			NM_003105*:Homo sapiens sortilin-related	3.9	3.1
20	426054	U12431	Hs.166109	ELAV (embryonic lethal, abnormal vision,	3.9	3.9 3.3
30	429290 408777	AF203032 U71204	Hs.198760 Hs.47626	neurofilament, heavy polypeptide (200kD) Ric (Drosophila)-like, expressed in neur	3.8 3.8	3.3 3.8
	442676	AI733585	Hs.130897	ESTs	3.8	3.8
	414699	AI815523	Hs.76930	synuclein, alpha (non A4 component of am	3.8	4.5
	436476	AA326108	Hs.33829	bHLH protein DEC2	3.8	3.3
35	434998	AW975157	Hs.26037	ESTs	3.7	3.7
	412049	N53437	Hs.18268	adenylate kinase 5	3.7 3.7	10.7 4.5
	416220 459697	N49776 AA406062	Hs.170994 Hs.98002	hypothetical protein MGC10946 ESTs	3.7 3.7	5.4
	435648	H24347	Hs.27524	ESTs	3.7	8.1
40	442042	AI990506	Hs.8077	Homo sapiens mRNA; cDNA DKFZp547E184 (fr	3.7	6.2
	456765	Al497900	Hs.33067	ESTs	3.7	3.7
	434933	R91095	Hs.4276	KIAA1701 protein	3.6	6.1
	419518	U79289	Hs.90798	Human clone 23695 mRNA sequence	3.6 3.6	3.6 3.6
45	452667 436773	T87219 AW078629	Hs.13219	ESTs PC4 and SFRS1 interacting protein 1	3.6	3.6
73	408119	W26213	Hs.101672	ESTs, Weakly similar to T00331 hypotheti	3.6	3.6
	453534	NM_014796	Hs.33187	KIAA0748 gene product	3.6	4.7
	449093	AB035356	Hs.22998	neurexin 1	3.6	3.6
50	442738	AW002370	Hs.131055	ESTs, Weakly similar to NPM_HUMAN NUCLEO	3.5	3.5
50	447746	AW015920	Hs.161359	ESTs ESTs, Weakly similar to HSS2_HUMAN HEPAR	3.5 3.5	9.9 3.5
	449117 447750	AW449310 AI422234	Hs.210262 Hs.143434	contactin 1	3.5	9.8
	453590	AF150278	Hs.33578	KIAA0820 protein	3.5	22.3
	409339	AB020686	Hs.54037	ectonucleotide pyrophosphatase/phosphodi	3.5	3.6
55	410240	AL157424	Hs.61289	synaptojanin 2	3.5	4.6
	410224	M55513	Hs.150208	potassium voltage-gated channel, shaker-	3.4 3.4	3.4 3.4
	400098 450181	H05254	Hs.201198	Eos Control ESTs	3.4	7.2
	459080	AW192083	Hs.290855	ESTs	3.4	13.5
60	417063	N50515	Hs.45061	ESTs	3.3	3.3
	424918	R13982	Hs.169309	myelin-associated oligodendrocyte basic	3.3	5.3
	453431	AF094754	Hs.32973	glycine receptor, beta	3.3	4.6
	412453	R20205	Hs.75236	ESTs .	3.3 3.3	3.3 3.3
65	450561 415527	R49674 F11624	Hs.25909	ESTs qb:HSC2ZD101 normalized infant brain cDN	3.3	3.3
03	426968	U07616	Hs.173034		3.3	15.3
	427386	AW836261	Hs.6727	ESTs	3.3	3.3
	424001	W67883	Hs.137476		3.2	5.4
70	439450	R51613	Hs.125304		3.2	8.3
70	442879	AF032922	Hs.8813	syntaxin binding protein 3	3.2 3.2	3.2 3.2
	417284 410343	N62889 AA084273	Hs.107242 Hs.76561	Homo sapiens cDNA FLJ12965 fis, clone NT ESTs, Weakly similar to S47072 finger pr	3.2	3.2
	410909	AW898161	Hs.53112	ESTs, Moderately similar to ALUS_HUMAN A	3.2	12.5
	453919	AW959912	Hs.7076	KIAA1705 protein	3.2	3.2
75	424087	N69333	Hs.143434	contactin 1	3.1	3.1
	428963	AW382682	Hs.258208		3.1	3.3
	419852	AW503756	Hs.286184		3.1 3.1	4.1 3.1
	422234 423829	AF119818 R44107	Hs.113287 Hs.240905		3.1	4.4
80	443297	AI049864	Hs.133029		3.1	3.1
	453302			glutamate receptor, metabotropic 1	3.1	4.6
	405819			NM_002578:Homo sapiens p21 (CDKN1A)-acti	3.1	13.5
	445725	AK000956	Hs.13209	hypothetical protein FLJ 10094	3.0	3.0

	44-670		N. 402205	Ect.	3.0	3.0
	447673 433670	A1823987 AA604405		ESTs gb:no87h09.s1 NCI_CGAP_AA1 Homo sapiens	3.0	3.9
	450757	BE081050		ESTs, Weakly similar to KIAA1324 protein	3.0	3.2
_	424724	T06532		Homo sapiens cDNA: FLJ22674 fis, clone H	3.0 3.0	3.0 3.1
5	433315	R96754	Hs.239706	GRB2-associated binding protein 1 Homo sapiens mRNA; cDNA DKFZp564P116 (fr	3.0	3.1 4.9
	451032 423346	W03692 AI267677	Hs.323079 Hs.127416	synaptojanin 1	3.0	20.1
	439274	AF086092	Hs.48372	ESTs	3.0	18.3
10	425649	U30930	Hs.158540	UDP glycosyltransferase 8 (UDP-galactose	2.9 2.9	38.6 14,9
10	441869	NM_003947	Hs.8004	huntingtin-associated protein interactin protine-rich Gta (G-carboxygtutamic acid	2.9	3.3
	407868 410765	NM_000950 Al694972	Hs.40637 Hs.66180	nucleosome assembly protein 1-like 2	2.9	8.0
	428001	H97428	Hs.219907	ESTs, Moderately similar to Transforming	2.8	5.9
	448533	AL119710	Hs.21365	nucleosome assembly protein 1-like 3	2.8	9.6 3.1
15	425130	AA448208	Hs.99163	ESTs nuclear receptor co-repressor/HDAC3 comp	2.8 2.8	3.7
	408554 452238	AA836381 F01811	Hs.315111 Hs.345757	ESTs	2.8	3.8
	446544	Al631932	Hs.7047	ESTs, Weakly similar to Unknown [H.sapie	2.8	12.4
	433803	AI823593	Hs.27688	ESTs	2.8	4.1
20	407728	AW071502	Hs.175931	ESTS	2.7 2.7	10,2 3.4
	414931	AK000342	Hs.77646 Hs.65746	Homo sapiens mRNA; cDNA DKFZp761M0223 (f KtAA0318 protein	2.7	6.1
	410711 452738	A8002316 AL133800	Hs.7086	hypothetical protein MGC12435	2.7	3.5
	451516	AI800515	Hs.12024	ESTs	2.7	6.3
25	454053	AW023006	Hs.27172	ESTs, Moderately similar to PC4259 femi	2.7 2.7	3.6 7.2
	450474	AW872844	Hs.117494 Hs.13701	ESTs ESTs	2.7	5.3
	422414 428186	AW875237 AW504300	Hs.295605	mannosidase, alpha, class 2A, member 2	2.7	3.9
	431342	AW971018	Hs.21659	ESTs	2.7	8.0
30	423449	Al497900	Hs.33067	ESTs .	2.6 2.6	14.5 3.0
	427283	AL119796	Hs.174185	ectonucleotide pyrophosphatase/phosphodi ELAV (embryonic lethal, abnormal vision,	2.6	9.0
	426919 437117	AL041228 AL049256	Hs.122593	ESTs	2.6	3.8
	422491	AA338548	Hs.117546	neuronatin	2.6	3.6
35	438068	AI927209	Hs.306210	Homo sapiens cDNA: FLJ23133 fis, clone L	2.6	5.1 9.9
	432809	AA565509	Hs.131703	ESTs protocadherin 9	2.5 2.5	18.1
	433551 444783	AI985544 AK001468	Hs.12450 Hs.62180	anilin (Drosophila Scraps homolog), act	2.5	43.2
	417417	F05745	Hs.89512	ATPase, Ca transporting, plasma membrane	2.5	17.1
40	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	2.5	5.7
	448902	245998	Hs.22543	Homo sapiens mRNA; cDNA DKFZp76111912 (f	2.5 2.5	21.8 14.5
	442910 423135	Al365130 N67655	Hs.11307 Hs.26411	ESTs, Wealthy similar to T19326 hypotheti ESTs	2.5	8.2
	452311	AW304029	Hs.252744	ESTs	2.5	3.5
45	418940	H17739	Hs.288513	Human DNA sequence from clone RP5-899C14	2.5	7.0
	432882	NM_013257		serum/glucocorticoid regulated kinase-li	2.5 2.5	4.2 12.0
	422411	AW749443	Hs.22511	ESTs spastic paraptegia 4 (autosomal dominant	2.4	3.1
	451386 404819	AB029006	Hs.26334	NM_002688°:Homo sapiens peanut (Drosophi	2.4	5.8
50	429656	X05608	Hs.211584	neurofilament, light polypeptide (68kD)	2.4	13.1
	431988	AC002302	Hs.77202	protein kinase C, beta 1	2.4 2.4	10.5 11.2
	411379	AI816344	Hs.12554	ESTs, Weakly similar to NPL4_HUMAN NUCLE CCAAT/enhancer binding protein (C/EBP).	2.4	45.2
	422980 429859	N46569 NM_007050	Hs.76722 Hs.225952	protein tyrosine phosphatase, receptor t	2.4	5.1
55	430287	AW182459	Hs.125759		2.4	7.6
-	422890	Z43784		ankyrin 3, node of Ranvier (ankyrin G)	2.4	3.6
	427658	H61387	Hs.30868	nogo receptor hypothetical protein dJ462O23.2	2.4 2.3	3.0 3.6
	446100 412266	AW967109 N59006	Hs.13804 Hs.26133	ESTs	2.3	30.9
60	435059	245270	Hs.235873		2.3	4.8
	420173	AA256151	Hs.22999	ESTs	2.3	4.1
	452371	R40990	Hs.21658	ESTs hypothetical protein	2.3 2.3	3.3 4.7
	430456 409953	AA314998 AA332277	Hs.241503 Hs.57691	cadherin 18, type 2	2.3	5.5
65	429006	AA443143	Hs.50929	hypothetical protein FLJ13842	2.3	6.6
	445194	AJ215667	Hs.175044		2.3	3.1
	428392		Hs.2265	secretory granute, neuroendocrine protei	2.3 2.3	42.3 4.8
	434460 416490		Hs.3852 Hs.79348	KIAA0368 protein regulator of G-protein signalling 7	2.3	12.5
70	437924		Hs.164118		2.3	3.2
	418738			solute carrier family 7, (cationic amino	2.2	16.9
	424945		11_ 20204	hypothetical protein FLJ10582	2.2 2.2	30.5 4.4
	416530		Hs.79361 Hs.30142	kallikrein 6 (neurosin, zyme) 3 calcium binding protein 1 (calbrain)	2.2	3.0
75	422927 438831			synapsin II	2.2	3.4
	449078				2.2	16.1
	410631	AA086469	Hs.47171		2.2	5.8 7.5
	419271		Hs.23853 Hs.33578		2.2 2.2	13.4
80	452752 446574		Hs.33593		2.2	3.5
	452106		Hs.21342	ESTs	2.2	3.4
	415910	U20350	Hs.78913		2.2	28.9 7.7
	444458	BE041526	Hs.31746	hypothetical protein DKFZp547F072	2.2	7.7

		744544		the continue with the Mile at 202 and in	2	.2	33.0
	445692	Z44514 AA120960	Hs.198416	Homo sapiens mRNA for KIAA1763 protein, ESTs			8.5
	412788 419103	Z40229	Hs.96423	hypothetical protein FLJ23033			8.4
	424474	AA308883	Hs.148680	calcyon; O1 dopamine receptor-interactin	2	2.2	3.6
5	451783	R42554	Hs.210862	T-box, brain, 1		2.1	11.2
	434792	AA649253	Hs.132458	ESTs		2.1	3.8
	424922	BE386547	Hs.217112	hypothetical protein MGC10825		21	3.7 4.9
	455364	H72176	Hs.4273	hypothetical protein FLJ13159		2.1 2.1	4.9 5.1
10	413988	M81883	Hs.324784	glutamate decarboxylase 1 (brain, 67kD)		2.1	3.6
10	452744	A1267652 A1034467	Hs.246107 Hs.34650	Homo sapiens mRNA; cDNA DKFZp434E082 (fr ESTs		21	7.6
	443150 453220	AB033089	Hs.32452	Homo sapiens mRNA for KIAA1263 protein,		2.1	19.9
	420050	AL118615	Hs.94653	neurochondrin		2.1	6.5
	408449	NM_004408	Hs.166161	dynamin 1		2.1	5.1
15	423641	AL137256	Hs. 130489	ATPase, aminophospholipid transporter-li		2.1	6.2
	430347	NM_002039	Hs.239706	GRB2-associated binding protein 1		2.1	3.2
	449568	AL157479	Hs.23740	KIAA1598 protein		2.1 2.1	3.6 3.3
	412675	AA460716	Hs.9788	hypothetical protein MGC10924 similar to		2.1	6.4
20	429550	AW293055 Al653048	Hs.119357 Hs.144006	ESTs ESTs		2.1	9.0
20	445782 453924	R49295	Hs.24886	ESTs		2.1	13.4
	437948	AA772920	Hs.303527	ESTs		2.1	24.8
	451952	AL120173	Hs.301663	ESTs		2.0	19.2
	453754	AW972580	Hs.172753	ESTs		2.0	3.4
25	448765	R15337	Hs.21958	Homo sapiens mRNA; cDNA DKFZp547D086 (fr		2.0	3.9
	447163	AW292770	Hs.5542	DnaJ (Hsp40) homolog, subfamily C, membe		2.0 2.0	3.4 11.5
	448299	AA497044	Hs.20887	hypothetical protein FLJ10392		2.0	6.6
	411666	AF106564	Hs.71346 Hs.1780	neurofilament 3 (150kD medium) myetin associated glycoprotein		2.0	10.1
30	424458 434277	M29273 X77748	Hs.3786	glutamate receptor, metabotropic 3		2.0	28.5
30	440152	AB002376	Hs.7006	KIAA0378 protein		2.0	14.2
	429956	AJ374651	Hs.22542	ESTs		2.0	3.2
	450590	AJ701507	Hs.273740	ESTs		20	3.8
	429024	A1652297	Hs.119302	complement-c1q tumor necrosis factor-rel		20	3.7
35	430643	AW970065	Hs.287425	MEGF10 protein		2.0	4.1 27.4
	415734	NM_014747	Hs.78748	KIAA0237 gene product		20 20	3.3
	419757	AA773820	Hs.63970 Hs.103042	ESTs		20	23.8
	421264 439607	AL039123 BE540565	Hs.159460	microtubule-associated protein 18 ESTs		2.0	5.6
40	435624	AF218942	Hs.24889	formin 2		2.0	12.2
70	425121	AI797511	Hs.154679	synaptotagmin I		2.0	3.9
	431677	AK000496	Hs.306989	hypothetical protein FLJ20489		2.0	3.1
	442593	R39804	Hs.31961	ESTs		2.0	6.7
	410366	AJ267589	Hs.302689	hypothetical protein	•	2.0	10.4
45	426575	M74826	Hs.170808			2.0	4.6 10.7
•	452856	AF034799	Hs.30881	protein tyrosine phosphatase, receptor t		2.0 2.0	3.8
	437380	AL359577	Hs.112198			2.0	3.8
	424893 436734	AW295112 AI937612	Hs.153648 Hs.273758			2.0	4.7
50	422544	AB018259	Hs.118140			2.0	11.8
-	440105	AA694010	Hs.6932	Homo sapiens clone 23809 mRNA sequence		2.0	8.2
	425741	AF052152	Hs.159412	Homo sapiens clone 24628 mRNA sequence		2.0	6.5
	450310	N62341	Hs.94116	ESTs		2.0	3.6
<i>c c</i>		_					
55	TABLE 2			- at idealifies sumbas			
	Pkey:	_		set identifier number			
	CAT num Accessio		ne chuster num nbank accessio				
	ACCESSIO	ii. Gei	IDDIK BACSSK	AT NUMBER			
60	Pkey	CAT Numbe	r Accession				
	415527	1539393_1	F11624 Z4	3212 H08936 R56332 H09256 R52303 R13075			
	415666	1543492_1		08673 H72694 F20990 R08580			
	418866	179788_1	T65754 A	A229857 AA229658	CE AMMONANON DES	A363A 736A3	32 AA805324 AA449241 AI651825 AI264863 AW196918
45	422890	222707_1	Z43/84 R1	A1953735 A1263703 AA319159 AW964436 A1903440	NO AVVOUAUSU BES NAMEGA 171 AIRET.	W2530 2230. AA7 AW2040	71 AW956110 C15616 D81142 H17038 AW162343
65			T87230 AI		7 MII 334 17 1 MOUT	AIIE	
	422949	223184_1	A A 310435	NEGAGE AA319377 AW961532 T48452 AAR94424			
	424945	245223_1	A1221010	710067 AARARTRO AWQ64077 AW166028 RES40193	N94800 AA45236	B N99604 AI3	341345 AW298800 AA724961 AA931158 AI741227
	727070	£40220	AI806660	AI982626 D81263 D53937 D52496 AA974487 AWO4	3854 N50483 Z399	97 AI492961	AI361526 F04002 AA452141 T23551 AI472655
70			A1193667	AIRA1			
	426919	273507_1		D82004 D61361 AI203314 AI990307 AW900295 AI0	18308 AW087473	AW183530 A	(A393346 H50055 AA935601
	433670	372721_1		8E062234 AW748386			
	433921	377350_1	AA618174	A1114549 R36464 R36465	70¢ €00042 ₹0200	C DODGER AC	E112220
75	433940	37787_1	HU5129 N	63433 A1651350 AA984734 A1368716 N40915 A1989 9 A1857375 N64357 AA731069	. UJ FUJUIZ 1W3U		
13	436773	426857_1	7/451/ A	1352097 A1803984 AW235923 AW196558 A1954637 /	AJ336983		
	446692	689623_1	C-4314 W	Paris Pari			
	TABLE :	20C:					
	Pkey:	l le	ique number o	corresponding to an Eos probeset			a dia dia mandra dia mandra dia dia dia dia dia dia dia dia dia di
80	Ref:	Se	quence source	 The 7 digit numbers in this column are Genbank Id 	entifier (GI) number	s. Dunham,	, et al. reters to the publication entitled "The DNA
	_	50	quence of hum	nan chromosome 22" Dunham, et al. (1999) Nature 40	12:489-495.		
	Strand:		SICERES UNA SI	rand from which exons were predicted. ide positions of predicted exons.			
	NL_posi	uur. IIX	moiss muceu				
				2/	14 4		

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	Pkey	Ref	Strand	Nt_position
	400844	9188605	Plus	24746-24872,25035-25204
5	404819	4678240	Plus	16223-16319,16427-16513,16736-16859,16941-17075,17170-17287,17389-17529,18261-18357,18443-18578
	405560	183148	Plus	5495-5655,6077-6241,6495-6692
	405819	4007557	Plus	2830-2967
	406311	9211559	Minus	137114-139033

TABLE 21A: ABOUT 410 GENES SIGNIFICANTLY DOWN-REGULATED IN GLIOBLASTOMA MULTIFORMA COMPARED TO NORMAL ADULT CNS
Table 21A lists about 410 genes significantly down-regulated in glioblastoma multiforma (GBM) compared to normal adult CNS tissues. These were selected from 59680 probesets
on the Affymetriv/Eos Hu03 GeneChip array such that the ratio of "average" normal CNS to "average" GBM was greater than or equal to 2. The "average" normal CNS tevel was set
to the 75th percentile amongst various normal CNS tissues. The "average" GBM level was set to the 95th percentile amongst various tumor samples. In order to remove gene-specific
background levels of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before 10 15

the ratio was evaluated.

Pkey: Unique Eos probeset identifier number

Exacon: Exemptar Accession number, Genbank accession number

UnigenetD: Unigene number Unigene Title:

Unigene gene title Ratio of CNS to GLIOBLASTOMA MULTIFORMA 20 R1:

	Pkey	ExAcon	UnigenetD	Unigene Title	R1
	417275	X63578	Hs.295449	parvafoumin	18.6
25	428505	AL035461	Hs.2281	chromogranin B (secretogranin 1)	13.8
25	415672	N53097	Hs.193579	ESTs	13.5
	459080	AW192083	Hs.290855	ESTs TO THE TOTAL	12.9
	432298	AL118812	Hs.274293	Homo sapiens mRNA; cDNA DKFZp761G1111 (f	11.7
	400302 418318	N48056 U47732	Hs.1915 Hs.84072	folate hydrolase (prostate-specific memb	10.9 10.1
30	424645	NM_014682	Hs.151449	transmembrane 4 superfamily member 3	8.2
20	415274	AF001548	Hs.78344	KIAA0535 gene product myosin, heavy polypeptide 11, smooth mus	7.5
	413324	V00571	Hs.75294	corticotropin releasing hormone	7.5
	417167	AW206437	Hs.4290	ESTs	7.3
	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	6.8
35	410330	AW023630	Hs.159425	ESTs	6.5
	450590	A1701507	Hs.273740	ESTs	6.5
	453165	S74727	Hs.32042	aspartoacylase (aminoacylase 2, Canavan	6.5
	454076	AW204712	Hs.61957	ESTs	6.3
4.0	419956	AL137939	Hs.40096	ESTs	6.3
40	416851	AW963951	Hs.85618	ESTs	6.2
	428874	W32133	Hs.194366	transthyretin (prealbumin, amyloidosis t	6.0
	409743	N48721	Hs.183506	hypothetical protein FLJ14213	5.9
	449078	AK001256	Hs.22975	KIAA1576 protein	5.6
45	448072	AI459306	Hs.24908	ESTs	5.6
45	412622	AW664708	Hs.171959	ESTs	5.6
	428414	AL049980	Hs.184216	DKFZP564C152 protein	5.5
	427322	AK002017	Hs.176227	hypothetical protein FLJ11155	5.5
	411498 453344	NM_014210	Hs.70499 Hs.44571	ecotropic viral integration site 2A	5.4
50	441790	BE349075 AW294909	Hs.132208	ESTs ESTs	5.4 5.3
30	443037	AW500305	Hs.8906	syntaxin 7	5.3
	445529	H14421	Hs.180513	ATP-binding cassette, sub-family A (ABC1	5.2
	447750	AI422234	Hs. 143434	contactin 1	5.2
	444409	AI792140	Hs.49265	ESTs	5.2
55	409031	AA376836	Hs.288856	ESTs	5.1
	453220	AB033089	Hs.32452	Horno sapiens mRNA for KIAA1263 protein,	5.0
	452022	AW072330	Hs.293875	ESTs	4.9
	408428	NM_014787	Hs.44896	DnaJ (Hsp40) homolog, subfamily 8, membe	4.8
C 0	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	4.8
60	443622	AJ911527	Hs.11805	ESTs	4.8
	442023	A1187878	Hs.144549	ESTs	4.7
	445618	H79667	Hs.237642	Homo sapiens cDNA FLJ12052 ffs, done HE	4.6
	429611	AI889077	Hs.211388	Homo sapiens BAC clone CTB-60N22 from 7q	4.5
65	414290	AI568801	Hs.71721	ESTs	4.4
03	450715 428508	AI266484 BE252383	Hs.31570 Hs.184668	ESTs, Weakly similar to KIAA1324 protein	4.4
	4255649	U30930	Hs.158540	SBBI31 protein UDP glycosyltransferase 8 (UDP-galactose	4.4 4.3
	459247	N46243	Hs.110373	ESTs, Highly similar to T42626 secreted	4.3
	434064	AL049045	Hs.180758	hypothetical protein PRO0082	4.3
70	414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZo564B1264 (f	4.3
	416133	NM_001683	Hs.89512	ATPase, Ca transporting, plasma membrane	4.3
	426471	M22440	Hs.170009	transforming growth factor, alpha	4.2
	409231	AA445644	Hs.692	GA733-2 antigen; epithelial glycoprotein	4.2
	448958	AB020651	Hs.22653	KIAA0844 protein	4.2
75	410657	AF063228	Hs.65248	dynein, cytoplasmic, intermediate polype	4.1
	447138	Al439112	Hs.93828	ESTs, Weakly similar to 2109260A B cell	4.1
	440736	D56919	Hs.265848	myomegalin	4.1
	407245	X90568	Hs.172004	tiin	4.1
80	441976	AA428403	Hs.106131	ESTs	4.1
00	450642	R39773	Hs.7130	copine IV	4.1
	432799 428465	NM_016161 AW970976	Hs.278960 Hs.293653	alpha-1,4-N-acetylglucosaminyltransferas ESTs	4.0
	407868	NM_000950	Hs.40637	proline-rich Gla (G-carboxyglutamic acid	4.0
	407000	141M_000930	10.4007	housement one (o-resonny distriction and	4.0

	433558	AA833757	Hs.201769	ESTs, Wealthy similar to T24435 hypotheti	4.0 4.0
	429470 415666	AI878901 H72693	Hs.203862	guanine nucleotide binding protein (G pr gb:yu03c11.r1 Soares fetal liver spleen	3.9
_	407988	N47760	Hs.285107	hypothetical protein FLJ13397	3.9
5	427061	AB032971	Hs.173392	KIAA1145 protein	3.9
	430261	AA305127	Hs.237225	hypothetical protein HT023	3.9 3.8
	440624 431668	AF017987 AW969610	Hs.7306 Hs.151179	secreted frizzled-related protein 1 ESTs	3.8
	446692	Z44514	113.131113	Homo sapiens mRNA for KIAA1763 protein,	3.8
10	408739	W01556	Hs.238797	ESTs, Moderately similar to 138022 hypot	3.8
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (lg),	3.8
	450103	R08665	Hs.17244	hypothetical protein FLJ13605	3.7 3.7
	426775 403469	AA384564	Hs.3628	ESTs Target Exon	3.7
15	450181	H05254	Hs.201198	ESTs	3.7
	438202	AW169287	Hs.22588	ESTs	3.7
	445279	R41900	Hs.22245	ESTs	3.7 3.7
	422546 435712	AB007969 AA694607	Hs.301478 Hs.176956	KIAA0500 protein ESTs	3.6
20	417620	R02530	Hs.191198	ESTs	3.6
	421952	AA300900	Hs.98849	ESTs, Moderately similar to AF161511 1 H	3.6
	453655	AW960427	Hs.342874	transforming growth factor, beta recepto	3.6
	426365 416982	AA376667 J05401	Hs.10283 Hs.80691	RNA binding motif protein 88 creatine kinase, mitochondrial 2 (sarcom	3.6 3.6
25	438086	AA336519	Hs.83623	nuclear receptor subfamily 1, group I, m	3.6
	424704	AI263293	Hs.152096	cytochrome P450, subfamily IU (arachido	3.6
	414631	AW970130	Hs.65406	ESTs	3.6
	453698	AA037615	Hs.42746	ESTs	3.6 3.5
30	438704 437073	A1435060 A1885608	Hs.32825 Hs.94122	ESTs ESTs	3.5
50	434460	AA478486	Hs.3852	KIAA0368 protein	3.5
	414541	BE293116	Hs.76392	aldehyde dehydrogenase 1 family, member	3.5
	423665	BE167153	Hs.24380	ESTs	3.5
35	446390	AA233393	Hs.14992	hypothetical protein FLJ11151	3.5 3.5
33	441264 433629	AA927170 R13140	Hs.23290 Hs.13359	ESTs ESTs	3.5
	411811	AW864370	113.13333	gb:PM4-SN0016-100500-004-h09 SN0016 Homo	3.5
	410140	AL134435	Hs.247837	neurexin 3	3.4
40	415114	D60468	Hs.94181	ESTs	3.4
40	455649	BE065051		gb:RC1-8T0313-110500-017-c04 BT0313 Homo	3.4 3.4
	433670 417175	AA604405 R44558	Hs.94002	gb:no87h09.s1 NCI_CGAP_AA1 Homo sapiens ESTs	3.4
	427176	AW381569	Hs.40334	ESTs	3.4
	448519	AW175665	Hs.278695	Homo sapiens prostein mRNA, complete cds	3.4
45	457012	R41480	Hs.302754	ESTs	3.3
	405354	AIC01573	Lin 200021	CX000321:gij6671579 ref NP_031518.1 ari Homo sapiens cDNA FLJ11997 fis, clone HE	3.3 3.3
	445872 433803	AI681573 AI823593	Hs.288671 Hs.27688	ESTs	3.3
	449017	AW002425	Hs.224142	ESTs	3.3
50	414545	AA149287	Hs.76605	ESTs	3.3
	409010	AI648675	Hs.103441	Homo sapiens, Similar to RIKEN cDNA 1700	3.3 3.3
	426158 422411	NM_001982 AW749443	Hs.199067 Hs.22511	v-erb-b2 avian erythroblastic leukemia v ESTs	33
	428850	AA934975	Hs.185076	ESTs	3.3
55	406922	S70284	Hs.119597	gb:stearoyl-CoA desaturase [human, adipo	3.2
	429556	AW139399	Hs.98988	ESTs	3.2 3.2
	434104 427229	AF116691 AI799751	Hs.116459 Hs.5635	hypothetical protein PRO2198 ESTs	3.2
	444458	BE041526	Hs.31746	hypothetical protein DKFZp547F072	3.2
60	433328	AW298159	Hs.23544	ESTs, Wealdy similar to S65824 reverse t	3.2
	412786	AW900654	Hs.285729	ESTs, Wealdy similar to unnamed protein	3.2
	440808	AK001339 AW664964	Hs.7432 Hs.128899	hypothetical protein FLJ10477 ESTs; hypothetical protein for IMAGE:447	3.2 3.1
	442117 429876	AB028977	Hs.225974	KIAA1054 protein	3.1
65	450757	BE081050	Hs.31570	ESTs. Wealdy similar to KIAA1324 protein	3.1
	414327	BE408145	Hs.185254	ESTs, Weakly similar to T24435 hypotheti	3.1
	459399	BE407712	Hs.153998	creatine kinase, mitochondrial 1 (ubiqui	3.1 3.1
	433582 452752	BE548749 AW044058	Hs.148016 Hs.33578	ESTs KIAA0820 protein	3.0
70	439165	AA029517	Hs.95162	KCNQ1 overlapping transcript 1	3.0
	409403	AA568224	Hs.6634	Homo sapiens cDNA: FLJ22547 fis, clone H	3.0
	422414	AW875237	Hs.13701	ESTs	3.0
	407173	T64349	Un 21642	gb:yc10d08.s1 Stratagene lung (937210) H KIAA1035 protein	3.0 3.0
75	448583 429043	NM_015239 AI824977	Hs.21542 Hs.145319		3.0
	452990	AA887428	Hs.246970		3.0
	412258	AA376768	Hs.324841	hypothetical protein FLJ22622	3.0
	429968	AA322503	Hs.227011		3.0
80	434348	BE393191 AW972853	Hs.181795 Hs.112237		2.9 2.9
30	427115 430538	AW972855 AB032435	Hs.242821		2.9
	449561	AI022240	Hs.17924	ESTs, Moderately similar to ALU1_HUMAN A	2.9
	405403			Target Exon	2.9

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	452197			ESTs	2.9 2.9
	437357 436427			Homo sapiens mRNA; cDNA DKFZp76202215 (f ESTs	2.9
	417787	R14948		ESTs .	2.9
5	439272	AA832474		ESTs	2.9 2.9
	454247	AJ243950		deafness locus associated putative guani ESTs	2.9
	415839 408814	R40611 N62499	Hs.94694 Hs.176227	hypothetical protein FLJ11155	2.9
	408468	AI909712	Hs.93837	phosphatidylinositol transfer protein, m	2.9
10	431304	BE157283		gb:RC4-HT0373-130200-011-a03 HT0373 Homo	2.9 2.9
	410240 444783	AL157424 AK001468	Hs.61289 Hs.62180	synaptojanin 2 anillin (Drosophila Scraps homolog), act	2.8
	408438	AB011180	Hs.100960	KIAA0608 protein	2.8
	458793	N80159	Hs.121849	microtubule-associated proteins 1A/18 li	2.8
15	429788	U87791	Hs.221040	HBS1 (S. cerevisiae)-like	2.8 2.8
	424264 433109	D80400 N58907	Hs.239388 Hs.162430	Human DNA sequence from clone RP1-304B14 EST	2.8
	427974	BE093023	Hs.188767	ESTs	2.8
20	432266	AK000385	Hs.274222	hypothetical protein FLJ20378	2.8 2.8
20	414764	AW013887	Hs.31522	ESTs gb:PM4-PT0019-141299-009-F08 PT0019 Homo	2.8
	411918 404563	AW876354		Target Exon	2.8
	446468	AI765890	Hs.16341	MAWD binding protein	2.8
0.5	444755	AA431791	Hs.113823	ClpX (caseinolytic protease X, E. coli)	2.8 2.7
25	445898	AF070623	Hs.13423 Hs.174185	Homo sapiens clone 24468 mRNA sequence ectonucleotide pyrophosphatase/phosphodi	2.7
	427283 400138	AL119796	NS.174100	Eos Control	2.7
	458676	AI692464	Hs.202263	EST _S	2.7
20	459697	AA406062	Hs.98002	ESTs	2.7 2.7
30	444420	AI148157	Hs.146766 Hs.240112	ESTs KIAA0276 protein	2.7
	430371 449117	D87466 AW449310	Hs.210262	ESTs, Weakly similar to HSS2_HUMAN HEPAR	2.7
	424994	AW954525	110.2 10202	gb:EST366595 MAGE resequences, MAGC Homo	2.7
26	400339	X57131	Hs.248209	H2A histone family, member F, pseudogene	2.7 2.7
35	417494	A1369494	Hs.222137 Hs.99154	ESTs ESTs	2.7
	427166 404746	AA431576	FIG. 33134	CX000138*:gi]7512767[pir][T12477 hypothe	2.7
	411361	AW839073		gb:CM2-LT0066-030100-109-d06 LT0066 Homo	27
40	428358	AA993222	Hs.101915	Stargardt disease 3 (autosomal dominant)	2.7 2.7
40	406625 416101	Y13647 R24854	Hs.119597 Hs.268806	stearoyl-CoA desaturase (della-9-desatur ESTs	2.7
	404606	F(24034	115.200000	Target Exon	2.7
	433921	AA618174		gb:nq14f01.s1 NCI_CGAP_Thy1 Homo sapiens	2.7
45	414272	AI651603	Hs.46988	ESTs	2.7 2.7
45	418047 421089	R37633 AB037771	Hs.4847 Hs.101799	ESTs KIAA1350 prolein	2.7
	412244	AW948175	113.101733	gb:RC0-MT0013-280300-021-c10 MT0013 Homo	2.7
	432434	AL161977	Hs.2994	PCTAIRE protein kinase 3	2.6 2.6
50	424153	AA451737	Hs.141496	MAGE-like 2 ESTs	2.6
30	427189 454454	H82453 AW612264	Hs.5635 Hs.131705		2.6
	426747	AA535210	Hs.171995	kaltikrein 3, (prostate specific antigen	2.6
	456791	H05202	Hs.133968	FGF receptor activating protein 1	2.6 2.6
55	405715 425494	N55540	Hs.78026	ENSP00000005198*:Mixed lineage kinase ML ESTs, Wealdy similar to similar to ankyr	2.6
55	430865	AI073424	Hs.5232	HSPC125 protein	2.6
	435767	H73505	Hs.117874		2.6 2.6
	410119	F07841	Hs.13926 Hs.115960	ESTs KIAA0939 protein	2.6
60	432146 448871	AW081072 BE616709	Hs.159265		2.6
50	414516	AI307802	Hs.135560	ESTs, Weakly similar to T43458 hypotheti	2.6
	429477	AJ275514	Hs.6658	ESTs	2.6 2.5
	400269	4144022229	Hs.322922	Eos Control 2 ESTs	2.5
65	443992 451926	AW022228 AW134519	Hs.96125	Homo sapiens, Similar to clone FLB3816,	2.5
05	435145	A1277259	Hs.116631	I ESTs	2.5
	420309		Hs.21766		2.5 2.5
	449709 416530		Hs.23918 Hs.79361	hypothetical protein PP5395 kallikrein 6 (neurosin, zyme)	2.5
70	411678		Hs.71465		2.5
	408119	W26213	Hs.10167	2 ESTs, Weakly similar to T00331 hypotheti	2.5
	436624		40545	fatty acid binding protein 1, liver	2.5 2.5
	458268 451336		Hs.10613 Hs.3610	1 ESTs ESTs	2.5
75	456924		Hs.19695		2.5
	455040			gb:QV0-CT0225-100400-187-d08 CT0225 Homo	2.5
	420033		Hs.29259		2.5 2.5
	448786		Hs.17907 Hs.23216		2.5
80	432251 408206			kinesin family member 3A	2.5
	440205	T86950	Hs.10544	8 ESTs, Wealdy similar to B34087 hypotheti	2.5
	442138	AA445973			2.5 2.4
	420912	AW853156	Hs.90787	ESTs	2.4

	439180	Al393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	2.4
	421025	AW958975	Hs.29397	Homo sapiens cDNA FLJ13226 fis, clone OV	2.4
	439973	A1733308	Hs.124663	ESTs	2.4
5	446847	T51454	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	24
3	414672 451522	Al218038 BE565817	Hs.48504 Hs.26498	ESTs, Moderately similar to ALU5_HUMAN A hypothetical protein FLJ21657	2.4 2.4
	433068	NM_006456	Hs.288215	sialytransferase	24
	446620	AA128808	Hs.179902	transporter-like protein	2.4
	423803	NM_005709	Hs.132945	POZ-73 protein	2.4
10	407978	AW385129	Hs.41717	phosphodiesterase 1A, calmodulin-depende	2.4
	425907	AA365752	Hs.155965	ESTs	24 24
	433819 446066	AW511097 Al343931	Hs.112765 Hs.149383	ESTs ESTs	24
	430573	AA744550	Hs.136345	ESTs	2.4
15	444992	R37658	Hs.21375	ESTs	24
	434975	AA657884	Hs.314413	ESTs	2.4
	458227	Z40670	Hs.181340	ESTs	24 24
	443244 432408	AI457235 N39127	Hs.166479	ESTs Weakly similar to A46010 X-linked	24
20	401600	BE247275		U5 snRNP-specific protein, 116 kD	2.3
	419066	Z98492	Hs.6975	PRO1073 protein	2.3
	424823	NM_006226	Hs.153322	phospholipase C, epsilon	2.3
	402124	1100440		NM_031891:Homo sapiens cadherin 20, type	2.3 2.3
25	416678 444897	N80448 AW137088	Hs.269106 Hs.144857	ESTs ESTs	2.3
23	425111	BE018485	Hs.30977	ESTs, Weakly similar to B34087 hypotheti	2.3
	400536	240.0.00		NM_000681°:Homo sapiens adrenergic, alph	2.3
	427544	AJ767152	Hs.181400	ESTs, Weakly similar to 178885 serine/th	2.3
20	459511	AJ142379	070044	gb:qg64c01.r1 Soares_testis_NHT Homo sap	23
30	415111	R39039 AI738815	Hs.279041 Hs.117323	EST . ESTs	2.3 2.3
	433331 440293	AI004193	Hs.22123	ESTs	2.3
	411770	NM_014278	Hs.71992	heat shock protein (hsp110 family)	2.3
26	416964	D87467	Hs.80620	guanine nucleotide exchange factor for R	2.3
35	419386	AA236867		ESTs, Wealthy similar to 138022 hypotheti	2.3 2.3
	402493	AI743260		mannosidase, alpha, class 1A, member 1 NM_003771*:Homo sapiens keratin, hair, a	2.3 2.3
	401783 420548	AA278246	Hs.920	ESTs	23
	419763	AI039691	Hs.127486	ESTs	2.3
40	421750	AK000768	Hs.107872	hypothetical protein FLJ20761	2.3
	406023			Target Exon	23
	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	2.3 2.3
	401586 404091			Target Exon Target Exon	23
45	456773	AI038192	Hs.129764	EGF-like repeats and discoidin Hike do	2.3
	414106	BE300325	Hs.77135	RNA binding protein	2.3
	454288	BE222648	Hs.241432	ESTs, Highly similar to c380A1.1b [H.sap	2.3
	441879	AI521936	Hs.107149	novel protein similar to archaeal, yeast	2.3 2.3
50	424724 415692	T06532 N51935	Hs.287709 Hs.47374	Homo sapiens cDNA: FLJ22674 fis, clone H Homo sapiens cDNA FLJ13561 fis, clone PL	2.3
50	416282	R86664	Hs.167257	brain link protein-1	2.2
	404659			ENSP00000239999*:HYPOTHETICAL 34.7 kDa P	2.2
	429956	AI374651	Hs.22542	ESTs ·	2.2
55	429670	L01087	Hs.211593	protein kinase C, theta	2.2 2.2
55	429655 458921	U48959 AI682088	Hs.211582 Hs.79375	myosin, light polypeptide kinase holocarboxylase synthetase (biotin-[prop	2.2
	436463	H06502	Hs.6656	ESTs	22
	408994	AW299520	Hs.43052	ESTs	2.2
<i>4</i> 0	413303	AW836130	Hs.75277	hypothetical protein FLJ 13910	2.2
60	418154	BE165866 AL044818	Hs.84928	nuclear receptor subfamily 1, group I, m nuclear transcription factor Y, beta	2.2 2.2
	418407 422907	ALU44616 AI879263	Hs.77273	Human glucose transporter pseudogene	2.2
	446377	AW014022	Hs.170953	ESTs	2.2
	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	2.2
65	449714	AB033015	Hs.23941	KIAA1189 protein	2.2
	408480	AI350337	Hs.164568	fibroblast growth factor 7 (keratinocyte DKFZP586L2024 protein	2.2 2.2
	410066 410912	AL117664 AW810224	Hs.58419	gb:MR4-ST0125-021199-017-e07 ST0125 Homo	2.2
	447163	AW292770	Hs.5542	DnaJ (Hsp40) homolog, subfamily C, membe	2.2
70	421709	AA159394	Hs.107056	CED-6 protein	2.2
	403728			Target Exon	2.2
	453359	AA448787	Hs.24872	ESTS	2.2 2.2
	411379 413427	AI816344 U31120	Hs.12554 Hs.845	ESTs, Weakly similar to NPL4_HUMAN NUCLE interleukin 13	2.2
75	409028	AB014513	Hs.49998	Z-band alternatively spliced POZ-motif	2.2
	413924	AL119964	Hs.75616	seladin-1	2.2
	403463			Target Exon	22
	408068	AW148652	Hs.167398		2.2 2.2
80	407819 414203	R42185 BE262170	Hs.102720 Hs.78629	ATPase, Na? transporting, beta 1 polypep	22
	448045	AJ297436	Hs.20166	prostate stem cell antigen	2.2
	449835	AW979300	Hs.293813	ESTs	22
	458547	AW204314	Hs.170784	ESTs	2.2

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	414276	BE297862		pb:601174780F1 NIH_MGC_17 Homo sapiens c Farget CAT	2.2
	427493 458441	H09037 AW842283	Hs.288232 (cyclin I	2.1
_	410705	BE004107	1	gb:CM0-BN0102-150300-288-112 BN0102 Homo	2.1
5	444647	H14718		Human clone 23589 mRNA sequence	2.1 2.1
	405502 400818			C7000609*:gi[628012 pir [A53933 myosin1 Target Exon	21
	435059	Z45270	Hs.235873	hypothetical protein FLJ22672	2.1
• •	426559	AB001914		paired basic amino acid cleaving system	2.1 2.1
10	445200	AA084460		somatostatin ESTs	2.1
	453396 443819	AW162768 AB033076		likely homolog of rat kinase D-interacti	2.1
	401929	ABUSSOID		C17001690;qil6005701 ref NP_009099.1 AT	2.1
	451032	W03692	Hs.323079	Homo sapiens mRNA; cDNA DKFZp564P116 (fr	2.1 2.1
15	433862	D86960		KIAAD205 gene product ESTs	2.1
	458694 417063	F12832 N50515		ESTs	2.1
	416935	AA190712		gb:zp87f09.r1 Stratagene HeLa cell s3 93	2.1
••	414446	AA147534	Hs.142019	ESTs, Wealdy similar to 1207289A reverse	2.1 2.1
20	434581	AA642402	Hs.59142 Hs.249163	ESTs fatty acid hydroxylase	2.1
	413835 426137	AI272727 AL040683	Hs.167031	DKFZP566D133 protein	2.1
	424481	R19453	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	2.1
	454339	AW381980		gb:QV4-HT0316-091199-028-d05 HT0316 Homo	21 21
25	407786	AA687538	Hs.38972 Hs.103253	tetraspan 1 perilipin	21
	421296 444200	NM_002666 AA327113	Hs.149057	ESTs	21
	409339	AB020686	Hs.54037	ectonucleotide pyrophosphatase/phosphodi	2.1
20	418410	AA811441	Hs.107393	chromosome 3 open reading frame 4	21 21
30	414759	AW295157	Hs.47587 Hs.296261	ESTs guanine nucleotide binding protein (G pr	2.1
	449511 451606	AI436187 AA018791	Hs.7945	AIF-75 binding protein protein	2.1
	437924	A1935344	Hs.164118	ESTs, Weakly similar to SL51_HUMAN SODIU	2.1
	449119	AI631195	Hs.232193	ESTs	2.1 2.1
35	431568	AW972316	Hs.283703	ESTs vesicle-associated membrane protein 1 (s	2.1
	447932 433516	AA837474 AA595802	Hs.20021 Hs.33410	ESTs, Wealdy similar to T17279 hypotheti	2.1
	441987	AW452234	Hs.128293	ESTs	2.1
40	414055	AW818687	Hs.5366	hypothetical protein FLJ21522	2.1 2.1
40	445066	BE178734	Hs.197422	ESTs gb:RC3-BN0036-090200-011-g06 BN0036 Homo	2.1
	455546 413607	AW994075 T64741		gb:yc48f11.r1 Stratagene liver (937224)	2.1
	456401	W28146		gb:43f11 Human retina cDNA randomly prim	2.0
4.5	407341	AA918886	Hs.204918	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.0 2.0
45	425055	AW961959	Hs.96940	ESTs DKFZP58680923 protein	2.0
	426917 419647	AA913814 AA348947	Hs.172854 Hs.91816	hypothetical protein	2.0
	412266	N59006	Hs.26133	FSTs	2.0
60	449658	AI964033	Hs.195730		2.0 2.0
50	424505	AA445131	Hs.124918 Hs.257194	KIAA1795 protein ESTs	2.0
	438219 425068	AI916151 AL048716	Hs.154387		2.0
	412949	AI471639	Hs.71913	ESTs	2.0
<i>E E</i>	418866	T65754		gbryc11c07.s1 Stratagene lung (937210) H	2.0 2.0
55	445071 456529	AI280246 AF014643	Hs.149504 Hs.100072		2.0
	406475	A 014043	113.100072	C15000508*:gi 2558825 gb AAC53387.1 (AF	2.0
	429656	X05608	Hs.211584	neurofilament, light polypeptide (68kD)	20 20
60	431542	H63010	Hs.5740	ESTs	2.0
60	452625 410378	AA724771 R23324	Hs.61425 Hs.41693	ESTs DnaJ (Hsp40) homolog, subfamily B, membe	2.0
	409767	AW501470	110,11000	gb:UI-HF-8P0p-aid-b-03-0-UI.r1 NIH_MGC_5	20
	446873		Hs.30724	ESTs	2.0 2.0
65	453938		Hs.36794	D-type cyclin-interacting protein 1 catherin 19, type 2	2.0
05	423605 420061		Hs.129887 Hs.29410		2.0
	439559			ESTs, Wealdy similar to 2109260A B cell	2.0
	449901			gb;wd15h01.x1 Soares_NFL_T_GBC_S1 Homo s	2.0 2.0
70	428304		Hs.98422 Hs.27425		2.0
70	432278 458480		TI3.21423	p30 DBC protein	2.0
	404559			Target Exon	2.0
	445831	NM_00605			2.0 2.0
75	427523		Hs.17952 Hs.75183		2.0
13	413055 444904				2.0
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80	42818				2.0
60	44877 45399				2.0
	42029	0 AW977318	B Hs.19448	O ESTs	2.0
	43146	7 N71831	Hs.25639	8 Homo sapiens mRNA; cDNA DKFZp434E0528 (f	2.0

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447965
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AA026735
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  60
                            59843_1
                                             A1792298 H14121 A1375113 AA960851 AA744592 AV648739 A1298360 AW293609
               458480
               TABLE 21C:
                                     Unique number corresponding to an Eos probeset Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA
               Pkey:
               Ref:
  65
                                      sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
                                      Indicates DNA strand from which exons were predicted.
               Strand:
               Mt_position:
                                      Indicates nucleotide positions of predicted exons.
               Pkey
400536
                                             Strand
                                                            Nt position
                             Ref
  70
                            9797380
                                                             170994-172025
                                             Minus
                                             Plus
                                                             172644-172765,173085-173200
                             8569994
               400818
                                                            93974-94099
               401586
                             9838242
                                             Micus
                                                             27363-27518,28727-28891,29526-29731
               401600
                             4388746
                                             Minus
                                                             139369-139827,140509-140591,140834-140990,141496-141657,141757-141882,142063-142283
                             7249190
               401783
                                             Plus
  75
                                                             3167-3286.4216-4310
                401929
                             3810670
                                              Minus
                                                             164206-164459
                             4033680
                                             Plus
                402124
                                                             205146-205240,205428-205542
                             9797670
                402493
                                             Minus
                                                             102596-102879
                             9929538
                                              Plus
                403463
                             9929739
                                              Minus
                                                             4831-7707
                403469
   80
                                                             18308-18458
                403582
                             8101186
                                             Plus
                                                             34481-34671
               403728
404091
                             7534291
                                              Minus
                             7684554
                                                             82121-83229
                                              Minus
                                                             73499-73651,89575-89739
                404559
                             8748893
```

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	404563	9838310	Plus	100136-100343
	404606	9212936	Minus	22310-23269
	404659	9797068	Minus	65026-67930
_	404746	7219894	Minus	32643-32834
5	405354	2642452	Plus	52213-53089
	405403	6850244	Minus	37491-37670,40951-41031
	405502	9211311	Minus	50360-50584
	405715	4156209	Plus	26293-26706
	406023	8272661	Plus	205623-205936
10	406475	9797684	Plus	125417-125563,128052-128180

TABLE 22A: ABOUT 301 GENES SIGNIFICANTLY DOWN-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT CNS
Table 22A lists about 301 genes significantly down-regulated in glioblastoma compared to normal adult CNS tissues. These were selected from 59680 probesets on the
Affymetriv/Eos Hu03 GeneChip array such that the ratio of "average" normal CNS to "average" glioblastoma was greater than or equal to 2. The "average" normal CNS level was set to the 75th percentile amongst various normal CNS issues. The "average" glioblastoma level was set to the 95th percentile amongst various tumor samples. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Prizey:

Unique Eos probeset identifier number

Exemplar Accession number, Genbank accession number

Unique either the problem of the p 15

20

UnigenelD: Unigene Title: R1:

Unigene number Unigene gene fille Ratio of CNS to GLIOBLASTOMA

	••••	, 200	,, 00 0		
	Pkev	ExAcon	UnigenelD	Unigene Title	RI
25	418318	U47732	Hs.84072	transmembrane 4 superfamily member 3	10.1
	445529	H14421	Hs.180513	ATP-binding cassette, sub-family A (ABC1	9.4
	415274	AF001548	Hs.78344	myosin, heavy polypeptide 11, smooth mus	7.5
	417167	AW206437	Hs.4290	ESTs	7.3
••	453165	S74727	Hs.32042	aspartoacytase (aminoacytase 2, Canavan	6.5
30	454076	AW204712	Hs.61957	ESTs	6.3 6.2
	417275	X63578	Hs.295449	parvalbumin	6.0
	412636	NM_004415		desmoptakin (DPI, DPII)	5.9
	409743	N48721	Hs.183506	hypothetical protein FLJ14213	5.6
25	424645	NM_014682	Hs.151449	KIAA0535 gene product	5.5
35	427322	AK002017	Hs.176227	hypothetical protein FLJ11155	5.2
	446390	AA233393	Hs.14992	hypothetical protein FLJ11151	5.2
	444409	AI792140	Hs.49265	ESTS	5.1
	409031	AA376836	Hs.288856	ESTs DnaJ (Hsp40) homolog, subfamily B, membe	4.8
40	408428	NM_014787	Hs.44896	DKFZP564C152 protein	4.8
40	428414	AL049980	Hs.184216	transthyretin (prealburnin, amyloidosis t	4.6
	428874	W32133	Hs.194366 Hs.99291	HSPC156 protein	4.6
	420605	BE391491		Homo sapiens cDNA FLJ12052 fis, clone HE	4.6
	445618	H79667	Hs.237642 Hs.31570	ESTs, Weakly similar to KIAA1324 protein	4.4
45	450715	A1266484 BE252383	Hs.184668	SBB131 protein	4.4
43	428508		Hs.180758	hypothetical protein PRO0082	4.3
	434064 410330	AL049045 AW023630	Hs.159425	ESTs	4.2
	426471	M22440	Hs.170009	transforming growth factor, alpha	4.2
	409231	AA446644	Hs.692	GA733-2 antigen; epithelial glycoprotein	4.2
50	448958	AB020651	Hs.22653	KIAA0844 protein	4.2
50	428465	AW970976	Hs.293653	ESTs	4.0
	429470	AI878901	Hs.203862	guanine nucleotide binding protein (G pr	4.0
	432298	AL118812	Hs.274293	Homo sapiens mRNA; cDNA DKFZp761G1111 (f	3.9
	427061	AB032971	Hs.173392	KIAA1145 protein	3.9
55	430261	AA305127	Hs.237225	hypothetical protein HT023	3.9
• •	435145	AI277259	Hs.116631	ESTs	3.8
	416101	R24854	Hs.268806	ESTs	3.8
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (lg),	3.8
	438202	AW169287	Hs.22588	ESTs	3.8
60	433558	AA833757	Hs.201769	ESTs, Weakly similar to T24435 hypotheti	3.7
	419956	AL137939	Hs.40096	ESTs	3.7
	430573	AA744550	Hs.136345	ESTs	3.7
	422546	AB007969	Hs.301478		3.7
	453344	BE349075	Hs.44571	ESTs	3.6
65	417620	R02530	Hs.191198		3.6 3.6
	421952	AA300900	Hs.98849	ESTs, Moderately similar to AF161511 1 H	3.6
	414631	AW970130	Hs.65406	ESTs	3.5
	437073	AI885608	Hs.94122	ESTs	3.5
70	441264	AA927170	Hs.23290	ESTs	3.5
70	433629	R13140	Hs.13359	ESTs	3.4
	415114	D60468	Hs.94181 Hs.71992	ESTs heat shock protein (hsp110 family)	3.4
	411770	NM_014278	NS./ 1992	gb:yu03c11.r1 Soares fetal liver spleen	3.4
	415666	H72693 AW963951	Hs.85618	ESTs	3.4
75	416851		Hs.8906	syntaxin 7	3.4
, 3	443037 449511	AW500305 Al436187	Hs.296261		3.4
	427176	AW381569	Hs.40334	ESTs	3.4
	42/1/6	AW361369 AW35060	Hs.32825	ESTs	3.3
	430/04	R44558	Hs.94002	ESTs	3.3
80	430865	AI073424	Hs.5232	HSPC125 protein	3.3
	457012	R41480	Hs.302754		3.3
	405354	1171700	10.000	CX000321:gij6671579 ref[NP_031518.1] ari	3.3
	432799	NM_016161	Hs.278960		3.3
	-GE: 33	0.0.0			

	429876 434348	A8028977 BE393191	Hs.225974 Hs.181795	KIAA1054 protein putative b,b-carotene-9',10'-dioxygenase	3.3 3.3
	441071	D79550	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	3.3
_	445279	R41900	Hs.22245	ESTs	3.2
5	414541	BE293116	Hs.76392	aldehyde dehydrogenase 1 family, member	3.2 3.2
	448072 402429	A1459306	Hs.24908	ESTs Target Exon	3.2
	433328	AW298159	Hs.23644	ESTs, Wealthy similar to S65824 reverse t	3.2
••	400138			Eos Control	3.1
10	414327	BE408145	Hs.185254	ESTs, Weakly similar to T24435 hypotheti	3.1 3.1
	459399 433582	BE407712 BE548749	Hs.153998 Hs.148016	creatine kinase, mitochondrial 1 (ubiqui ESTs	3.1
	434104	AF116691	Hs.116459	hypothetical protein PRO2198	3.0
1.5	404606			Target Exon	3.0
15	407173	T64349 N53097	Hs.193579	gb:yc10d08.s1 Stratagene lung (937210) H ESTs	3.0 3.0
	415672 448583	NM_015239	Hs.21542	KIAA1035 protein	3.0
	429043	AJ824977	Hs.145319	ESTs	3.0
20	439165	AA029517	Hs.95162	KCNQ1 overlapping transcript 1	29 29
20	449561 436427	A)022240 A)344378	Hs.17924 Hs.143399	ESTs, Moderately similar to ALU1_HUMAN A ESTs	29
	405403	MOTIO	113.170003	Target Exon	29
	452197	AW023595	Hs.232048	ESTs	29
25	437357	AL359559	Hs.331666	Homo sapiens mRNA; cDNA DKFZp762O2215 (f	2.9 2.9
23	439272 415839	AAB32474 R40611	Hs.25851 Hs.94694	ESTs ESTs	29
	411906	AW875765	1 0.0 100 1	gb:QV2-PT0012-020500-186-a08 PT0012 Homo	2.9
	409403	AA668224	Hs.6634	Homo sapiens cDNA: FLJ22547 fis, clone H	2.9
30	412258	AA376768 AW292532	Hs.324841 Hs.343667	hypothetical protein FLJ22622 hornolog of yeast long chain polyunsatura	2.8 2.8
30	435836 433109	N58907	Hs.162430	EST	28
	404563			Target Exon	2.8
	427974	BE093023	Hs.188767	ESTs	2.8
35	413324 409263	V00571 AA069573	Hs.75294 Hs.50319	conticotropin releasing hormone ESTs	2.7 2.7
55	454247	AJ243950	Hs.46735	deafness locus associated putative guani	2.7
	449180	AI633836	Hs.195649	ESTs	2.7
	416004	D11880	Hs.299254	Homo sapiens cDNA: FLJ23597 fis, clone L	2.7 2.7
40	424994 430371	AW954525 D87466	Hs.240112	gb:EST366595 MAGE resequences, MAGC Homo KIAA0276 protein	2.7
40	449117	AW449310	Hs.210262	ESTs, Wealty similar to HSS2_HUMAN HEPAR	2.7
	451007	H38108	Hs.32759	ESTs	2.7
	414502	AL133721	Hs.224680	ESTS	2.7 2.7
45	458793 459053	N80159 AI807052	Hs.121849 Hs.210361	microtubule-associated proteins 1A/1B li ESTs	27
	427229	AI799751	Hs.5635	ESTs	2.7
	425649	U30930	Hs.158540	UDP glycosyltransferase 8 (UDP-galactose	2.7 2.7
	444922 433921	AI921750 AA618174	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL gb:nq14f01.s1 NCI_CGAP_Thy1 Homo sapiens	2.7
50	414272	AI651603	Hs.46988	ESTs	2.7
	418047	R37633	Hs.4847	ESTs	2.7
	421089	AB037771	Hs.101799	KIAA1350 protein	2.7 2.6
	416498 414290	U33632 AI568801	Hs.79351 Hs.71721	potassium channel, subfamily K, member 1 ESTs	2.6
55	433703	AA210863	Hs.3532	nemo-like kinase	2.6
	408739	W01556	Hs.238797	ESTs, Moderately similar to 138022 hypot	26
	414602 422137	AW630088 AJ236885	Hs.76550 Hs.112180	Homo sapiens mRNA; cDNA DKFZp564B1264 (f zinc finger protein 148 (pHZ-52)	2.6 2.6
	442023	A1187878	Hs.144549		2.6
60	421709	AA159394	Hs.107056	CED-6 protein	2.6
	426747	AA535210	Hs.171995	kaffikrein 3, (prostate specific antigen gb:RC0-MT0013-280300-021-c10 MT0013 Homo	2.6 2.6
	412244 419386	AW948175 AA236867		ESTs, Weakly similar to 138022 hypotheti	2.6
	423665	BE167153	Hs.24380	ESTs	2.6
65	430320	BE245290	Hs.239218		2.6
	408468	AJ909712 AF063228	Hs.93837 Hs.65248	phosphatidylinositol transfer protein, m dynein, cytoplasmic, intermediate polype	2.6 2.6
	410657 448871	BE616709	Hs. 159265		2.6
	414516	Al307802	Hs.135560		2.6
70	459080	AW192083	Hs.290855	ESTs	2.5 2.5
	455040 435712	AW852286 AA694607	Hs.176956	gb:QV0-CT0225-100400-187-d08 CT0225 Homo ESTs	2.5
	431662	AA513406	Hs.152307		2.5
25	435902	AA701867	Hs.297726	ESTs	2.5
75	436624	T64297	U- 3377A	fatty acid binding protein 1, liver	2.5 2.5
	443155 439183	R54485 AW970600	Hs.23772 Hs.303261	ESTs ESTs	2.5
	426365	AA376667	Hs.10283	RNA binding motif protein 68	2.5
00	420033	059502	Hs.292590		2.5
80	408438 440205	AB011180 T86950	Hs.100960 Hs.105448		2.5 2.5
	448786		Hs.179075	Homo sapiens cDNA FLJ11881 fis, clone HE	2.5
	432251	AW972983			2.5

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					2.4
			Hs.112237 (ESTs pb:no87h09.s1 NCI_CGAP_AA1 Homo sapiens	2.4
	433670	AA604405 AW072330		ESTs	2.4
	452022 408814			hypothetical protein FLJ11155	2.4
5	403469			Target Exon	24 24
	450374		Hs.60293	Homo sapiens clone 122482 unknown mRNA Homo sapiens, Similar to clone FLB3816,	2.4
	451926	AW134519 AI911527		ESTs	2.4
	443622 456791	H05202	Hs.133968	FGF receptor activating protein 1	24
10	414672	AI218038	Hs.48504	ESTs, Moderately similar to ALU5_HUMAN A	2.4 2.4
	451522	8E565817		hypothetical protein FLJ21657	2.4
	4 <u>22</u> 414	AW875237		ESTs Down syndrome critical region gene 1-lik	2.4
	425383	D83407 AA336519	Hs.156007 Hs.83623	nuclear receptor subfamily 1, group 1, m	2.4
15	438086 410240	AL157424	Hs.61289	synaptojanin 2	24
10	432408	N39127		ESTs, Weakly similar to A46010 X-linked	2.4 2.4
	458227	Z40670	Hs.181340	ESTS	2.4
	431325	AW026751	Hs.5794	ESTs, Wealdy similar to 2109260A B cell US snRNP-specific protein, 116 kD	23
20	401600 422963	BE247275 M79141	Hs.13234	ESTs	23
20	444897	AW137088	Hs.144857	ESTs	2.3
	418207	C14685	Hs.34772	ESTs	2.3 2.3
	445071	AJ280246	Hs.149504	ESTs profine-rich Gla (G-carboxyglutarnic acid	2.3
25	407868	NM_000950	Hs.40637 Hs.117323	ESTs	2.3
23	433331 440293	A1738815 A1004193	Hs.22123	ESTs	23
	428850	AA934975	Hs.185076	ESTs	2.3 2.3
	401783			NM_003771*:Homo sapiens keratin, hair, a	2.3 2.3
20	419763	AI039691	Hs.127486	ESTs proprotein convertase subtilisin/kexin t	2.3
30	416018	AW138239 AW853156	Hs.78977 Hs.90787	ESTs	2.3
	420912 442097	AW015799	Hs.128474	ESTs	2.3
	425907	AA365752	Hs.155965	ESTs	2.3 2.3
	404091			Target Exon	2.3
35	414106	8E300325	Hs.77135	RNA binding protein ESTs, Highly similar to c380A1.1b [H.sap	2.3
	454288 441040	BE222648 AW449782	Hs.241432 Hs.178803	ESTs	2.3
	424724	T06532	Hs.287709	Homo sapiens cDNA: FLJ22674 fis, clone H	2.3
	441879	AI521936	Hs.107149	novel protein similar to archaeal, yeast	2.3 2.2
40	407988	N47760	Hs.285107	hypothetical protein FLJ13397 centrin, EF-hand protein, 3 (CDC31 yeast	2.2
	452420	BE564871	Hs.29463 Hs.202263	ESTs	2.2
	458676 418407	A1692464 AL044818	Hs.84928	nuclear transcription factor Y, beta	2.2
	453938	AF082569	Hs.36794	D-type cyclin-interacting protein 1	2.2
45	407978	AW385129	Hs.41717	phosphodiesterase 1A, calmodulin-depende	2.2 2.2
	420548	AA278246	Hs.920	ESTs Human glucose transporter pseudogene	2.2
	422907 446351	A1879263 AW444551	Hs.77273 Hs.35380	x 001 protein	2.2
	442117	AW664964	Hs.128899	· · · · · · · · · · · · · · · · · ·	2.2
50	429598	AA811257	Hs.269710	ESTs	2.2 2.2
	408480	AI350337	Hs.164568	fibroblast growth factor 7 (keratinocyte gb:CM2-LT0066-030100-109-d06 LT0066 Homo	2.2
	411361	AW839073 AA406062	Hs.98002	ESTs	2.2
	459697 409856		113.30002	gb:UI-HF-BR0p-ajq-g-04-0-UI.r1 NIH_MGC_5	2.2
55	444760	AI796296	Hs.208062	P ESTs	2.2 2.2
	443258		Hs.9098	sulfate transporter 1	2.2
	428206		Hs.183006 Hs.13926	KIAA0836 prolein ESTs	2.2
	410119 413427		Hs.845	interleukin 13	2.2
60	438021		Hs.32427	5 WW domain-containing protein 1	2.2 2.2
	428652		Hs.33622		2.2
	429655		Hs.21158 Hs.14149		2.2
	424153 413303				2.2
65	427287			8 KIAA0938 protein	2.2
	449658		Hs.19573		2.2 2.2
	441984		Hs.8059	synaptotagmin IV hypothetical protein PP5395	22
	449709 408068			. 100	2.2
70	407819		Hs.10272	O ESTs	22
. •	41420		Hs.78629	ATPase, Na? transporting, beta 1 polypep	2.2 2.2
	45433	9 AW381980		gb:OV4-HT0316-091199-028-d05 HT0316 Homo	2.2
	44804		Hs.20166	prostate stem cell antigen p30 DBC protein	2.2
75	45848 44983		0 Hs.2938		2.2
,,	44963 45854			B4 ESTs	2.2
	41167	8 Al907114	Hs.7146	5 squalene epoxidase	21 21
	44478	3 AK001468			2.1
80	42463			gb:wd15h01.x1 Soares_NFL_T_GBC_S1 Homo s	2.1
00	44990 43158			76 S-adenosytmethionine decarboxylase 1	2.1
	41053	8 AW75311	5	gb:PMO-CT0248-131099-001-h12 CT0248 Homo	2.1 2.1
	42677		4 Hs.3628	ESTs	21

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	433862	D86960	Hs.3610	KIAA0205 gene product	2.1
	458694 417063	F12832	Hs.3610 Hs.45061	ESTs ESTs	2.1 2.1
	416935	N50515 AA190712	ns.43001	gb:zp87f09ur1 Stratagene HeLa cell s3 93	2.1
5	436489	AJ272269	Hs.121429	zinc-binding protein Rbcc728	2.1
	431128	AJ203545	Hs.296169	S-phase response (cyclin-related)	2.1
	442310	AF033199	Hs.8198	zinc finger protein 204	2.1 2.1
	432434 400339	A£161977 X57131	Hs.2994 Hs.248209	PCTAIRE protein kinase 3 H2A histone family, member F, pseudogene	2.1
10	432266	AK000385	Hs.274222	hypothetical protein FLJ20378	21
	414759	AW295157	Hs.47587	ESTs	2.1
	438219	AI916151	Hs.257194	ESTs	2.1
	451336 430538	AI264643 AB032435	Hs.3610 Hs.242821	ESTs differentiation-associated Na-dependent	2.1 2.1
15	413493	BE144444	113.242021	gb:MR0-HT0168-141199-002-09 HT0168 Homo	2.1
	428501	ALD41162	Hs.98587	ESTs	2.1
	431568	AW972316	Hs.283703	ESTs	2.1
	456177 441976	NM_012391 AA428403	Hs.79414 Hs.106131	prostate epithelium-specific Ets transcr ESTs	2.1 2.1
20	421311	N71848	Hs.283609	hypothetical protein PRO2032	2.1
	428358	AA993222	Hs.101915	Stargardt disease 3 (autosomal dominant)	21
	439973	AI733308	Hs.124663	ESTs	21
	446185 451606	AI279191 AA018791	Hs.149454 Hs.7945	ESTs, Wealthy similar to DSR6_HUMAN DOWN AIE-75 binding protein protein	2.1 2.1
25	433516	AA595802	Hs.33410	ESTs, Weakly similar to T17279 hypotheti	2.1
	441987	AW452234	Hs.128293	ESTs	2.1
	457140	Al279960	Hs.178140	ESTs	2.1
	414055 445066	AW818687 BE178734	Hs.5366 Hs.197422	hypothetical protein FLJ21522 ESTs	2.1 2.1
30	459265	A#003616	113.13/422	gb:AJ003616 Selected chromosome 21 cDNA	2.0
	425337	AA355442	Hs.169054	ĚSTs	2.0
	409339	AB020686	Hs.54037	ectonucleotide pyrophosphatase/phosphodi	2.0
	453023 425055	AW028733 AW961959	Hs.31439 Hs.96940	serine protease inhibitor, Kunitz type, ESTs	2.0 2.0
35	425068	AL048716	Hs.154387	KIAA0103 gene product	2.0
	444700	NM_003645	Hs.11729	fatty-acid-Coenzyme A ligase, very long-	2.0
	424823	NM_006226	Hs.153322	phospholipase C, epsilon	2.0
	450103	R08665	Hs.17244	hypothetical protein FLJ13605	2.0 2.0
40	448519 440808	AW175665 AK001339	Hs.278695 Hs.7432	Horno sapiens prostein mRNA, complete cds hypothetical protein FLJ 10477	2.0
	429968	AA322503	Hs.227011	G-substrate	2.0
	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	2.0
	433068	NM_006456	Hs.288215	sialyltransferase	2.0 2.0
45	416982 423479	J05401 NM_014326	Hs.80691 Hs.129208	creatine kinase, mitochondrial 2 (sarcom death-associated protein kinase 2	2.0
	407341	AA918886	Hs.204918	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.0
	452625	AA724771	Hs.61425	ESTS	2.0
	410378	R23324	Hs.41693	DnaJ (Hsp40) homotog, subfamily B, membe qb;UI-HF-BP0p-aid-b-03-0-UI.r1 NIH_MGC_5	2.0 2.0
50	409767 415925	AW501470 H09474	Hs.202341	Homo sapiens cDNA: FLJ23573 fis, clone L	2.0
	405670	*****	1 10.12.22	C2000627":gij12034653lgbjAAG45951.1JAF22	2.0
	408206	AF041853	Hs.43670	kinesin family member 3A	2.0
	458660	AJ299739	Hs.99601	hypothetical protein FLJ 12553	2.0 2.0
55	432278 404559	AL137506	Hs.274256	hypothetical protein FLJ23563 Target Exon	2.0
	403728			Target Exon	2.0
	413055	AV655701	Hs.75183	cytochrome P450, subfamily IIE (ethanol-	2.0
	407786 413266	AA687538 BE300352	Hs.38972	tetraspan 1 gb:600944231F1 NiH_MGC_17 Homo sapiens c	2.0 2.0
60	453994	BE180964	Hs.165590	ribosomal protein S13	20
	451583	AI653797	Hs.24133	ESTs	2.0
	443244	AI457235	Hs.166479	ESTs	2.0
	453396	AW162768	Hs.22620 Hs.339283	ESTs Human DNA sequence from clone RP1-187J11	2.0 2.0
65	415694 459511	AW194301 AI142379	ns.333263	gb:gg64c01.r1 Soares_testis_NHT Homo sap	2.0
•-	450757	BE081050	Hs.31570	ESTs. Weakly similar to KIAA1324 protein	2.0
	451032	W03692	Hs.323079	Homo sapiens mRNA; cDNA DKFZp564P116 (fr	2.0
	440509	BE410132	Hs.134202 Hs.11506	ESTs, Weakly similar to T17279 hypotheti Human clone 23589 mRNA sequence	2.0 2.0
70	444647 447932	H1471B AA837474	Hs.20021	vesicle-associated membrane protein 1 (s	2.0
	444749	Al190672	Hs.65926	ESTs	2.0
	446277	AI284218	Hs.159204		2.0
	452550	AA026735	Hs.326048	Homo sapiens mRNA; cDNA DKFZp434M0420 (I hect domain and RLD 3	2.0 2.0
75	453843 445725	D25215 AK000956	Hs.35804 Hs.13209	hypothetical protein FLJ10094	2.0
	409265	T78737	Hs.321062		2.0
	TABLE 2	220.			
	1 ABLE 4	LEAD.			

80

TABLE 228:
Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey CAT Number Accession

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AW501470 AW502931 AW499500
                                          1154015_1
1156268_1
                    409767
                                                                       AW502082 AW502979 AW502807 AW501876
                    409856
                                                                        AW753115 AW753113 R45779
                                           1207341_1
                    410538
                                                                        AW839073 AW839234 AW839230 AW878302 AW839109 AW843897
                                           1240611_1
                    411361
                                                                      AW875765 H50294 AW875444

AW948175 AW947637 AW902869 AW947537 AW947531 AW947532 AW947530

NM_004415 AL031058 M77830 BE149760 AW752599 AW848723 AW376897 AW376817 AW376699 AW848371 AW376782 AW848789 AW361413

AW849074 AW997139 AW799304 AW799309 BE077002 BE077017 BE185187 AW997196 BE156621 BE179915 BE005561 BE143155 AW890985

BE002107 AW103521 AAB57316 AW383133 BE011378 AW170253 BE185750 AW885475 BE160433 J05211 BE082576 BE082584 BE004047

AW607238 AW377700 AW377699 BE082556 BE082505 BE082507 BE082514 AW178000 AW177933 AJ905935 AW747877 AW748114 BE148516

AW265328 AW847678 AW847688 AW365115 AW365148 AW365153 AW365156 AW365175 AW365154 AW066840 BE092272 AW365145

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AW999515 BE182166 BE144243 BE001923 AJ951766 AJ434518 BE184920 BE184933 AJ284090 BE184941 AW804674 BE184924 CV4715 W39488

AW999515 BE184948 BE159646 AW606653 AA099891 AA131128 AA337270 AA340777 AW384371 AA852212 RB6704 AW366566 AW364859

AA025851 AA025852 AA455100 AA719958 AW352220 AW996245 BE165351 BE073467 AA377127 AW390264 AW609750 AW391912 AW849690

T87267 AW853312 AA852213 W74149 BE009090 AA056401 H91011 AW366529 AW390272 C18467 AW674920 NS7176 AA026680 AW177787 AA026654 AW177786 BE092137 BE092138 AW1777784 AI022862 BE091653 AW376811 AW848592

AA040018 BE185331 BE182164 AA368564 AW951576 T29918 AA131077 W95048 W25458 AW205789 H90899 N29754 W32490 R20904 BE167181
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                                                                        AW875765 H50294 AW875444
                    411906
                                           1265204_1
                                           1284692_1
                    412244
                                           13165 1
                    412636
10
15
                                                                        H93284 AA026863 AW177787 AA026654 AW177786 BE092134 BE092137 BE092136 AW177784 AI022862 BE091653 AW376811 AW848592
AA040018 BE185331 BE182164 AA368564 AW951576 T29918 AA131077 W95048 W25458 AW205789 H90899 N29754 W32490 R20904 BE167181
BE167165 N84767 H27408 H30146 A1190590 C03378 AI554403 AI205263 AA128470 AI392926 AF139065 AW370813 AW370827 AW798417
AW798780 AW798883 AW798569 R33557 AA149190 C03029 AW177783 AA088866 AW370829 AA247685 BE002273 AI760816 AI439101 AW879451
AI700963 AA451923 AI340326 AI590975 T48793 AI568096 AI142882 AA039975 AI470146 AA946936 BE002273 AI760816 AI439101 AW879451
AI700963 AA451923 AI340326 AI590975 T48793 AI568096 AI142882 AA039975 AI470146 AA946936 BE067737 BE067786 W19287 AA644381
AA702424 A417612 AI306554 AI668869 AI568892 AW190555 AI571075 AI220573 AA065627 AI471874 AI304772 AW517828 AI915596 AI627383
AIZ70345 AW021347 AW166807 AW105614 AI346078 AA552300 W95070 AI494069 AI911702 AA149191 AA026864 AI830049 AI887258 AW780435
AI910434 AI819984 AI858282 AI078449 AI025932 AI860584 AI635878 AA026047 AA703232 D12062 AW192085 AA658154 AW514597 AW591892
T87181 AA782066 AW243815 AW150038 AW268383 AW004633 AI927207 AA782109 AW473233 AI804485 AW169216 AI572669 AA602182
AW015480 AW771865 AI270027 AA961816 AA283207 AI076962 AI498487 AI348053 AI783914 H44405 AW799118 AA128330 AA515500 AA918281
W02156 AI905927 AA022701 W38382 R20795 T77861 AW860878
20
 25
                                                                          W02156 Al905927 AA022701 W38382 R20795 T77861 AW860878
                                                                          BE300352 BE299274 BE075351 BE297444
                       413266
                                             1356260 1
                                             1373555_1
                                                                           BE144444 BE144430
                       413493
                                                                          H72693 R08673 H72694 F20990 R08580
                       415666
                                              1543492_1
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 30
                                             163179_1
184356_1
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                                                                          AA236867 AA237066 AA354236 AW957759 H08961
                       419386
                                                                          AW954525 A1372685 AA349501 A1372687 H10564
N39127 F20776 A1082691 AA865520 F36964 F33894
AA604405 BE062234 AW748386
                                             245786_1
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                        432408
                                              346286_2
                        433670
                                             372721_1
                                                                            AA618174 AI114549 R36464 R36465
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                                                                            T64297 AA894931 NM_001443 M10050 AW843109 AI698516 T53219 T48785 T64166 AA706930 R29613 T55913 T56518 T64679 R29666 M10617
                                              4237 5
                        436624
                                                                            AJ768596 AA 101894 W90338 AJ742193 AW752206 AA099433 T53220 AW082135 AW272775 T29562 T55862 AJ343047 AJ345671 T68235 T68121
                                                                            AW842284
                                                                            AI674072 BE268487
                        449901
                                              818599 1
                                                                            AW381980 BE152244 BE152235 BE152238 BE152232
  40
                                              1122972 1
                        454339
                                                                            AW852286 AW851934 AW852096 AW852274
AI792298 H14121 AI375113 AA960851 AA744592 AV648739 AI298360 AW293609
                                              1250028_1
                        455040
                         458480
                                               59843_1
                                                                            AJ003616 AJ003654 AJ003617
                         459265
                                              966590 1
   45
                        TABLE 22C:
                                                               Unique number corresponding to an Eos probeset
Sequence source. The 7 digit numbers in this column are Senbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA
                          Pkey:
                          Ref.
                                                               sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
                                                                Indicates DNA strand from which exons were predicted.
                          Strand:
    50
                                                                Indicates nucleotide positions of predicted exons.
                          Nt_position:
                                                                                                        Nt position
                                                Ref
                                                                             Strand
                                                                                                       27363-27518, 28727-28891, 29526-29731
139369-139827,140509-140591, 140834-140990, 141496-141657, 141757-141882, 142063-142283
                                                4388746
                                                                             Minus
                          401600
                          401783
                                                7249190
                                                                                                        57622-57793,59282-59402,59624-59827
    55
                          402429
                                                9796372
                                                                             Minus
                                                                                                        4831-7707
                          403469
                                                9929739
                                                                             Minus
                           403728
                                                7534291
                                                                              Minus
                                                                                                        34481-34671
                                                                                                        82121-83229
73499-73651,89575-89739
                           404091
                                                7684554
                           404559
                                                8748893
                                                                               Mirus
                                                                                                         100136-100343
     60
                                                9838310
                           404563
                                                                               Plus
                                                                                                         22310-23269
                           404606
                                                9212936
                                                                               Minus
                           405354
                                                 2642452
                                                                               Plus
                                                                                                         52213-53089
                                                                                                         37491-37670.40951-41031
                           405403
                                                 6850244
                                                                               Minus
                                                                                                         96543-96870
                           405670
                                                 4662655
                                                                               Plus
     65
                           TABLE 23A: ABOUT 441 GENES SIGNIFICANTLY DOWN-REGULATED IN LOWER GRADE GLIOBLASTOMA COMPARED TO NORMAL ADULT CNS
                          TABLE 23A: ABOUT 441 GENES SIGNIFICANTLY DOWN-REGULATED IN LOWER GRADE GLIBBLASTOMA COMPARED-TO NORMAL ADULT ONS
Table 23A lists about 441 genes significantly down-regulated in lower grade glioblastoma (LGG) compared to normal adult CNS tissues. These were selected from 59680 probesets
on the Afymetrix/Eos Hx/03 GeneChip array such that the ratio of "average" normal CNS to "average" LGG was greater than or equal to 2.5. The "average" normal CNS to level was set
to the 75° percentile amongst various normal CNS tissues. The "average" LGG level was set to the 95° percentile amongst various normal CNS tissues. The "average" LGG level was set to the 95° percentile amongst various normal cns to remove gene-specific
background levels of non-specific hybridization, the 10° percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before
      70
                            the ratio was evaluated.
                                                                  Unique Eos probeset identifier number
                            Pkey:
                                                                   Exemplar Accession number, Genbank accession number
                            ExAccn:
       75
                            UnigenelD:
                                                                   Unigene number
                                                                   Unigene gene title
Ratio of CNS to LOWER GRADE GLIOBLASTOMA
                             Unigene Title:
                             R1
                                                                                UnigenelD
                                                                                                         Unigene Title
                                                                                                          collagen, type XVIII, alpha 1
transmembrane 4 superfamily member 3
        80
                                                                                Hs.78409
                             415388
                                                   AF018081
                                                                                                                                                                                                                                            10.1
                                                                                Hs.84072
                             418318
                                                   U47732
                                                                                                          ATP-binding cassette, sub-family A (ABC1
                                                                                 Hs.180513
                                                   H14421
                             445529
                                                                                                          5T4 oncofetal trophoblast glycoprotein
                                                                                Hs.82128
                                                   BE270266
```

	422746	NM_004484	Hs.119651	glypican 3	7.7
	448362	AA641767	Hs.21015	hypothetical protein DKFZp564L0864 simil	7.7
	430573	AA744550	Hs.136345	ESTs	7.6
5	415274	AF001548	Hs.78344	myosin, heavy polypeptide 11, smooth mus	7.5 7.4
,	419290 424670	AI128114 W61215	Hs.112885 Hs.116651	spinal cord-derived growth factor-B epithelial V-like antigen 1	7.3
	417167	AW206437	Hs.4290	ESTs	7.3
	416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin (7.3
10	424632	AB014523	Hs.151406	KIAA0623 gene product	6.9 6.5
10	453165 411770	S74727 NM_014278	Hs.32042 Hs.71992	aspartoacytase (aminoacytase 2, Cenavan heat shock protein (hsp110 family)	6.5
	439272	AA832474	Hs.25851	ESTs	6.5
	414831	M31158	Hs.77439	protein kinase, cAMP-dependent, regulato	6.4
16	454076	AW204712	Hs.61957	ESTs	6.3
15	446390 430865	AA233393	Hs.14992	hypothetical protein FLJ11151 HSPC125 protein	6.3 6.3
	434064	A1073424 AL049045	Hs.5232 Hs.180758	hypothetical protein PR00082	6.2
	417458	NM_005655	Hs.82173	TGFB inducible early growth response	6.1
20	412636	NM_004415		desmoplakin (DPI, DPII)	6.0
20	409743	N48721	Hs.183506	hypothetical protein FLJ14213	5.9 5.8
	430998 434725	AF128847 AK000796	Hs.204038 Hs.4104	indolethylamine N-methyltransferase hypothetical protein	5.6
	417175	R44558	Hs.94002	ESTs	5.6
0.5	417275	X63578	Hs.295449	parvalbumin	5.5
25	427322	AK002017	Hs.176227	hypothetical protein FLJ11155	5.5
	431009 420297	BE 149762 AI628272	Hs.48956 Hs.88323	gap junction protein, beta 6 (connexin 3 ESTs, Wealdy similar to ALU1_HUMAN ALU S	5.4 5.4
	412472	AW975398	Hs.293836	ESTs	5.4
	443258	AF169301	Hs.9098	sulfate transporter 1	5.3
30	427210	BE396283	Hs.173987	eukaryotic translation initiation factor	5.3
	442064	AI422867	Hs.88594	ESTS	5.2 5.2
	438868 444409	AW246243 A1792140	Hs.334800 Hs.49265	hypothetical protein FLJ20974 ESTs	5.2 5.2
	442310	AF033199	Hs.8198	zinc finger protein 204	5.1
35	409031	AA376836	Hs.288856	ESTs	5.1
	438460	AB020702	Hs.6224	KIAA0895 protein	5.1
	411939	AI365585	Hs.146246	ESTs	5.0 5.0
	448429 413293	D17408 AL047483	Hs.21223 Hs.302498	catponin 1, basic, smooth muscle GTP-binding protein homologous to Saccha	5.0
40	408968	AI652236	Hs.49376	hypothetical protein FLJ20544	5.0
	443491	AW499665	Hs.9456	SWI/SNF related, matrix associated, acti	4.9
	448960	AF006513	Hs.22670	chromodomain helicase DNA binding protei	4.9
	416101 433558	R24854 AA833757	Hs.268806 Hs.201769	ESTs ESTs, Weakly similar to T24435 hypotheti	4.9 4.9
45	424645	NM_014682	Hs.151449	KIAA0535 gene product	4.8
	437679	NM_014214	Hs.5753	inositol(myo)-1(or 4)-monophosphatase 2	4.8
	408428	NM_014787	Hs.44896	OnaJ (Hsp40) homolog, subfamily B, membe	4.8
	414502	AL133721	Hs.224680	ESTs	4.8 4.8
50	442572 -412700	A1001922 BE222433	Hs.135121 Hs.239208	hypothetical protein FLJ22415 ESTs, Weakly similar to I38022 hypotheti	4.8
50	422603	BE242587	Hs.118651	hernatopoietically expressed homeobox	4.8
	420605	BE391491	Hs.99291	HSPC156 protein	4.7
	422482	AI439905	Hs.344476	gb:ti57g08.x1 NCI_CGAP_Lym12 Homo sapien	4.7
55	416636 409263	N32536 AA069573	Hs.42645 Hs.50319	solute carrier family 16 (monocarboxylic ESTs	4,7 4,7
JJ	410657	AF063228	Hs.65248	dynein, cytoplasmic, intermediate polype	4.6
	457216	AA452554	Hs.283697	ESTs, Weakly similar to A41796 neural re	4.6
	433423	BE407127	Hs.8997	heat shock 70kD protein 1A	4.6
60	449901	AI674072	Hs.237642	gb:wd15h01.x1 Soares_NFL_T_GBC_S1 Homo s Homo saniens cONA FI 112052 fis clone HE	4.6 4.6
JU	445618 431582	H79667 F07136	Hs.237642 Hs.261828	Homo sapiens cDNA FLJ12052 fis, clone HE G protein-coupled receptor kinase 7	4.5
	424675	NM_005512	Hs.151641	glycoprotein A repetitions predominant	4.5
	449511	AI436187	Hs.296261	guanine nucleotide binding protein (G pr	4.5
65	401500	BE247275		U5 snRNP-specific protein, 116 kD	4.5 4.5
03	447135 426689	T58148 BE245550	Hs.171825	gb:yb98g06.s1 Stratagene tung (937210) H basic helix-loop-helix domain containing	4.4
	429598	AA811257	Hs.269710		4.4
	428206	AB020643	Hs.183006	KIAA0836 protein	4.4
70	450715	AI266484	Hs.31570	ESTs, Wealthy similar to KIAA1324 protein	4.4
70	428508	BE252383 A)277259	Hs.184668 Hs.116631		4.4 4.4
	435145 405670	NIZ11233	ID. 110031	C2000627*:gij12034653lgblAAG45951.1JAF22	4.4
	442321	AF207664	Hs.8230	a disintegrin-like and metalloprotease (4.3
75	427670	BE612888	Hs.180224	myosin regulatory light chain	4.3
75	428465	AW970976	Hs.293653		4.3
	449180	AI633836 AV653231	Hs.195649	ESTs CCAAT/enhancer binding protein (C/EBP),	4.3 4.3
	402364 426471	M22440	Hs.170009		4.2
00	419386	AA236867		ESTs, Weakly similar to 138022 hypotheti	4.2
80	441408	A1733249	Hs.126897		4.2
	419631 409231	AW188117 AA446644	Hs.303154 Hs.692	popeye protein 3 GA733-2 antigen; epithelial glycoprotein	4.2 4.2
	448958	AB020651	Hs.22653	KIAA0844 protein	4.2
				•	

	404020	A A 2000CE 2	Un 111100	Name and an artist of the complete	4.2
	421878 422278	AA299652 AF072873	Hs.111496 Hs.114218	Homo sapiens cDNA FLJ11643 fis, clone HE frizzled (Drosophila) homolog 6	4.2
	459053	AI807052	Hs.210361	ESTs	4.1
_	450600	BE079478	Hs.24880	ESTs	4.1
5	415839	R40611	Hs.94694	ESTs	4,1 4,1
	450374	AA397540 AF114494	Hs.60293 Hs.114062	Homo sapiens clone 122482 unknown mRNA protein tyrosine phosphatase-like (proli	4.1
	422270 405674	AF 114454	NS.114002	NM_022775:Homo sapiens hypothetical prot	4.1
	453906	AW444952	Hs.257054	ESTs	4.1
10	419318	AW969742	Hs.291005	ESTs	4.0
	456382	NM_001126	Hs.90011	adenylosuccinate synthase	4.0 4.0
	435902	AA701867	Hs.297726	ESTs	4.0 4.0
	449483 434228	AK001971 Z42047	Hs.23607 Hs.283978	hypothetical protein FLJ11109 Horno sapiens PR02751 mRNA, complete cds	4.0
15	403890	242041	115.200310	C5002036*:gi[10241574]emb[CAC09416.1] (A	4.0
	429470	AI87B901	Hs.203862	guanine nucleotide binding protein (G pr	4.0
	409856	AW502082		gb:UI-HF-BR0p-eig-g-04-0-UI.r1 NIH_MGC_5	4.0
	443682	AI383061	Hs.47248	ESTs, Highly similar to similar to Cdc14	4.0 4.0
20	420230 410509	AL034344 AW840743	Hs.284186	forkhead box C1 gb:QV1-CN0002-080300-102-f07 CN0002 Homo	4.0
20	428414	AL049980	Hs.184216	DKFZP564C152 protein	3.9
	400138			Eos Control	3.9
	451522	BE565817	Hs.26498	hypothetical protein FLJ21657	3.9
25	436521	AW203986	Hs.213003	ESTs C15000810":gi[11131272 sp P79331 ATS2_BO	3.9 3.9
23	401507 449785	AI225235	Hs.288300	hypothetical protein FLJ23231	3.9
	434815	AF155582	Hs.46744	core1 UDP-galactose:N-acetylgalactosamin	3.9
	411906	AW875765		gb:QV2-PT0012-020500-186-a08 PT0012 Homo	3.9
20	440509	BE410132	Hs.134202	ESTs, Weakly similar to T17279 hypotheti	3.9
30	427061	AB032971	Hs.173392	KIAA1145 protein	3.9 3.9
	430261 449658	AA305127 AI964033	Hs.237225 Hs.195730	hypothetical protein HT023 ESTs, Weakly similar to CTXN RAT CORTEXI	3.8
	429876	AB028977	Hs.225974	KIAA1054 protein	3.8
	410330	AW023630	Hs.159425	ESTs	3.8
35	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (3.8
	437659	AB007944	Hs.5737	KIAA0475 gene product	3.8 3.8
	438171	AW976507	Hs.293515 Hs.84728	ESTs Kruppel-like factor 5 (intestinal)	3.8
	418394 405586	AF132818	NS.04720	NM_000299:Homo sapiens plakophilin 1 (ec	3.8
40	432298	AL118812	Hs.274293	Homo saciens mRNA; cDNA DKFZp761G1111 (f	3.8
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (lg),	3.8
	438202	AW169287	Hs.22588	ESTs	3.8
	404606	41004044	11- 445444	Target Exon	3.8 3.8
45	425329 407604	AJ961644 AW191962	Hs.145444 Hs.288061	Homo sapiens cDNA FLJ11494 fis, clone HE collagen, type Vill, alpha 2	3.8
73	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	3.7
	430868	W93178	Hs.5232	HSPC125 protein	3.7
	457008	AA410446	Hs.112011	ESTs, Weakly similar to unknown [H.sapie	3.7
50	458660	AI299739	Hs.99601	hypothetical protein FLJ12553	3.7 3.7
30	408732 436281	AL117490 AW411194	Hs.47225 Hs.85195	Ras-associated protein Rap1 myeloid leukemia factor 1	3.7
	413493	BE144444	113.00133	gb:MR0-HT0168-141199-002-f09 HT0168 Homo	3.7
	418407	AL044818	Hs.84928	nuclear transcription factor Y, beta	3.7
55	445797	A1253414		gb:aq14f04.x1 Stanley Frontal NS pool 2	3.7
55	457121	A1743770 R02530	Hs.180513		3.6 3.6
	417620 421952	AA300900	Hs.191198 Hs.98849	ESTs, Moderately similar to AF161511 1 H	3.6
	454247	AJ243950	Hs.46735	deafness locus associated putative guani	. 3.6
	431662	AA513406	Hs.152307	ESTs	3.6
60	426908	AW815163	Hs.172851		3.6
	438519	AI186033	Hs.147025	ESTs, Wealty similar to C57785 zinc fing gb:zd51e10.r1 Soares_fetal_heart_NbHH19W	3.6 3.6
	415606 444859	W70022 AW449137	Hs.157487		3.6
	414631	AW970130	Hs.65406	ESTs	3.6
65	428897	AJ245719	Hs.194385	hypothetical protein FLJ20234	3.5
	437073	A1885608	Hs.94122	ESTs	3.5
	427287	NM_014903		KIAA0938 protein Kell blood group precursor (McLeod pheno	3.5 3.5
	415927 450235	AL120168 AA007512	Hs.78919 Hs.17538	ESTs	3.5
70	447263	AW965667	Hs.322406		3.5
-	419440	AB020689	Hs.90419	KIAA0882 protein	3.5
	427254	AL121523	Hs.97774	ESTs	3.5
	434348	BE393191	Hs.18179		3.5 3.5
75	441264	AA927170 R13140	Hs.23290 Hs.13359	ESTs ESTs	3.5
	433629 446494	AA463276	Hs.28890		3.5
	441585		Hs.20238	3 ESTs	3.5
	438704	AI435060	Hs.32825		3.4
80	445279		Hs.22245		3.4 3.4
30	415114 449561	D60468 AI022240	Hs.94181 Hs.17924		3.4
	452420		Hs.29463		3.4
	416517	AA775987	Hs.79357		3.4

	441134	W29092	Hs.346950	cellular retinoic acid-binding protein 1	3.4
	427176	AW381569	Hs.40334	ESTs	3.4
	415668	AW957684	Hs.306814	hypothetical protein FLJ21889	3.4
5	450928	AJ744417	11- 202254	gb:tr10h12.x1 NCI_CGAP_Ov23 Homo sapiens	3.4 3.3
)	457012 405354	R41480	Hs.302754	ESTs CX000321:gij6671579 ref NP_031518.1 ari	3.3
	408855	T83061	Hs.319946	Homo sapiens mRNA for KIAA1727 protein,	3.3
	418525	AW450369	Hs.86937	ESTs	3.3
10	420174	AI824144	Hs.23912	ESTs	3.3
10	437124	AA554458	Hs.279860	KIAA0666 protein	3.3 3.3
	419211 424335	BE270817 AW021508	Hs.37617 Hs.28170	ESTs, Wealthy similar to A53933 myosin t ESTs	3.3
	453344	BE349075	Hs.44571	ESTS	3.3
	428065	AI634046	Hs.157313	ESTs	3.3
15	417248	AA329449	Hs.247302	twisted gastrulation	3.3
	429415	NM_002593	Hs.202097	procollagen C-endopeptidase enhancer	3.3 3.3
	411393 406976	AW797437 M60299	Hs.69771	B-factor, properdin gb:Human alpha-1 collagen type II gene,	3.3
	441071	D79550	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	3.3
20	414327	BE408145	Hs.185254	ESTs, Wealdy similar to T24435 hypotheti	3.3
	433703	AA210863	Hs.3532	nemo-like kinase	3.3
	418880	N87353 AW612084	Hs.89421	CBF1 Interacting corepressor ESTs	3.3 3.3
	445947 437334	AU353947	Hs.298494 Hs.283780	hypothetical protein DKFZp761N1814	3.3
25	434795	BE620794	Hs.4147	translocating chain-associating membrane	3.2
	400127			Eos Control	3.2
	414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	3.2
	402429	AI355647	Un 100000	Target Exon purinergic receptor (family A group 5)	3.2 3.2
30	428695 427699	AW965076	Hs.189999 Hs.180378	hypothetical protein 669	3.2
-	403442		1.0.100010	Target Exon	3.2
	419272	AA663904	Hs.89862	TNFRSF1A-associated via death domain	3.2
	456614	AV653110	Hs.106650	hypothetical protein FLJ20533	3.2
35	407581 412633	R48402 AF001691	Hs.173508 Hs.74304	P3ECSL oeriptakin	3.2 3.2
"	433328	AW298159	Hs.23644	ESTs, Weakly similar to S65824 reverse t	3.2
	449294	AI651786	Hs.195045	ESTs	3.1
4	442799	AI564739	Hs.68505	ESTs	3.1
40	434045	AI065133	Hs.152316	hypothetical protein PRO0971	3.1 3.1
40	409403 420033	AA668224 D59502	Hs.6634 Hs.292590	Homo sapiens cDNA: FLJ22547 fis, clone H ESTs	3.1 3.1
	422137	AJ236885	Hs.112180	zinc finger protein 148 (pHZ-52)	3.1
	444760	AI796296	Hs.208062	ESTs	3.1
4.5	403488			ENSP00000201948:KARYOPHERIN BETA2B HOMOL	3.1
45	411359	H86088	Hs.22635	ESTs	3.1
	443037 407127	AW500305 R45970	Hs.8906 Hs.236349	syntaxin 7 EST	3.1 3.1
	416851	AW963951	Hs.85618	ESTs	3.1
	416838	D84109	Hs.80248	RNA-binding protein gene with multiple s	3,1
50	443030	R68048	Hs.9238	hypothetical protein FLJ23516	3.1
	410389	AW954049	Hs.8177	ESTs, Weakly similar to PIHUB6 salivary	3.1 3.1
	459399 433582	BE407712 BE548749	Hs.153998 Hs.148016	creatine kinase, mitochondrial 1 (ubiqui ESTs	3.1
	431128	AI203545	Hs.296169	S-phase response (cyclin-related)	3.1
55	420411	AI581085	Hs.24678	sphingosine-1-phosphatase	3.1
	459584	Al910884	Hs.346429	ESTs	3.1
	449883	AI004464	Hs.344156	gb:ot56e06.s1 Soares_testis_NHT Homo sap Homo sapiens cDNA: FLJ21362 fis, clone C	3.1 3.1
	445320 410786	AA503887 AW803340	Hs.167011	gb:(L2-UM0079-090300-050-D02 UM0079 Homo	3.1
60	418207	C14685	Hs.34772	ESTs	3.0
	420521	AI915734	Hs.87298	ESTs	3.0
	425890	H24530	Hs.273294	hypothetical protein FLJ20069	3.0
	416749	AW068550.0 AA376768	omp Hs.79732 Hs.324841	fibulin 1 hypothetical protein FLJ22622	3.0 3.0
65	412258 407173	T64349	NS.324041	gb:yc10d08.s1 Stratagene lung (937210) H	3.0
•••	415672	N53097	Hs.193579	ESTs	3.0
	448583	NM_015239	Hs.21542	KIAA1035 protein	3.0
	429043	AJ824977	Hs.145319		3.0
70	404091 406085			Target Exon Target Exon	3.0 3.0
, 0	438825	BE327427	Hs.79953	ESTs	3.0
	457441	BE467737	Hs.146125	ESTs	3.0
	403512			C3000579*:gi 12643308 sp 09Y4K1 AIM1_HUM	3.0
75	416866	AA297356 H39685	Hs.80324	serine/threonine protein phosphatase cat	3.0 3.0
, ,	439877 441984	AB037763	Hs.250700 Hs.8059	tryptase bela 1 synaptotagmin IV	3.0
	436765	AB028952	Hs.5307	synaptopodin	3.0
	445071	A1280246	Hs.149504	ESTs	3.0
80	404333	41070000	11. 22024	C7001735*:gi7768636 dbj BAA95483.1 (AB	3.0
οU	422907 413266	AJ879263 BE300352	Hs.77273	Human glucose transporter pseudogene gb:600944231F1 NIH_MGC_17 Homo sapiens c	3.0 3.0
	429393	AA383024	Hs.201603		3.0
	415337	Z44881	Hs.9012	ESTs, Wealthy similar to \$26650 DNA-bindi	3.0

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	415044	AA419108	Hs.77840	annexin A4	2.9
	403469	74113100		Target Exon	2.9
	416928	AA190573	Hs.85902	ESTs, Weakly similar to MCHU calmodulin	2.9
•	430195	AW969308	Hs.188594	ESTs	2.9 2.9
5	458544	A1631036 BE076969	Hs.196843 Hs.7337	ESTs hypothetical protein FLJ10936	2.9
	440667 424641	AB001106	Hs.151413	glia maturation factor, bela	2.9
	428820	AA436187	Hs.172631	integrin, alpha M (complement component	2.9
	405403			Target Exon	2.9
10	452197	AW023595	Hs.232048	ESTs	2.9 2.9
	437357	AL359559	Hs.331666	Homo sapiens mRNA; cDNA DKFZp762O2215 (f death-associated protein kinase 2	2.9
	423479 404559	NM_014326	Hs.129208	Target Exon	2.9
	406270			Target Exon	2.9
15	422190	H17399	Hs.11506	Human clone 23589 mRNA sequence	2.9
	431300	AA502346		gb:ne26b03.s1 NCI_CGAP_Co3 Homo sapiens	2.9
	420286	A1796395	Hs.111377 Hs.256895	ESTs ESTs	2.9 2.9
	422964 431583	AW439476 AL042613	Hs.262476	S-adenosylmethionine decarboxylase 1	2.9
20	428595	AB037795	Hs.186547	KIAA1374 protein	29
	402198			NM_024323:Homo sapiens hypothetical prot	2.9
	416246	U47413	Hs.79101	cyclin G1	2.9 2.9
	427593	AK001132	Hs.179752	Homo sapiens cDNA FLJ10270 fis, clone HE x 001 protein	2.9 2.9
25	446351 440432	AW444551 AI239637	Hs.35380 Hs.202653	ESTs, Weakly similar to T14267 Xin prote	2.9
23	446525	AW967069	Hs.211556	hypothetical protein MGC5487	2.8
	400965			C11002190*:gij12737279 ref XP_012163.1	2.8
	436489	AJ272269	Hs.121429	zinc-binding protein Rbcc728	2.8 2.8
20	458793	N80159	Hs.121849	microtubule-associated proteins 1A/1B li teukocyte immunoglobulin-like receptor,	2.8
30	406810 445577	U82275 N40696	Hs.94498 Hs.137064	cytoplasmic polyadenylation element bind	2.8
	428874	W32133	Hs.194366	transthyretin (prealburnin, amyloidosis t	2.8
	418745	AW882645	Hs.88044	sprouty (Drosophila) homolog 1 (antagoni	2.8
2.5	433095	AK001092	Hs.302480	Homo sapiens cDNA FLJ10230 fis, clone HE	2.8 2.8
35	425580	L11144	Hs.1907	galanin	2.8
	416233 438219	AA176633 AI916151	Hs.257194	gb:zp13g01.s1 Stratagene fetal retina 93 ESTs	2.8
	404661	M310131	113.201101	C9000306*:gi 12737280 ref XP_006682.2 k	2.8
	435836	AW292532	Hs.343667	homolog of yeast long chain polyunsatura	2.8
40	423665	BE167153	Hs.24380	ESTs	2.8 2.8
	430320	BE245290	Hs.239218	uncharacterized hypothalamus protein HCD NM_003771*:Homo sapiens keratin, hair, a	2.8 2.8
	401783 423837	AW937063	Hs.275150	gb:PM3-DT0037-231299-001-g11 DT0037 Homo	2.8
	447271	AL041747	Hs.170261	ESTs	2.8
45	438913	Al380429	Hs.172445	ESTs	2.8
	441962	AW972542	Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone H	2.8 2.8
	444385	BE278964	Hs.11085	CGI-111 protein	2.8 2.8
	432278 415666	AL137506 H72693	Hs.274256	hypothetical protein FLJ23563 gb:yu03c11.r1 Soares fetal liver spleen	2.8
50	452345	AA293279	Hs.29173	hypothetical protein FLJ20515	2.8
••	445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	2.8
	439556	Al623752	Hs.163603		2.8 2.8
	405474	AI370379	LL 122216	NM_001093*:Homo sapiens acetyl-Coenzyme ESTs	2.8
55	426208 419461	AI370379 AI452601	Hs.132216 Hs.288869		2.8
55	428501	AL041162	Hs.98587	ESTs	2.8
	413427	U31120	Hs.845	interleukin 13	2.8
	433109	N58907	Hs.162430		2.8 2.8
60	427974 455040	BE093023 AW852286	Hs.188767	ESTs gb:QV0-CT0225-100400-187-d08 CT0225 Homo	2.8
oo	453994	BE180964	Hs.165590	ribosomal protein S13	2.8
	459171	AW967801	Hs.64783	ESTs, Weakly similar to T42705 hypotheti	2.8
	404845			C22000163*:gij10242166jgbjAAG15318.1jAF2	2.8
65	408182	AA047854	U- 42250	gb:zf49g04.r1 Soares retina N2b4HR Homo serine (or cysteine) proteinase inhibito	2.8 2.7
05	427111 414541	AA351026 BE293116	Hs.173594 Hs.76392	aldehyde dehydrogenase 1 family, member	2.7
	432815	Z30045	Hs.293676		2.7
	404036			Target Exon	2.7
70	418157	W99382	Hs.283709		2.7
70	426403	NM_00036		thrombomodulin Homo sapiens cDNA FLJ14471 fis, clone MA	2.7 2.7
	439659 443932		Hs.59483 Hs.9973	Homo sapiens corva PL314471 hs, done ma lensin	2.7
	444930		Hs.30118		2.7
	419269			gb:zs41b04.s1 Soares_NhHMPu_S1 Homo sapi	2.7
75	416004	D11880	Hs.29925		2.7
	430371		Hs.24011 Hs.21026		2.7 2.7
	449117 451007		Hs.32759		2.7
	421202		Hs.10250		2.7
80	405308			NM_025192:Homo sapiens hypothetical prot	2.7
	413208			gb:RCO-BT0522-071299-011-b10 BT0522 Homo	2.7 2.7
	421420 445693		Hs.12329 Hs.76507		2.7
	-4-2031	A11000177			

	******	44005047		-him-OC-404 -4 Co-esse foted board MINISTER	2.7
	452351 410538	AA025647 AW753115		gb:ze85d01_r1 Soares_letal_heart_NbHH19W gb:PM0-CT0248-131099-001-h12 CT0248 Homo	2.7
	448072	AI459306	Hs.24908	ESTs	2.7
_	420912	AW853156	Hs.90787	ESTs	2.7
5	453830	AA534296	Hs.20953	ESTs	2.7
	457791	AW117431	Hs.191906	ESTs	2.7
	417735	AA188175	Hs.82506	KIAA1254 protein	2.7 2.7
	411773 417076	NM_006799 AW973454	Hs.72026 Hs.238442	protease, serine, 21 (testisin) ESTs, Moderataly similar to ALU7_HUMAN A	27
10	436476 ·		Hs.33829	bHLH protein DEC2	2.7
	440945	AW505345	Hs.7540	f-box and teucine-rich repeat protein 3A	2.7
	425826	U97698		mucin 6, gastric	2.7
	422795	AB033109	Hs.120866	KIAA1283 protein	2.7
16	433921	AA618174		gb:nq14f01.s1 NCI_CGAP_Thy1 Homo saplens	2.7
15	414272 418047	AI651603	Hs.46988 Hs.4847	ESTs ESTs	2.7 2.7
	421089	R37633 AB037771	Hs.101799	KIAA1350 protein	2.7
	419763	AI039691	Hs.127486	EST ₈	2.7
	459265	AJ003616		gb:AJ003616 Selected chromosome 21 cDNA	2.7
20	410970	AW812151		gb:RC5-ST0178-081099-011-A06 ST0178 Homo	2.7
	401925	N98378		sialyltransferase 1 (beta-galactoside al	27
	418504	BE159718	Hs.85335	Homo sapiens mRNA; cDNA DKFZp564D1462 (f	2.6 2.6
	433789 418308	AA220977 AA215738	Hs.182514	gb:zr01a08.r1 Stratagene NT2 neuronal pr ESTs, Wealdy similar to A46010 X-linked	2.6
25	444618	AV653785	Hs.173334	ELL-RELATED RNA POLYMERASE II, ELONGATIO	2.6
	406299	***************************************		Target Exon	2.6
	422963	M79141	Hs.13234	ESTs	2.6
	441244	BE612935	Hs.184052	PP1201 protein	2.6
20	439954	AL046748	Hs.6790	OnaJ (Hsp40) homolog, subfamily B, membe	2.6 2.6
30	405088			Target Exon Target Exon	26
	404741 451927	AL355687	Hs.27261	Homo sapiens mRNA full length insert cDN	26
	439103	AF085959	Hs.38705	ESTs	26
	437241	AL137318	Hs.306450	Homo sapiens mRNA; cDNA DKFZp434L171 (fr	2.6
35	442379	NM_004613	Hs.8265	transglutaminase 2 (C polypeptide, prote	2.6
	457394	M86528	Hs.266902	neurotrophin 5 (neurotrophin 4/5)	2.6
	427229	A1799751	Hs.5635	eSTs gb:601301177F1 NIH_MGC_21 Homo sepiens c	2.6 2.6
	414630 406744	BE410857 AA554082	Hs.16064 Hs.279860	tumor protein, translationally-controlle	2.6
40	443984	AI424415	Hs.143719	ESTs	2.6
70	421221	AW276914	Hs.326714	Homo sapiens clone IMAGE:713177, mRNA se	2.6
	421709	AA159394	Hs.107056	CED-6 protein	2.6
	426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen	2.6
A.E	439480	AL038511	Hs.125316	ESTs, Wealdy similar to S33990 finger pr	2.6
45	419567	AW339890	Hs.128187	ESTs	2.6 2.6
	421922 421859	AW295043 AA356620	Hs.109590 Hs.108947	genethanin 1 KIAA0050 gene product	2.6
	431441	U81961	Hs.2794	sodium channel, nonvoltage-gated 1 alpha	2.6
	444843	AA400172		gb:zu69e01.r1 Soares_testis_NHT Homo sap	2.6
50	416729	U46165	Hs.1027	Ras-related associated with diabetes	2.6
	439238	N47305	Hs.302161	ESTs	26
	439183	AW970600	Hs.303261	ESTs	26 26
	408739 412061	W01556 AA833763	Hs.238797 Hs.330211	ESTs, Moderately similar to 138022 hypot ESTs	2.6
55	432114	AL036021	Hs.8934	ESTs	2.6
	425337	AA355442	Hs.169054		2.6
	424299	AK000377	Hs.82294	homolog of mouse C2PA	2.6
	448871	BE616709	Hs.159265		2.6
60	414516	AI307802	Hs.135560	ESTs, Weakly similar to T43458 hypotheti	2.6 2.6
OU	456235 410429	AA203637 AA310600	Hs.63657	gb:zx58b12.r1 Soares_fetal_liver_spleen_ peptide:N-glycanase similar to yeast PNG	2.6
	449251	AW151660	Hs.31444	ESTs	2.6
	436546	AW023329	Hs.132743		2.6
	450546	AA010200	Hs.175551		2.6
65	437255	R58970	Hs.9887	ESTs	2.6
	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	2.6
	427983	M17706	Hs.2233	colony stimulating factor 3 (granulocyte ESTs, Weakly similar to T18967 hypotheti	2.5 2.5
	413341 423763	H78472 R98203	Hs.191325 Hs.132724	== · · · · · · · · · · · · · · · · ·	2.5
70	413282	BE078159	113.132724	gb:CM0-8T0615-140200-175-e06 BT0615 Homo	2.5
, ,	415590	T74068	Hs.170081		2.5
	406215			Target Exon	2.5
	453938	AF082569	Hs.36794	D-type cyclin-interacting protein 1	2.5
75	424310	AA338648	Hs.50334	testes development-related NYD-SP22	2.5
75	442097	AW015799	Hs.128474 Hs.106773		2.5 2.5
	456650 413231	AA620501 D87461	Hs.75244	BCL2-like 2	2.5
	457297	AW968188	110.10444	gb:EST380383 MAGE resequences, MAGJ Horno	2.5
	444942	AW293458	Hs.283807	chromosome 11 open reading frame 16	2.5
80	425764	AW996009	Hs.112577	Homo sapiens cDNA FLJ14130 fis, clone MA	2.5
	435712	AA694607	Hs.176956	ESTs	2.5 2.5
	436624 443155	T64297 D54485	Hs.23772	fatty acid binding protein 1, liver ESTs	2.5 2.5
	443155	R54485	113.23/12	Luis	2.0

	425907	AA365752	Hs.155965	ESTs	2.5
	414759	AW295157	Hs.47587	ESTs	2.5 2.5
	414699	AI815523	Hs.76930	synuclein, alpha (non A4 component of am gb:QV0-HT0101-061099-032-c04 HT0101 Homo	25
5	411426 404492	BE141714		C8000067*:gi 10432400 emb CAC10290.1 (A	25
,	425153	AW023193	Hs.27046	ESTs	25
	426372	BE304680	Hs.169531	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	2.5
	434803	AW974640	Hs.303413	ESTs	2.5
_	425694	U51333	Hs.159237	hexokinase 3 (white cell)	2.5
10	433069	X76732	Hs.3164	nucleobindin 2	2.5
	428054	AI948688	Hs.266619	ESTs	2.5
	424823	NM_006226	Hs.153322	phospholipase C, epsilon	2.5 2.5
	456972	AI054347	Hs.2017	ribosomal protein L38	2.5 2.5
1.5	431405	AI470895	Hs.334895	ribosomal protein L10a	25
15	427982	NM_016156	Hs.181326 Hs.143314	KIAA1073 protein ESTs	25
	412831 437114	AA121352 AA836641	Hs.163085	ESTs	2.5
	426157	AA370977	Hs.345728	STAT induced STAT inhibitor 3	2.5
	448786	BE048842	Hs.179075	Homo sapiens cDNA FLJ11881 fis, clone HE	2.5
20	432251	AW972983	Hs.232165	polycythemia rubra vera 1; cell surface	2.5
	449239	T24653	Hs.23360	likely ortholog of yeast ARV1	2.5
	453572	AA382590	Hs.46366	KIAA0948 protein	2.5
25	TABLE 23		Fb	ant identifier number	
23	Pkey:		e cluster numb	set identifier number	
	CAT numl Accession		bank accessio		
	MUUGSSIUI	L 061	Dain accoss	11 (10)100.0	
	Pkey	CAT Number	Accession		•
30	408182	104479_1		AA057506 AA053841	
	409856	1156268_1		AW502979 AW502807 AW501876	
	410509	1206699_1		AW752404 H43469	
	410538	1207341_1	AW753115	AW753113 R45779	1003473
25	410786	1221063_1	AW803340	AW803280 AW803275 AW803415 AW803343 AV	1003422
35	410970	1228131_1		AW812186 AW812166 AW845993 AW845989	
	411426 411906	1245515_1 1265204_1	414076766	LICODO A AMOTEARA	
	412636	13165_1	NINA 00441	6 AL 021058 M77820 RE149760 AW752599 AW84	8723 AW376697 AW376817 AW376699 AW848371 AW376782 AW848789 AW361413
	412000	13103_1	A14/04007/	I AMANO 7420 AM/70030/I AM/700300 RE077020 RE	177017 RF185187 AW997196 BE156621 BE179915 BEU06561 BE143133 AW690903
40			00000103	AMMINGER A ARETRIE AWRESTED REN11378 AWI	70253 RF185750 AW886475 BE160433 J05211 BE082576 BE082504 BE094947
. •			414557777	A A M 277700 A M 277700 DED 27676 DED 27676 REI	182507 RE082514 AW178000 AW177933 AI905935 AW/4/8// AW/48114 BE1402 IO
			AW265320	3 AW847678 AW847688 AW365151 AW365148 AV	V365153 AW365156 AW365175 AW365157 AW365154 AW068840 BE005272 AW365145
			BE001925	BE182166 BE144243 BE001923 AI951766 AI434	518 BE184920 BE184933 A1284090 BE184941 AW804674 BE184924 C04715 W39488
40			AW99561	5 BE184948 BE159646 AW606653 AA099891 AA1	31128 AA337270 AA340777 AW384371 AA852212 R58704 AW366566 AW364859 96245 BE165351 BE073467 AA377127 AW890264 AW609750 AW391912 AW849690
45			AA025851	AA025852 AA455100 AA719958 AW352220 AW3	H91011 AW368529 AW390272 C18467 AW674920 N57176 AA026480 AW576767
			LICODO A A	AAACOCA AWATTTRT AAAACGGA AWATTTRG RFA92	134 RE092137 BE092136 AW177784 AU2Z862 BEU91653 AW376611 AW646392
			A A 0.4 0.04 C	DE106331 DE183164 AA368564 AW951576 T29	118 AA131077 W95048 W25458 AW205789 H90899 N29754 W32490 K20904 BE 107 10 1
			00107100	: NOATET LIDTARO LIBRIAE AITONSON MRRRADA MISSA	MO3 AI205263 AA128470 AI392926 AF139065 AWJ/U81J AWJ/U82/ AW/9041/
50			AM7097R	n AW708883 AW798569 R33557 AA149190 CD30	29 AW177783 AA088866 AW370829 AA247685 BEUUZZ73 AI760816 AI439101 AW679451
			A17000C2	A A 45 1022 A 1240226 A 1500275 T48792 A 1568096	A1142882 AA039975 A1470146 AA946936 BE067737 BE067786 W19287 AA944301
			AA702424	AI417612 AI306554 AI686869 AI568892 AW1905	55 AI571075 AI220573 AA056527 AI471874 AI304772 AW517828 AI915596 AI627383
			AI270345	AW021347 AW166807 AW105614 AI346078 AA5	52300 W95070 A1494069 A1911702 AA149191 AA026864 A1830049 A1887258 AW780435
<i>E E</i>			AI910434	A1819984 A1858282 A1078449 A1025932 A1850584	A1635878 AA026047 AA703232 D12062 AW192085 AA658154 AW514597 AW591892 4633 A1927207 AA782109 AW473233 A1804485 AW169216 A1572669 AA602182
55			18/181 A	A AMPERA DOC A 1070007 A AGE 1818 A A 283207 A 107	6962 AI498487 AI348053 AI783914 H44405 AW799118 AA128330 AA515500 AA918281
			W01540	A1905927 AA022701 W38382 R20795 T77861 AW	050274304078
	413208	1353610_1		9 BE071804 BE071798	 -
	413266	1356260_1		2 BE299274 BE075351 BE297444	
60	413282	1358147_1		9 BE078276 BE078163 BE078277 BE078279 BE0	78158
	413493		BE14444	4 BE144430	
	415606	1540470_1	W70022	R35201 F12763 T74725 H63485 Z45782 H61126	
	415666			R08673 H72694 F20990 R08580	
45	416233			3 AW961842 AA309418	
65	419269			8 BE180775 7 AA237066 AA354236 AW957759 H08961	
	419386		1107608	NW915264 AIZ91966 AIZ32669 AAS88236 AI5216	2 AI804760 AI955717 AW292169 AI468227 AI420483 AA603459 AI868225 AI919551
	425826 431300			6 BE159863	•
	433789			7 AF091029 AA701227	
70	433921		AA61817	4 Al114549 R36464 R36465	7,0044 1,00000 1,000
	436624		TEA207	4A894931 NM_001443 M10050 AW843109 AI6985	16 T53219 T48785 T64166 AA706930 R29613 T55913 T56518 T64679 R29666 M10617
		_			433 T53220 AW082135 AW272775 T29562 T55862 AI343047 AI345671 T68235 T68121
			AW8422		
75	444843			72 AA400146 AV651691	
75	445797			4 A1366014 R34822 ANKE16670 ANKIDEOGO3	
	447135			AW516579 AW059603 2 BE268487	•
	449901 450928			7 R91614 H77365	
	452351			17 R45716 AW753786	
80	455040		1 AW8522	86 AW851934 AW852096 AW852274	
	45623		AA2036	37 AA832266 H67452	
	457297	7 313764_1	AW9681	88 AA468196 AA468269 AA468298	
	45926	5 966590_1	AJ0036	I6 AJ003654 AJ003617	
					217

TABLE 23C: Unique number corresponding to an Eos probeset Pkey: Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495. 5 Strand: Indicates DNA strand from which exons were predicted. Indicates nucleotide positions of predicted exons. Nt_position: Nt_position 173043-173564 Pkey Strand 10 400965 7770576 Minus 401507 7534110 71055-71259 Plus 4388746 27363-27518,28727-28891,29526-29731 401600 Minus 13365-139827,140509-140391-140334-140990,141496-141657,141757-141882,142063-142283 138252-138469,140239-140364,140437-140598,141037-141193,141925-142007,142787-143230 7249190 401783 Plus 401925 3892083 Minus 15 8576116 79041-79191 402198 Ptus 54983-55240,56507-56785,56982-57365 9454515 Minus 402364 402429 9796372 57622-57793,59282-59402,59624-59827 Minus 403442 7210003 Ptus 174560-175270 403469 9929739 9966615 Minus 4831-7707 20 403488 12450-12753 Minus 403512 7656757 Minus 114487-114610 403890 7710561 83165-83350 Plus 65247-67529,112537-114863 404036 8567760 7684554 Minus 404091 82121-83229 Minus 25 137948-138024,138111-138300 404333 9802821 Minus 404492 8123400 Minus 138612-138803 73499-73651,89575-89739 8748893 9212936 404559 Minus 22310-23269 404606 Minus 404661 9797073 33374-33675,33769-34008 Ptus 30 143025-143467 47174-47326,52928-53146,53312-53602 404741 8574139 404845 7958980 Minus 115690-117621 405088 8072518 Minus 2642452 52213-53089 Plus 405354 405403 6850244 37491-37670,40951-41031 Minus 35 172005-172175 38810-39017 405474 B439781 Plus 405586 5002511 Plus 96543-96870 405670 4662655 Plus 405674 4589984 Plus 68302-68429 406085 9123888 Plus 18665-18843 40 406215 7342161 Plus 310-432 13136-13591 7534217 406270 Plus 35655-36119 5686278 Minus 406299 406308 9211532 358408-358651 45 TABLE 24A: ABOUT 1260 GENES UP-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT TISSUES Table 24A lists about 1260 genes up-regulated in glioblastoma compared to normal adult tissues. These were selected from 59680 probesets on the Affymetric/Eos Hu03 GeneChip array such that the ratio of "average" glioblastoma to "average" normal adult tissues was greater than or equal to 2.5. The "average" glioblastoma level was set to the 75° percentile amongst various glioblastoma tumors. The "average" normal adult tissue level was set to the 85° percentile amongst various glioblastoma tumors. The "average" normal adult tissue level was set to the 85° percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10° percentile value amongst the various non-malignant tissues was subtracted from both the numerator and the denominator 50 before the ratio was evaluated. Unique Eos probeset identifier number Pkey: ExAccn: Exemplar Accession number, Genbank accession number UnigenelD: Unigene number 55 Unigene Title: Unigene gene title Ratio of 75th percentile turnor to 85th percentile normal body tissue R1 UnigeneID Unigene Title Pkey ExAcon peripheral myelin protein 2 431917 D16181 Hs.2868 60 427343 AI880044 Hs.176977 protein kinase C binding protein 2 74.6 74.2 455601 A1368680 Hs.816 SRY (sex determining region Y)-box 2 71.6 428321 AI699994 Hs.2868 peripheral myelin protein 2 ESTs Hs.129911 AW016610 412719 Hs.315369 Homo sapiens cDNA: FLJ23075 fis, clone L 66.3 449494 AW237014 65 U88967 BE242870 BE259150 64.3 415817 Hs.78867 protein tyrosine phosphatase, receptor-t solute carrier family 1 (gliaf high affi delta (Drosophila)-like 3 60.1 Hs.75379 Hs.127792 413472 456759 Homo sapiens mRNA; cDNA DKFZp761C1712 (f 46.7 435147 AL133731 Hs.4774 Hs.159623 40.1 425842 AI587490 NK-2 (Drosophila) homolog B 70 39.0 412733 AA984472 Hs.74554 KIAA0080 protein NM 003081 Hs.84389 synaptosomal-associated protein, 25kD 418375 Hs.32964 SRY (sex determining region Y)-box 11 Homo sapiens mRNA; cDNA DKFZp761J1324 (f 37.2 453392 U23752 AL157425 Hs.133315 36.8 423849 Hs.75297 Hs.80220 fibroblast growth factor 1 (acidic) catenin (cadherin-associated protein), d 32.8 413333 M74028 75 31.8 416829 AB013805 AK000106 Hs.272227 Homo sapiens cDNA FLJ20099 fis, clone CO 431941 BE465204 Hs.47448 **ESTs** 31.4 436878

30.9 30.4

30.2

28.3

26.9 25.9

426325

425057 445711

439415

430838

429466

80

D28114

AAR26434

AF169692

F05538

N46664

MR5835

Hs.169309

Hs.1619

Hs.12450

Hs.12825

Hs.12827

Hs. 169395

myelin-associated oligodendrocyte basic

hypothetical protein FLJ 12015

protocadherin 9

ESTs

ESTs

achaete-scute complex (Drosophila) homol

PCT/US02/29560 WO 03/025138

			11. 457500	FOT:	25.3
	447004 424581	AW296968 M62062	Hs.157539 Hs.150917	ESTs catenin (cadherin-associated protein), a	24.8
	452744	AI267652	Hs.30504	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	24.8
_	441285	NM_002374	Hs.167	microtubule-associated protein 2	24.3
5	453642	A1370936	Hs.34074	dipeptidy/peptidase VI	24.3 24.2
	424140 450133	Z48051 AW969769	Hs.141308 Hs.105201	myelin oligodendrocyte głycoprotein ESTs	24.2
	408562	A1436323	Hs.31141	Homo saplens mRNA for KIAA1568 protein,	23.3
	448672	Al955511	Hs.225106	ESTs	22.7
10	435708	AI362949	Hs.75169	ESTs	22.0 21.9
	407034	U84540	Lin 447102	gb:Human dystrobrevin isoform DTN-3 (DTN ESTs	21.7
	407168 431019	R45175 NM_005249	Hs.117183 Hs.2714	forkhead box G1B	21.5
	409049	AI423132	Hs.146343	ESTs	21.4
15	433896	AW294729	Hs.274461	ESTs	21.1
	445041	T64183 AW388633	Hs.282982	solute carrier solute carrier family 7, (cationic amino	21.0 20.4
	418738 444378	R41339	Hs.6682 Hs.12569	ESTs	20.0
	411305	BE241596	Hs.69547	myelin basic protein	19.9
20	437414	AW894071	Hs.48448	hypothetical protein DKFZp547C176	19.8
	441016	AW138653	Hs.25845	ESTS	19.6 18.5
	440435 438209	AL042201 AL120659	Hs.21273 Hs.6111	transcription factor NYD-sp10 aryl-hydrocarbon receptor nuclear transl	18.4
	452461	N78223	Hs.108106	transcription factor	18.1
25	409395	U46745	Hs.54435	dystrobrevin, alpha	18.1
	417183	R52089	Hs.172717	ESTs	18.0 18.0
	409638 428392	AW450420 H10233	Hs.21335 Hs.2265	ESTs secretory granule, neuroendocrine protei	18.0
	420392 449611	AI970394	Hs.197075	ESTs	17.0
30	446692	Z44514	Hs.156829	Homo sapiens mRNA for KIAA1763 protein,	16.9
	425088	AA663372	Hs.169395	hypothetical protein FLJ12015	16.9
	444471	AB020684	Hs.11217	KIAA0877 protein protocadherin 17	16.8 16.7
	421659 431725	NM_014459 X65724	Hs.106511 Hs.2839	Norrie disease (pseudoglioma)	16.6
35	429276	AF056085	Hs.198612	G protein-coupled receptor 51	16.6
	416892	L24498	Hs.80409	growth arrest and DNA-damage-inducible,	16.5
	441440	AI807981	Hs.30495	ESTS	15.7 15.7
	449433 421264	Al672096 AL039123	Hs.9012 Hs.103042	ESTs, Weakly similar to S26650 DNA-bindi microtubule-associated protein 18	15.5
40	415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	15.3
	413597	AW302885	Hs.117183	ESTs	15.1
	424945	AJ221919	Hs.173438	hypothetical protein FLJ10582	14.9 14.9
	447414	D82343 H15302	Hs.18551 Hs.168950	neuroblastoma (nerve tissue) protein Homo sapiens mRNA; cDNA DKFZp566A1046 (f	14.8
45	426269 416857	AA188775	Hs.292453	ESTs	14.7
	419721	NM_001650	Hs.288650	aquaporin 4	14.6
	411078	AI222020	Hs.182364	CocoaCrisp	14.4
	453924	R49295	Hs.24886	ESTs Homo sapiens mRNA, chromosome 1 specific	14.4 14.3
50	409389 430130	AB007979 AL137311	Hs.301281 Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (14.1
50	410909	AW898161	Hs.53112	ESTs, Moderately similar to ALU8_HUMAN A	14.0
	412266	N59006	Hs.26133	ESTs	14.0
	412986 424790	X81120 AL119344	Hs.75110 Hs.13326	cannabinoid receptor 1 (brain) ESTs, Weakly similar to 2004399A chromos	14.0 14.0
55	439239	ALT 19544 AI031540	Hs.235331		14.0
-	441497	R51064	Hs.23172	ESTs	14.0
	445495	BE622641	Hs.38489	ESTs, Wealdy similar to 138022 hypotheti	14.0
	414245	BE148072	Hs.75850	WAS protein family, member 1	13.7 13.6
60	429900 448595	AA460421 AB014544	Hs.30875 Hs.21572	ESTs KIAA0644 gene product	13.6
•	449605	AW138581	Hs.198416		13.6
	452526	W38537	Hs.280740		13.6
	420547	AF155140	Hs.98738	gonadotropin-regulated testicular RNA he paraneoplastic antigen MA2	13.3 13.3
65	441350 420077	AB020690 AW512260	Hs.7782 Hs.87767	ESTs	13.2
05	424120	T80579	Hs.290270		13.2
	456965	AW131888	Hs.172792		13.2
	423361	AW170055	Hs.47628	ESTs	13.1 12.9
70	428409 417160	AW117207 N76497	Hs.98523 Hs.1787	ESTs proteolipid protein 1 (Pelizaeus-Merzbac	12.6
, 0	451621	AI879148	Hs.26770	fatty acid binding protein 7, brain	12.5
	411379	AI816344	Hs.12554	ESTs, Weakly similar to NPL4_HUMAN NUCLE	12.5
	436954	AA740151	Hs.13042		12.4 12.4
75	430691 433551	C14187 AI985544	Hs.103531 Hs.12450	B ESTs protocadherin 9	12.4
, ,	422544		Hs.11814		12.2
	427540	R12014	Hs.20976	ESTs	12.1
	435624		Hs.24889		12.1 12.1
80	415849 428845		Hs.6806 Hs.15361	ESTs 0 KIAA0751 gene product	11.9
	442671		Hs.13477		11.9
	444396	T65213	Hs.4257	ESTs	11.8
	452752	AW044058	Hs.33578	KIAA0820 protein	11.8
				319	

				•	
	425523	AB007948	Hs.158244	KIAA0479 protein	11.8
	416072	AL110370	Hs.79000	growth associated protein 43	11.7
	440184	AB002297	Hs.7022	dedicator of cyto-kinesis 3	11.7
	428976	AL037824	Hs.194695	ras homolog gene family, member I	11.6
5	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	11.6
,		AA497044	Hs.20887		11.6
	448299			hypothetical protein FLJ10392	
	414214	D49958	Hs.75819	glycoprotein M6A	11.5
	428982	NM_005097	Hs.194704	leucine-rich, glioma inactivated 1	11.5
	405238				11.4
10	420362	U79734	Hs.97206	huntingtin interacting protein 1	11.4
-	422980	N46569	Hs.76722	CCAAT/enhancer binding protein (C/EBP),	11.4
	424918	R13982	Hs. 169309	myelin-essociated oligodendrocyte basic	11,4
		X77748		glutamate receptor, metabotropic 3	11,4
	434277		Hs.3786		
1.5	451952	AL120173	Hs.301663	ESTs	11.3
15	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfot	11.3
	424278	AK000723	Hs.144517	hypothetical protein FLJ20716	11.3
	429418	AI381028	Hs.118769	ESTs	11.3
	429918	AW873986	Hs.119383	ESTs	11.3
	443912	R37257	Hs.184780	ESTs	11.3
20	448743	AB032962	Hs.21896	KIAA1136 protein	11.3
20				ESTs	11.2
	420092	AA814043	Hs.88045		11.2
	408081	AW451597	Hs.167409	ESTs	
	411642	NM_014932	Hs.71132	neuroligin 1	10.9
~-	415170	R44385	Hs.164578	ESTs	10.9
25	426320	W47595	Hs.169300	transforming growth factor, beta 2	10.8
	450568	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 fis, clone NT	10.8
	425799	T08133	Hs.182906	Homo sapiens mRNA for KIAA1872 protein,	10.8
	423853	AB011537	Hs.133466	stit (Drosophila) homolog 1	10.7
	400293		Hs.306480	Homo sapiens mRNA; cDNA DKFZp761E2112 (f	10.7
30		N51002			
JU	447773	AI423930	Hs.36790	ESTs, Weakly similar to putative p150 (H	10.7
	448321	NM_005883	Hs.20912	adenomatous polyposis coli like	10.5
	448533	AL119710	Hs.21365	nucleosome assembly protein 1-like 3	10.5
	440684	Al253123	Hs.127356	ESTs, Highly similar to S21424 nestin [H	10.3
	444017	U04840	Hs.214	neuro-oncological ventral antigen 1	10.3
35	438380	T06430	Hs.6194	chondroitin sulfate proteoglycan BEHAB/b	10.3
	440471	AA886145	Hs.307944	ESTs	10.2
	413063				10.1
		AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	
	439978	BE139460	Hs.124673	Homo sapiens cDNA FLJ11477 fis, clone HE	10.1
40	448902	Z45998	Hs.22543	Homo sapiens mRNA; cDNA DKFZp761I1912 (f	10.1
40	424932	R14070	Hs.315369	Homo sapiens cDNA: FLJ23075 fis, clone L	9.9
	431721	A8032996	Hs.268044	KIAA1170 protein	9,9
	419088	AI538323	Hs.52620	integrin, beta 8	9.8
	420602	AF060877	Hs.99236	regulator of G-protein signalling 20	9.8
	436511	AA721252	Hs.291502	ESTs	9.8
45		AF002020			9.7
73	414696		Hs.76918	Niemann-Pick disease, type C1	
	449539	W80363	Hs.58446	ESTs	9.7
	412959	D87458	Hs.75090	KIAA0282 protein	9.6
	412811	H06382	Hs.21400	ESTs	9.6
	449300	A1656959	Hs.222165	ESTs	9.6
50	426344	H41821	Hs.322469	transcriptional activator of the c-fos p	9.5
	419271	N34901	Hs.238532	ESTs	9.5
	419078	M93119	Hs.89584	insulinoma-associated 1	9.4
	451516	AJ800515	Hs.12024	ESTs	9.4
		AI870435			9.3
55	422656		Hs.1569	LIM homeobox protein 2	
55	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	9.3
	414175	Al308876	Hs.103849	hypothetical protein DKFZp761D112	9.3
	415279	F04237	Hs.1447	glial fibrillary acidic protein	9.2
	428784	Y12851	Hs.193470	purinergic receptor P2X, ligand-gated io	9.2
	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	9.2
60	424641	AB001106	Hs.151413	glia maturation factor, beta	9.1
	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	9.1
	449448	D60730	Hs.57471	ESTs	9.1
		AI806109	Hs.135736	KIAA1580 protein	9.0
	408508				9.0
45	452785	AL359942	Hs.296434	erythroid differentiation and denucleati	
65	448986	H42169	Hs.18653	hypothetical protein FLJ14627	8.9
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	8.9
	433800	AJ034361	Hs.135150	tung type-I cell membrane-associated gly	8.9
	408926	AF217525	Hs.49002	Down syndrome cell adhesion molecule	8.8
	449625	NM_014253		odz (odd Oz/ten-m, Drosophila) homolog 1	8.8
70	400292	AA250737	Hs.72472	ESTs	8.7
. •	417404	NM_007350		pleckstrin homology-like domain, family	8.7
				ESTs	8.7
	420345	AW295230	Hs.25231		
	429927	NM_001115		adenylate cyclase 8 (brain)	8.7
75	437528	N59646	Hs.169745		8.7
75	440152	AB002376	Hs.7006	KIAA0378 protein	8.7
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	8.6
	400780			•	8.6
	434891	AA814309	Hs.123583	ESTs	8.6
	449277	AA001064	Hs.172976		8.6
80	415709	AA649850	Hs.278558		8.5
U U		A8006627		astrolactin	8.5
	439947		Hs.6788		
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	8.5
	433042	AW193534	Hs.281895	Homo sapiens cDNA FLJ11660 fis, clone HE	8.4

	416370	N90470		ESTs, Weakly similar to I38022 hypotheti	8.4
	452786	R61362		ESTs, Wealdy similar to T09052 hypotheti ATPase, Na+/K+ transporting, beta 2 poly	8.4 8.3
	415796 426271	R87548 AF026547	Hs.78854 Hs.169047	chondroitin sulfate proteoglycan 3 (neur	8.3
5	408947	AL080093	Hs.49117	Homo sapiens mRNA; cDNA DKFZp564N1662 (f	8.3
	419863	AW952691	Hs.93485	Homo sapiens mRNA; cDNA DKFZp761D191 (fr neuronal pentraxin II	8.3 8.3
	433447 431467	U29195 N71831	Hs.3281 Hs.256398	Homo sapiens mRNA; cONA DKFZp434E0528 (f	8.3
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	8.3
10	414300	AI304870	Hs.188680	ESTs	8.2 8.2
	407728 422798	AW071502 R92347	Hs.175931 Hs.34574	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.2
	419704	AA429104	Hs.45057	ESTs	8.2
1.5	429007	D80642		gb:HUM092E09B Human fetal brain (TFujiwa	8.1 8.1
15	442710 425048	AI015631 H05468	Hs.23210 Hs.164502	ESTs ESTs	8.1
	429149	AW193360	Hs.197962	ESTs, Weakly similar to 138022 hypotheti	8.0
	445740	T78281	Hs.13226	Homo sapiens clone 25181 mRNA sequence	8.0 7.9
20	418771 422728	AA807881 AW937826	Hs.25329 Hs.103262	ESTs ESTs, Wealdy similar to ZN91_HUMAN ZINC	7.9
20	425984	AW836277	Hs.165636	hypothetical protein DKFZp761C07121	7.9
	448408	AA322866	Hs.21107	neuroligin	7.9 7.9
	455364	H72176 AU076643	Hs.4273 Hs.313	hypothetical protein FLJ13159 secreted phosphoprotein 1 (osteopontin,	7.9 7.9
25	446619 435501	AW051819	Hs.129908	KIAA0591 protein	7.8
	423600	AI633559	Hs.310359	ESTs	7.8 7.8
	450625	AW970107	Hs.5422	gb:EST382188 MAGE resequences, MAGK Homo glycoprotein M6B	7.0 7.7
	415314 420036	N88802 R60336	Hs.52792	Homo sapiens mRNA; cDNA DKFZp586i1823 (f	7.7
30	427687	AW003867	Hs.1570	histamine receptor H1	7.7
	449328	A1962493	Hs.197647 Hs.89768	ESTs gamma-aminobutyric acid (GABA) A recepto	7.7 7.7
	419249 407896	X14767 D76435	Hs.41154	Zic family member 1 (odd-paired Drosophi	7.7
	419103	Z40229	Hs.96423	hypothetical protein FLJ23033	7.6
35	438779	NM_003787	Hs.6414	nucleolar protein 4 gb:EST387475 MAGE resequences, MAGN Homo	7.6 7.6
	433532 448555	AW975367 Al536697	Hs.159863	ESTs	7.5
	439662	H97552	Hs.269060	ESTs	7.5
40	448543	AW897741	Hs.21380	Homo sapiens mRNA; cDNA DKFZp586P1124 (f KIAA0036 gene product	7.5 7.5
40	410099 431592	AA081630 R69016	Hs.169387 Hs.213194	hypothetical protein MGC10895	7.4
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	7.4
	405819			FOT-	7.4 7.4
45	407886 437416	AW969688 AL359605	Hs.100826 Hs.283851	ESTs Homo sapiens mRNA; cDNA DKFZp547G036 (fr	7.4
73	437698	R61837	Hs.7990	ESTs, Moderately similar to I84505 catci	7.4
	408604	D51408	Hs.21925	ESTs 20	7.4 7.3
	418506 447499	AA084248 AW262580	Hs.85339 Hs.147674	G protein-coupled receptor 39 protocadherin beta 16	7.3
50	454036	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	7.3
	409746	NM_004794		RAB33A, member RAS oncogene family	7.2 7.2
	410037 419318	AB020725 AW969742	Hs.58009 Hs.291005	KIAA0918 protein ESTs	7.2
	424051	AL110203	Hs.138411		7.2
55	442026	AI243749	Hs.8074	brain-specific angiogenesis inhibitor 3	7.2 7.2
	448243 436281	AW369771 AW411194	Hs.52620 Hs.85195	integrin, beta 8 myeloid leukemia factor 1	7.2
	426429	X73114	Hs.169849		7.2
۲0	407182	AA312551	Hs.230157		7.1 7.1
60	415293 422764	R49462 A1767727	Hs.106541 Hs.47522	ESTs ESTs	7.1
	451592	AI805416	Hs.213897	' ESTs	7.1
	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	7.0 7.0
65	415734 434149	NM_014747 Z43829	Hs.78748 Hs.19574	KIAA0237 gene product hypothetical protein MGC5469	7.0
05	436726		Hs.128993		7.0
	417632	R20855	Hs.5422	glycoprotein M6B	7.0 6.9
	422421		Hs.235873 Hs.110114		6.9
70	435267 437117		Hs.12259	3 ESTs	6.9
	445523	Z30118	Hs.29378	8 ESTs, Moderately similar to unnamed prot	6.9 6.9
	445900		Hs.13429 Hs.13245		6.9 6.9
	445745 424085				6.9
75	428588	F12101	Hs.18570	1 Homo sapiens mRNA full length insert cDN	6.8
	421723		Hs.30071		6.8 6.7
	447342 443297		Hs.19322 Hs.13302		6.7
00	443992	2 AW022228	Hs.32292	2 ESTs	6.7
80	453096				6.7 6.7
	453857 443761		Hs.35861 Hs.16060		6.6
	429609				6.6
				221	

	435056	AW023337	Hs.5422	glycoprotein M6B	6.5
	453431	AF094754	Hs.32973	glycine receptor, beta	6.5 6.5
	444190 418110	AI878918 R43523	Hs.10526 Hs.217754	cysteine and glycine-rich protein 2 hypothetical protein FLJ22202	6.5
5	413988	M81883	Hs.324784	glutamate decarboxytase 1 (brain, 67kD)	6.5
-	420805	L10333	Hs.99947	reticulon 1	6.4
	429125	AA446854	Hs.271004	ESTs, Weakly similar to 138022 hypotheti	6.4 6.4
	435256 407866	AF193766 AW088232	Hs.13872 Hs.89506	cytokine-like protein C17 paired box gene 6 (aniridia, keratitis)	6.3
10	440700	AW952281	Hs.296184	guanine nucleotide binding protein (G pr	6.3
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	6.3
	422949	AA319435	00030	gb:EST21657 Adrenal gland tumor Homo sap	6.2 6.2
	445102 452401	AW204610 NM_007115	Hs.22270 Hs.29352	ESTs tumor necrosis factor, alpha-induced pro	6.2
15	435538	AB011540	Hs.4930	low density lipoprotein receptor-related	6.2
	410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fls, clone HE	6.2
	416871	H98716	Hs.85591	gb:yx13d08.s1 Soares melanocyte 2NbHM Ho ESTs	6.1 6.1
	416702 419347	AA186428 C15944	Hs.90005	superiorcervical ganglia, neural specifi	6.1
20	424997	AL138167	Hs.96920	ESTs	6.1
	438660	U95740	Hs.6349	Homo sapiens, clone IMAGE:3010666, mRNA,	6.1 6.1
	453649 449444	Y07494 AW818436	Hs.34114 Hs.23590	ATPase, Na+/K+ transporting, atpha 2 (+) sotute carrier family 16 (monocarboxytic	6.1
	414117	W88559	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	6.0
25	425517	AF121179		gb:AF121179 Homo sapiens liver (Chang L-	6.0
	427457	AW779105	Hs.164682	ESTs	6.0 6.0
	437034 444170	AA742643 AW613879	Hs.102408	gb:my91c01.s1 NCI_CGAP_GCB1 Homo saplens ESTs	6.0
	457183	H91882	Hs.118569	DVI-binding protein IDAX (inhibition of	6.0
30	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	6.0
	454048	H05626	Hs.6921	ESTs	6.0 5.9
	439772 448944	AL365406 AB014605	Hs.10268 Hs.22599	Homo sapiens mRNA full length insert cDN atrophin-1 interacting protein 1; activi	5.9
	410011	AB020641	Hs.57856	PFTAIRE protein kinase 1	5.9
35	415485	H12214	Hs.13284	ESTs, Wealty similar to 2109260A B cell	5.9
	438993	AA828995		gb:od77b08.s1 NCI_CGAP_Ov2 Homo sapiens	5.9 5.9
	447350 451783	AJ375572 R42554	Hs.172634 Hs.210862	ESTs T-box, brain, 1	5.9
	447101	N72185	Hs.44189	ESTs	5.9
40	440492	R39127	Hs.21433	hypothetical protein DKFZp547J036	5.9
	440274	R24595	Hs.7122	scrapie responsive protein 1	5.9 5.9
	438461 418064	AW075485 BE387287	Hs.286049 Hs.83384	phosphoserine aminotransferase S100 calcium-binding protein, beta (neur	5.8
	437036	AI571514	Hs.133022	ESTs	5.7
45	412225	AW902042		gb:QVO-NN1022-170400-193-c02 NN1022 Homo	5.7
	426342	AF093419	Hs.169378	multiple PDZ domain protein	5.7 5.7
	444218 445828	AF070641 F05802	Hs.10684 Hs.81907	Homo sapiens clone 24421 mRNA sequence ESTs	5.7
	447198	D61523	Hs.283435	ESTs	5.7
50	427897	NM_017413			5.7
	448499	BE613280	Hs.77550	hypothetical protein MGC1780 butyrobetaine (gamma), 2-oxoglutarate di	5.7 5.6
	443672 412155	AA323362 R38167	Hs.9667 Hs.12449	Homo sapiens transmembrane protein HTMP1	5.6
	435718	R06569	Hs.269534	ESTs	5.6
55	449340	AW235786	Hs.195359	hypothetical protein MGC10954	5.6
	424481	R19453	Hs.1787 Hs.245510	proteolipid protein 1 (Pelizaeus-Merzbac ESTs	5.6 5.6
	451996 422411	AW514021 AW749443	Hs.22511	ESTs	5.6
	438328	AI492261	Hs.32450	ESTs	5.6
60	433244	AB040943	Hs.271285	KIAA1510 protein	5.6 5.5
	435191 418677	R15912 S83308	Hs.4817 Hs.87224	Homo sapiens clone 24461 mRNA sequence SRY (sex determining region Y)-box 5	5.5
	400859	505500	160,01227	or low committee of the control	5.5
	413625	AW451103	Hs.71371	ESTs	5.5
65	421863	AI952677	Hs.108972		5.5 5.5
	434933 438702	R91095 AI879064	Hs.4276 Hs.54618	KIAA1701 protein ESTs	5.5
	452055	AI377431	Hs.141693		5.5
70	430979	AI479755	Hs.129010		5.5
70	412709	AL022327	Hs.74518	KIAA0027 protein neurotrimin	5.5 5.5
	439920 424343	H05430 AW956360	Hs.288433 Hs.4748	adenylate cyclase activating polypeptide	5.4
	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	5.4
75	419235	AW470411	Hs.288433		5.4
75	418030	8E207573	Hs.83321 Hs.46786	neuromedin B ESTs	5.4 5.4
	410330 410781	AW023630 AI375672	Hs.165028		5.4
	420658	AW965215	Hs.336656	5 ESTs	5.4
οΛ	421308	AA687322	Hs.192843		5.4 5.4
80	443740 426457		Hs.21062 Hs.16996		5.4 5.4
	450375		Hs.8850	a disintegrin and metalloproteinase doma	5.4
	412494		Hs.792	ADP-ribosylation factor domain protein 1	5.4

				and the second s	5.4
	426600	NM_003378		VGF nerve growth factor inducible protocadherin 10	5.4
	424432 429250	AB037821 H56585		protocadnenn 10 tryptophan rich basic protein	5.4
_	443785	AW449952	Hs.190125	basic-helix-loop-helix-PAS protein	5.4
5	436282	R91913	Hs.272104	ESTs, Moderately similar to ALU1_HUMAN A	5.4
	404584	4 D000000	LI- 222022	MIA A 44 30 amelojo	5.3 5.3
	430091 439845	AB032958 AL355743		KIAA1132 protein Homo sapiens EST from clone 41214, full	5.3
	424001	W67883		paternally expressed 10	5.3
10	425073	W39609	Hs.22003	solute carrier family 6 (neurotransmitte	5.3
	426625	T78300		serologically defined colon cancer antig	5.3 5.3
	428137	AA421792	Hs.170999	ESTs gb:zw80c03.s1 Soares_testis_NHT Homo sap	5.3
*	428679 438176	AA431765 AW138970	Hs.122113	ESTs	5.3
15	440138	AB033023	Hs.318127	hypothetical protein FLJ10201	5.3
	451018	AW965599	Hs.247324	mitochondrial ribosomal protein S14	5.3
	416340	N31772	Hs.79226	fasciculation and elongation protein zet	5.3 5.3
	435244	N77221	Hs.187824 Hs.13565	ESTs Sam68-like phosphotyrosine protein, T-ST	5.3
20	446035 424624	NM_006558 AB032947	Hs.151301	Ca2+-dependent activator protein for sec	5.3
20	407748	AL079409	Hs.38176	KIAA0606 protein; SCN Circadian Oscillat	5.3
	430437	AI768801	Hs.169943	Homo sapiens cDNA FLJ13569 fis, clone PL	5.3
	414825	X06370	Hs.77432	epidermal growth factor receptor (avian	5.2 5.2
25	453941 424998	U39817 U58515	Hs.36820 Hs.154138	Bloom syndrome chitinase 3-like 2	5.2
23	423419	R55336	Hs.23539	ESTs	5.2
	424922	BE386547	Hs.217112	hypothetical protein MGC10825	5.2
	447359	NM_012093	Hs.18268	adenylate kinase 5	5.2 5.2
30	408206	AF041853	Hs.43670	kinesin family member 3A mutated in colorectal cancers	5.2
30	421013 429443	M62397 AB028967	Hs.1345 Hs.202687	potassium voltage-gated channel, Shal-re	5.2
	434367	AB020700	Hs.3830	KIAA0893 protein	5.2
	444861	R46789	Hs.76118	ubiquitin carboxyl-terminal esterase L1	5.2 5.2
25	446142	A1754693	Hs.145968	ESTs	5.2
35	448816 451050	AB033052 AW937420	Hs.22151 Hs.69662	KIAA1226 protein ESTs	5.2
	451106	BE382701	Hs.25960	v-myc avian myelocytomatosis viral relat	5.2
	439285	AL133916	Hs.172572	hypothetical protein FLJ20093	5.2
40	416737	AF154335	Hs.79691	LIM domain protein	5.2 5.2
40	424800 443695	AL035588 AW204099	Hs.153203 Hs.337720	MyoD family inhibitor ESTs, Weakly similar to AF126780 1 refin	5.2
	415257	F03016	Hs.27513	ESTs	5.2
	433929	A1375499	Hs.27379	ESTs	5.1
AE	415651	A1207162	Hs.3815	stathmin-like-protein RB3	5.1 5.1
45	451027 409172	AW519204 Z99399	Hs.40808 Hs.118145	ESTs ESTs	5.1
	423343	AA324643	Hs.246106	ESTs	5.1
	429172	AA447417	Hs.285491	ESTs	5.1
50	437268	A1754847	Hs.227571	regulator of G-protein signalling 4	5.1 5.1
50	451270 452904	AW341392 AL157581	Hs.235795 Hs.30957	ESTs Homo sapiens mRNA; cDNA DKFZp434E0626 (f	5.1
	420560	AW207748	Hs.59115	ESTs	5.1
	418097	R45137	Hs.21868	ESTs	5.1
6.5	442910	AJ365130	Hs.11307	ESTs, Weakly similar to T19326 hypotheti	5.1 5.1
55	434849 413554	AW292765 AA319146	Hs.8053 Hs.75426	ESTs secretogranin II (chromogranin C)	5.1
	414217	Al309298	Hs.279898		5.1
	412068	S72043	Hs.73133	metallothionein 3 (growth inhibitory fac	5.0
۲0	413627	BE182082	Hs.246973		5.0 5.0
60	418661 422438	NM_001949 AA445925	Hs.1189 Hs.270896	E2F transcription factor 3 ESTs. Moderately similar to Z195_HUMAN Z	5.0
	423728		Hs.132136		5.0
	431431		Hs.252953	Human DNA sequence from clone RP3-403A15	5.0
15	435087		Hs.23567	ESTs .	5.0 5.0
65	452097		Hs.27916 Hs.63668	a disintegrin-like and metalloprotease (toll-like receptor 2	4.9
	410434 408692		Hs.34074	dipeptidylpeptidase VI	4.9
	407808		Hs.279789	histone deacetylase 3	4.9
70	418940		Hs.288513		4.9 4.9
70	425977		Hs.165570		4.9
	426814 447112		Hs.172619 Hs.7154	myelin transcription factor 1-tike ESTs	4.9
	449574		Hs.17537		4.9
	453652	AW009640	Hs.28368	ESTs, Moderately similar to \$65657 alpha	4.9
75	423869		Hs.13401		4.9 4.9
	413248 449176		Hs.21433 Hs.19807		4.9
	448451			gb:UI-H-BiOp-abh-g-09-0-Ui.s1 NCI_CGAP_S	4.8
00	402604				4.8
80	436039		Hs.12107 Hs.38173		4.8 4.8
	448769 423678			ESTs	4.8
	43945			4 heterochromatin-like protein 1	4.8

	425870	R13406	Hs.56782	ESTs	4.8
	408777	U71204	Hs.47626	Ric (Drosophita)-like, expressed in neur	4.8
	413409	AI638418	Hs.78580	DEAD/H (Asp-Gtu-Ala-Asp/His) box polypep	4.8
_	413623	AA825721	Hs.246973	ESTs	4.8
5	417246	AI760098	Hs.21411	ESTs	4.8
	420900	AL045633	Hs.44269	ESTs	4.8
	424153	AA451737	Hs.141496	MAGE-like 2	4.8
	443539	AI076182	Hs.134074	ESTs, Moderately similar to ALU6_HUMAN A	4.8
10	448750	U95020	Hs.21903	calcium channel, voltage-dependent, beta	4.8 4.8
10	454030	AW021429	Hs.231980	ESTs	4.8
	424458 444119	M29273 R41231	Hs.1780 Hs.184261	myelin associated glycoprotein ESTs, Wealdy similar to T26686 hypotheti	4.8
	407792	AI077715	Hs.39384	putative secreted ligand homologous to f	4.8
	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	4.7
15	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	4.7
	429956	AJ374651	Hs.22542	ESTs	4.7
	435060	AI422719	Hs.233349	ESTs, Weakly similar to fork head like p	4.7
	436203	BE384982	Hs.5076	Homo sapiens cDNA: FLJ22128 fis, clone H	4.7
20	448475	BE613134	Hs.247474	hypothetical protein FLJ21032	4.7
20	422222	AJ699372	Hs.193247	hypothetical protein DKFZp434A171	4.7
	431733	AW298410	Hs.21475	ESTs	4.7 4.7
	449353 452022	AA001220 AW072330	Hs.271369 Hs.293875	ESTs ESTs	4.7
	454269	AI961060	Hs.129908	KIAA0591 protein	4.7
25	404541	71301000	13.125500	turboot protest	4.7
	428189	AA424030	Hs.46627	ESTs	4.7
	409125	R17268	Hs.259873	axonal transport of synaptic vesicles	4.7
	458435	Al418718	Hs.144121	ESTs, Weakly similar to T46916 hypotheti	4.6
20	425745	U44060	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	4.6
30	413492	D87470	Hs.75400	KIAA0280 protein	4.6
	419629	AB020695	Hs.91662	KIAA0888 protein	4.6
	407638	AJ404672	Hs.334483	hypothetical protein FLJ23571	4.6
	436140	W87355	Hs.269587	ESTs	4.6 4.6
35	439169	A1912122 A1034457	Hs.41095 Hs.34650	ESTs ESTs	4.6
55	443150 451073	AI758905	Hs.206063	ESTS	4.6
	451659	BE379761	Hs.14248	ESTs	4.6
	452106	AJ141031	Hs.21342	ESTs	4.6
	451407	AA131376	Hs.326401	fibroblast growth factor 128	4.6
40	448765	R15337	Hs.21958	Homo sapiens mRNA; cDNA DKFZp547D086 (fr	4.6
	430147	R60704	Hs.234434	hairy/enhancer-of-split related with YRP .	4.6
	437204	AL110216	Hs.12285	ESTs, Weakly similar to 155214 salivary	4.6
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	4.5
45	422175	N79885	Hs.6382	ESTs, Highly similar to T00391 hypotheti	4.5
43	407889	R34556	Hs.30800	ESTs, Weakly similar to S65657 alpha-1C-	4.5 4.5
	419343 421790	AA456245 AW896201	Hs.85603 Hs.22654	down-regulated by Ctnnb1, a sodium channel, voltage-gated, type 1, a	4.5
	429399	AA452244	Hs.16727	ESTs	4.5
	450149	AW969781	Hs.132863	Zic tamily member 2 (odd-paired Drosophi	4.5
50	453118	AW195849	Hs.252757	ESTs	4.5
	443455	AB001025	Hs.9349	ryanodine receptor 3	4.4
	442613	A1004002	Hs.130522	Kv channel-interacting protein 1	4.4
	429643	AA455889	Hs. 167279	FYVE-finger-containing Rab5 effector pro	4.4
55	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	4.4
55	418845	AA852985	Hs.89232	chromobox homolog 5 (Drosophila HP1 alph	4.4 4.4
	435202 437496	AI971313 AA452378	Hs.170204 Hs.170144	KIAA0551 protein Homo sapiens mRNA; cDNA DKFZp547J125 (fr	4.4
	451254	AJ571016	Hs.172967	ESTs	4.4
	439039	AI656707	Hs.48713	ESTs	4.4
60	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	4.4
-	441607	NM_005010	Hs.7912	neuronal cell adhesion molecule	4.4
	424983	AJ742434	Hs.169911	ESTs	4.4
	410611	AW954134	Hs.20924	KIAA1628 protein	4.4
45	402605				4.4
65	409248	AB033035	Hs.51965	KIAA1209 protein	4.4
	442222	AJ061301	Hs.164773		4.4 4.4
	454027 454293	R40192 H49739	Hs.21527 Hs.134013	Human DNA sequence from clone GS1-115M3 ESTs, Moderately similar to HK61_HUMAN H	4.4
	442832	AW206560	Hs.253569		4.4
70	407304	AA565832	1 13.230003	gb:nj32b03.s1 NCI_CGAP_AA1 Homo sapiens	4.4
. •	423279	AW959861	Hs.290943		4.3
	427194	AA399018	Hs.250835		4.3
	419723	AL120193	Hs.92614	longevity assurance (LAG1, S. perevisiae	4.3
75	445810	AW265700	Hs.155660		4.3
75	409734	BE161664	Hs.56155	hypothetical protein	4.3
	410389	AW954049	Hs.8177	ESTs, Wealty similar to PIHUB6 salivary	4.3 4.3
	411571	AA122393 AA573847	Hs.70811	hypothetical protein FLJ20516 KIAA1708 protein	4.3
	433024 453202	AW085781	Hs.26549 Hs.26270	hypothetical protein FLJ11588	4.3
80	425264	AA353953	Hs.20369	ESTs, Weakly similar to gonadotropin ind	4.3
- •	416427	BE244050	Hs.79307	Rac/Cdc42 guanine exchange factor (GEF)	4.3
	431789	H19500	Hs.269222	mitogen-activated protein kinase 4	4.3
	444600	R41398	Hs.6996	ESTs	4.3

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				. M. of an annual of 190002	4.3
	454042	H22570		ypothetical protein FLJ20093 ru3A protein	4.3
	441899 425256	AI372588 BE297611	He 155392 (collagasin response mediator protein 1	4.3
	410358	AW975168	Hs.13337	ESTs, Weakly similar to unnamed protein	4.2
5	430291	AV660345		CGI-49 protein	4.2
	433597	AA708205		ESTs	4.2 4.2
	444127	N63620	Hs.13281	ESTs Homo sapiens mRNA; cDNA DKFZp566N1047 (1	4.2
	448507	AL133109 AW452631	Hs.21333 Hs.313803	ESTs, Highty similar to AF157833 1 noncl	4.2
10	413589 408577	H50572	Hs 19515	FSTs. Highly similar to NRG3_HUMAN PRO-N	4.2
10	409719	AI769160	Hs.108681	Homo sapiens brain tumor associated prot	4.2
	428536	A1143139	Hs.2288	visinin-like 1	4.2 4.2
	429118	H20669	Hs.35406	ESTs, Highly similar to unnamed protein ESTs, Wealdy similar to 138022 hypotheti	4.2
15	432865	AI753709	Hs.152484 Hs.93828	ESTs, Weakly similar to 2109260A B cell	4.2
13	447138 450648	AI439112 AI703366		ESTs	4.2
	451459	AI797515	Hs.270560	ESTs, Moderately similar to ALU7_HUMAN A	4.2
	421686	AB011156		KIAA0584 protein	4.2 4.2
20	452776	AA194540	Hs.13522	ESTs, Weakly similar to 138022 hypotheti ESTs, Weakly similar to ZN22_HUMAN ZINC	4.2
20	436421	AI678031	Hs.122813 Hs.133483	Homo sapiens mRNA; cDNA DKFZp434B0650 (f	4.2
	423858 434001	AL137326 AW950905	Hs.3697	serine (or cysteine) proteinase inhibito	4.2
	437380	AL359577	Hs.112198	Homo sagiens mRNA; cDNA DKFZp547M073 (fr	4.2
	432328	A1572739	Hs.195471	6-phosphofructo-2-kinase/fructose-2,6-bi	4.1 4.1
25	439607	BE540565	Hs.159460	ESTS	4.1
	424028	AF055084	Hs.153692 Hs.47314	Homo sapiens cDNA FLJ14354 fis, clone Y7 ESTs	4.1
	446936 424240	H10207 AB023185	Hs.143535	calcium/calmodutin-dependent protein kin	4.1
	412446	A1768015	Hs.92127	ESTs	4.1
30	409953	AA332277	Hs.57691	cadherin 18, type 2	4.1
	416220	N49776	Hs.170994	hypothetical protein MGC10946	4.1 4.1
	419683	AA248897	Hs.48784	ESTs	4.1
	426071	AW138057	Hs.163835 Hs.301549	ESTs Homo sapiens mRNA; cDNA DKFZp564H172 (fr	4.1
35	428743 432809	AL080060 AA565509	Hs.131703	ESTs	4.1
33	440105	AA694010	Hs.6932	Homo sapiens clone 23809 mRNA sequence	4.1
	452039	A1922988	Hs.172510	ESTs	4.1 4.1
	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finge	4.1
. 40	457561	AA331517	Hs.286055 Hs.194766	chimerin (chimaerin) 2 seizure related gene 6 (mouse)-like	4.1
40	429038 433932	AL023513 AW954599	Hs.169330	neuronal protein	4.1
	436637	A1783629	Hs.26766	FSTs	4.1
	439231	AW581935	Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	4.1
4.5	450530	NM_006668		cytochrome P450, subfamily 46 (cholester	4.1 4.1
45	407721	Y12735	Hs.38018	dual-specificity tyrosine-(Y)-phosphoryl	4.1
	407881	AW072003	Hs.40968 Hs.69233	heparan sulfate (glucosamine) 3-0-sulfot zinc finger protein	4.0
	410486 413916	AW235094 N49813	Hs.75615	apolipoprotein C-II	4.0
	438703	AI803373	Hs.31599	ESTs	4.0
50	424726	AK001007	Hs.138760	Homo sapiens cDNA FLJ10145 fis, clone HE	4.0 4.0
	405771			to a describe timescatorie misteria proteira	4.0
	418841	NM_002332	Hs.89137 Hs.148135	low density lipoprotein-related protein serine/threonine kinase 33	4.0
	421764 424176	Al681535 AL137273	Hs.142307		4.0
55	425773		Hs.237749		4.0
	427304	AA761526	Hs.163853	ESTs	4.0 4.0
	428882		Hs.131748		4.0
	452834		Hs.105685 Hs.63908	KIAA1688 protein hypothetical protein MGC14726	4.0
60	453745 405239		Hs.11958	oxidative 3 alpha hydroxysteroid dehydro	4.0
00	413801		Hs.35406	ESTs, Highly similar to unnamed protein	4.0
	429698	AI685086	Hs.26339	ESTs, Weakly similar to S21348 probable	4.0 4.0
	435854		Hs.4996	putative ankyrin-repeat containing prote	4.0
65	439199		Hs.26299	ESTs I ESTs	4.0
05	439450 446782		Hs.125304 Hs.144006	S ESTs	4.0
	419687		Hs.227699		3.9
	402408				3.9
70	453362		Hs.10737	5 ESTs	3.9 3.9
70	414219		Hs.75823		3.9
	420578 425010		Hs.99034 Hs.4241	ESTs	3.9
	44423		Hs.14606		3.9
	44173	6 AW29277	9 Hs.16979	9 ESTs	3.9
75	41895		Hs.89506	paired box gene 6 (aniridia, keratitis)	3.9 3.9
	40631		Un 20557	4 ESTs	3.9
	40846 41065				3.9
	41469			synuclein, atpha (non A4 component of am	3.9
80	41884	9 AW47454	7 Hs.53565	Homo sapiens PIG-M mRNA for mannosyltran	3.9 3.0
	42947			ESTs	3.9 3.9
	43376			ESTs gb:Homo sapiens cDNA FLJ10197 fis, clone	3.9
	43619	~ ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	•	farm ratio and man and a series of an analysis and a series	

	447891 450221	R41754 AA328102	Hs.6496 Hs.24641	ESTs cytoskeleton associated protein 2	3.9 3.9
	404283			101.1.1.The	3.9
5	453919	AW959912	Hs.7076	KIAA1705 protein	3.9 3.9
,	429656 412754	X05608 AW160375	Hs.211584 Hs.74565	neurofilament, light polypeptide (58kD) amyloid beta (A4) precursor-like protein	3.9
	445314	AI689948	Hs.65489	Homo sapiens cDNA: FLJ21517 fis, clone C	3.9
	435652	N32388	Hs.334370	uncharacterized hypothalamus protein HBE	3.9
	407378	AA299264	Hs.57776	ESTs, Moderately similar to 138022 hypot	3.9
10	438054	AA776626	Hs.62183	ESTs	3.9
	436420	AA443966	Hs.31595	ESTs	3.9
	445133	AW157646	Hs.153506	ESTs	3.9 3.9
	432590 453331	AI609273 AI240665	Hs.110783 Hs.8895	ESTs ESTs	3.9
15	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	3.8
	424635	AA420687	Hs.115455	Homo sapiens cDNA FLJ14259 fis, clone PL	3.8
	451489	NM_005503	Hs.26468	armyloid beta (A4) precursor protein-bind	3.8
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 lis, clone NT	3.8
20	448302	AJ480208	Hs.182906	Homo sapiens mRNA for KIAA1872 protein,	3.8
20	415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito	3.8 3.8
	417355 446727	D13168 AB011095	Hs.82002 Hs.16032	endothelin receptor type B KIAA0523 protein	3.8
	424340	AA339036	Hs.7033	ESTs	3.8
	423346	AI267677	Hs.127416	synaptojanin 1	3.8
25	412788	AA120960	Hs.198416	ESTs	3.8
	404593			507 W. M. J. D. A. 199999 L	3.8
	416856	N27833	Hs.269028	ESTs, Weakly similar to 138022 hypotheti	3.8 3.8
	429896 439619	AA460367 AW975998	Hs.224223 Hs.58595	ESTs, Moderately similar to 138022 hypot ESTs, Weakly similar to 138022 hypotheti	3.8
30	439634	W79377	Hs.167	microtubule-associated protein 2	3.8
-	440322	AA879430		gb:oj91d08.s1 Soares_NFL_T_GBC_S1 Homo s	3.8
	447761	AF061573	Hs.19492	protocadherin 8	3.8
	452453	Al902519		gb:QV-BT009-101198-051 BT009 Homo sapien	3.8
35	439671	AW162840	Hs.6641	kinesin family member 5C Homo sepiens mRNA full length insert cDN	3.8 3.8
33	447937 459278	AL109716 AW294659	Hs.20034 Hs.34054	Homo sapiens cDNA: FLJ22488 fis, clone H	3.8
	447028	AI973128	Hs.167257	brain link protein-1	3.8
	449458	AJ805078	Hs.208261	ESTs	3.8
40	445888	AF070564	Hs.13415	Homo sapiens clone 24571 mRNA sequence	3.8
40	407385	AA610150	Hs.272072	ESTs, Weakly similar to 138022 hypotheti	3.8
	428841	AM18430	Hs.104935	ESTs NECETO and sin	3.8 3.8
	430643 422263	AW970065 AA307639	Hs.287425 Hs.129908	MEGF10 protein KIAA0591 protein	3.8
	422203 451625	R56793	Hs.106576	alanine-glyoxylate aminotransferase 2-li	3.8
45	439236	BE160952	Hs.247117	ESTs, Moderately similar to ALUF_HUMAN !	3.8
_	441928	Al370188	Hs.211454	ESTs	3.8
	441797	AI936933	Hs.214635	ESTs	3.7
	414922	D00723	Hs.77631	glycine cleavage system protein H (amino	3.7 3.7
50	425588 437007	F07396 AA741300	Hs.46751 Hs.202599	ESTs ESTs, Weakly similar to 138022 hypotheti	3.7
50	435793	AB037734	Hs.4993	KIAA1313 protein	3.7
	443682	AJ383061	Hs.47248	ESTs, Highly similar to similar to Cdc14	3.7
	425741	AF052152	Hs.159412	Homo sapiens clone 24628 mRNA sequence	3.7
55	418211	BE244746	Hs.247474	hypothetical protein FLJ21032	3.7 3.7
55	440080 452898	AW051597 AA814497	Hs.143707 Hs.78792	ESTs ESTs	3.7
	435575	AF213457	Hs.44234	triggering receptor expressed on myeloid	3.7
	409234	AI879419	Hs.27206	ESTs	3.7
60	420489	AA815089	Hs.193513		3.7
60	426890	AA393167	Hs.41294	ESTs	3.7 3.7
	438849 441869	W28948 NM_003947	Hs.10762 Hs.8004	ESTs huntingtin-associated protein interactin	3.7
	448796	AA147829	Hs.301431		3.7
	459318	NM_000038		gb:Homo sapiens adenomatosis polyposis c	3.7
65	459518	Al937419	Hs.294069		3.7
	434444	AI765276	Hs.101257		3.7
	421183	AL135740	Hs.102447	TSC-22-like a disintegrin and metalloproteinase doma	3.7 3.7
	410555 421637	U92649 AF035290	Hs.64311 Hs.106300		3.7
70	418522	AA605038	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	3.7
	420807	AA280627	Hs.57846	ESTs	3.7
	449961	AW265634	Hs.133100		3.7
	422634	NM_016010			3.7
75	421030	AW161357 AB032953	Hs.101174 Hs.173560		3.7 3.7
, ,	427099 452355	N54926	Hs.29202		3.7
	440483	AI200836	Hs.150386		3.7
	429597	NM_003816		a disintegrin and metalloproteinase doma	3.7
0Λ	423756	AA828125		gb:od71a09.s1 NCI_CGAP_Ov2 Homo sapiens	3.6
80	425187	AW014486	Hs.22509 Hs.299315	ESTs collapsin response mediator protein-5; C	3.6 3.6
	434859 413199	8E255080 M62843	Hs.75236	ELAV (embryonic lethal, abnormal vision,	16
	445729	H21066	Hs.13223	Homo sapiens mRNA full length insert cDN	3.6

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					26
	416120	H46739 AA448419	Hs.45209	gb:yo14h02.s1 Soares adult brain N2b5HB5 ESTs	3.6 3.6
	429239 419086	NM_000216	Hs.89591	Kallmann syndrome 1 sequence	3.6
٠.	446659	Al335361	Hs.226376	ESTs	3.6 3.6
5	426757 418819	AW205640 AA228776	Hs.158206 Hs.191721	ESTs ESTs	3.6
	458332	AI000341	Hs.220491	ESTs	3.6
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	3.6 3.6
10	410343 410507	AA084273 AA355288	Hs.76561 Hs.40834	ESTs, Weakly similar to \$47072 finger pr transitional epithelia response protein	3.6
10	422977	AA631498	113.70007	gb:np83h04.s1 NCI_CGAP_Thy1 Homo sapiens	3.6
	425305	AA363025	Hs.155572	Human clone 23801 mRNA sequence	3.6
	428002	AA418703	Un 2201	gb:zv98c03.s1 Soares_NhHMPu_S1 Homo sapi chromogranin B (secretogranin 1)	3.6 3. 6
15	428505 430530	AL035461 AA480870	Hs.2281 Hs.47660	ESTs	3.6
	436425	AI913146	Hs.318725	CGI-72 protein	3.6
	438078	AI016377	Hs.131693	ESTs ESTs	3.6 3.6
	442927 446242	A1024347 N66336	Hs.131519 Hs.7360	ESTs	3.6
20	448831	AL080123	Hs.22182	zinc finger protein 23 (KOX 16)	3.6
	450474	AW872844	Hs.201919	ESTs	3.6 3.6
	452198 455800	AI097560 R22479	Hs.61210 Hs.167073	ESTs, Wealdy similar to 138022 hypotheti Homo sapiens cDNA FLJ13047 fis, clone NT	3.6
	436443	AW138211	Hs.128746	ESTs	3.6
25	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	3.6 3.6
	456038 408902	AA203285 AW014869	Hs.294141 Hs.5510	ESTs, Weakly similar to alternatively sp ESTs	3.6
	442950	AI500417	Hs.46764	ESTs	3.6
20	423905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	3.6
30	425478	AB007953	Hs.268840 Hs.36232	ESTs KIAA0186 gene product	3.6 3.6
	453884 404721	AA355925	HS.30232	MANO 100 gene product	3.6
	408453	AI369838	Hs.45127	chondroitin sulfate proteoglycan 5 (neur	3.6
25	440553	AA889416	Hs.295362	Homo sapiens cDNA FLJ14459 fis, done HE	3.5 3.5
35	446372 413999	AB020644 N45124	Hs.14945 Hs.34460	long fatty acyl-CoA synthetase 2 gene ESTs	3.5
	421458	NM_003654	Hs.104576	carbohydrate (keratan sulfate Gal-6) sul	3.5
	425017	AL119305	Hs.288405	ESTs	3.5 3.5
40	435958 415101	H98180 R45531	Hs.117975 Hs.144534	ESTs ESTs	3.5
40	451320	AW118072	Hs.89981	diacylglycerol kinase, zeta (104kD)	3.5
	430290	AI734110	Hs.136355	ESTs	3.5 3.5
	416836 414821	D54745 M63835	Hs.80247 Hs.77424	cholecystokinin Fc tragment of IgG, high affinity Ia, re	3.5
45	419412	AW161058	Hs.90297	synuclein, beta	3.5
	437860	AA333063	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	3.5 3.5
	452689 .416661	F33868 AA634543	Hs.284176 Hs.79440	transferrin IGF-II mRNA-binding protein 3	3.5
	427491	R43279	Hs.22574	ESTs, Weakly similar to 138022 hypotheti	3.5
50	428037	N47474	Hs.89230	potassium intermediate/small conductance	3.5 3.5
	444584 408296	AJ 168422 AL 117452	Hs.44155	gb:ok30e11.x1 Soares_NSF_F8_9W_OT_PA_P_S DKFZP585G1517 protein	3.5
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	3.5
<i>e e</i>	412659	AW753865	Hs.74376	olfactomedin related ER localized protei	3.5 3.5
55	429077 436887	AB028983 AW953157	Hs.2352 Hs.193235	adenylate cyclase 2 (brain) hypothetical protein DKFZp547D155	3.5 3.5
	450784	AW246803	Hs.47289	ESTs	3.5
	446827	AW451243	Hs.157069		3.5 3.5
60	436434 412777	N50465 Al335773	Hs.92927 Hs.270123	putative 47 kDa protein ESTs	3.5
00	436476	AA326108	Hs.33829	bHLH protein DEC2	3.5
	408601	U47928	Hs.86122	protein A	3.4
	429401 448425	AW296102 AI500359	Hs.99272 Hs.233401	ESTs, Weakly similar to S32567 A4 protei ESTs	3.4 3.4
65	418727	AA227609	Hs.94834	ESTs	3.4
	451729	AW160725	Hs.312469		3.4
	435910	AI084152	Hs.21782 Hs.179769	ESTs, Wealdy similar to ALU7_HUMAN ALU S Homo sapiens cDNA: FLJ22487 fis, clone H	3.4 3.4
	434577 414598	R37316 Al094221	Hs.135150		3.4
70	439627	BE621702	Hs.29076	hypothetical protein FLJ21841	3.4
	413293		Hs.302490 Hs.137200		3.4 3.4
	423992 426249		Hs.16835		3.4
76	426968	U07616	Hs.17303	amphiphysin (Stiff-Mann syndrome with br	3.4
75	430388		Hs.24077		3.4 3.4
	435061 452291		Hs.16394 Hs.28853		3.4
	449714	AB033015	Hs.23941	KIAA1189 protein	3.4
80	443392		Hs.29342		3.4 3.4
OV.	410082 445337		Hs.15831 Hs.12523		3.4
	408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle)	3.4
	432731	R31178	Hs.28782	0 fibronectin 1	3.4

	448758	AB018311	Hs.21917	KIAA0768 protein	3.4 3.4
	432613 434164	AW081698 AW207019	Hs.80712 Hs.148135	KIAA0202 protein serine/threonine kinase 33	3.4
	425294	AF033827	Hs.155553	HNK-1 sulfotransterase	3.4
5	410108	AA081659	Hs.318775	OSBP-related protein 6	3.4
	406815	AA833930	Hs.288036	tRNA isopentenylpyrophosphate transferas	3.4
	402855	41304040	11: 449499	and he had a	3.3 3.3
	422170 445034	AI791949 AW293376	Hs.112432 Hs.143659	anti-Mullerian hormone ESTs	3.3 3.3
10	424378	W28020	Hs.167988	neural cell adhesion molecule 1	3.3
•	423611	A8011163	Hs.129908	KIAA0591 protein	3.3
	435593	R88872	Hs.4964	DKFZP586J1624 protein	3.3
	404819				3.3
15	436607 427315	AW661783 AA179949	Hs.211061 Hs.175563	ESTs Homo sapiens mRNA; cDNA DKFZp564N0763 (f	3.3 3.3
13	452693	T79153	Hs.48589	zinc finger protein 228	3.3
	454996	AW850180	15.40503	gb:IL3-CT0219-271099-022-C09 CT0219 Homo	3.3
	406927	M26460		gb:Homo sapiens (clone 104) retinoblasto	3.3
20	409045	AA635062	Hs.50094	Homo sapiens mRNA; cDNA DKFZp43400515 (f	3.3
20	415238	R37780	Hs.21422	ESTS	3.3
	417845	AL117461 AA833718	Hs.82719 Hs.204529	Homo sapiens mRNA; cDNA DKFZp586F1822 (f KIAA1806 protein	3.3 3.3
	421192 426695	AW118191	Hs.112729	ESTs	3.3
	438885	AI886558	Hs.184987	EST6	3.3
25 .	451762	AF222980	Hs.26985	disrupted in schizophrenia 1	3.3
	452103	R42764	Hs.339654	ESTs, Weakly similar to 138022 hypotheti	3.3
	453590	AF150278 NM_003462	Hs.33578	KIAA0820 protein	3.3 3.3
	453616 457285	AI038858	Hs.33846 Hs.130522	dynein, axonemal, light intermediate pol Kv channel-interacting protein 1	3.3
30	436045	AB037723	Hs.5028	DKFZP56400423 protein	3.3
• •	437470	AL390147	Hs.134742	hypothetical protein DKFZp547D065	3.3
	448520	A8002367	Hs.21355	doublecortin and CaM kinase-like 1	3.3
	436480	AJ271643	Hs.87469	putative acid-sensing ion channel	3.3 3.3
35	432656 443898	NM_000246 AW804296	Hs.3076 Hs.9950	MHC class II transactivator Sec61 gamma	3.3
55	423582	BE000831	Hs.23837	Homo sapiens cDNA FLJ11812 fis, done HE	3.3
	445953	AI612775	Hs.145710	ESTs	3.3
	427940	AA417812	Hs.38775	ESTs	3.3
40	414683	S78296	Hs.76888	hypothetical protein MGC12702	3.3
40	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino ESTs, Moderately similar to S65657 alpha	3.3 3.3
	420649 419498	AI866964 AL036591	Hs.124704 Hs.20887	hypothetical protein FLI10392	3.3
	457579	AB030816	Hs.36761	HRAS-like suppressor	3.3
	436556	Al364997	Hs.7572	ESTs	3.2
45	424369	R87622	Hs.26714	KIAA1831 protein	3.2
	457065	A1476318	Hs.192480	ESTs	3.2 3.2
	440210 444513	AW674562 AL120214	Hs.125296 Hs.7117	ESTs glutamate receptor, ionotropic, AMPA 1	3.2
	434353	AA630863	Hs.131375	ESTs, Moderately similar to ALUB_HUMAN !	3.2
50	414430	AJ346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	3.2
	439924	AI985897	Hs.125293	ESTs	3.2
	411505	AF155659	Hs.70565	molybdenum cofactor synthesis 2	3.2 3.2
	423175 415115	W27595 AA214228	Hs.18653 Hs.127751	hypothetical protein FLJ14627 hypothetical protein	3.2
55	407878	D87468	Hs.40888	activity-regulated cytoskeleton-associat	3.2
	410274	AA381807	Hs.61762	hypoxia-inducible protein 2	3.2
	437762	T78028	Hs.154679	synaptotagmin I	3.2
	438944	AA302517	Hs.92732	KIAA1444 protein	3.2 3.2
60	450313 409459	Al038989 D86407	Hs.332633 Hs.54481	Bardet-Biedl syndrome 2 low density lipoprotein receptor-related	3.2
00	410953	AW811766	Hs.334858	hypothetical protein MGC12250	3.2
	418527	AA450386	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	3.2
	420081	AW510776	Hs.94958	tubulin tyrosine ligase-like 1	3.2
65	429496	AA453800	Hs.192793	ESTs	3.2 3.2
UJ	430099 434928	AW194988 AW015595	Hs.20537 Hs.4267	hypothetical protein FLJ13942 Homo sapiens clones 24714 and 24715 mRNA	3.2
	435532	AW291488	Hs.117305	Homo sapiens, clone IMAGE:3682908, mRNA	3.2
	438306	AW188266	Hs.163645	ESTs	3.2
70	439274	AF086092	Hs.48372	ESTs	3.2
70	440847	AA907511	Hs.130178	ESTs	3.2 3.2
	447750 455350	Al422234 AW901809	Hs.143434	contactin 1 gb:QVO-NN1020-170400-195-h02 NN1020 Homo	3.2
	430890	X54232	Hs.2699	glypican 1	3.2
~~	420568	F09247	Hs.247735	protocadherin alpha 10	3.2
75	410768	AF038185	Hs.66187	Homo sapiens clone 23700 mRNA sequence	3.2
	427450		Hs.178121		3.2 3.2
	430456 430181	AA314998 AF065314	Hs.241503 Hs.234785		3.2
	418512	AW498974	Hs.89981	diacytolycerol kinase, zeta (104kO)	3.2
80	419912	AF249745	Hs.6066	Rho guanine nucleotide exchange factor (3.2
	450689	AJ369275	Hs.243010		3.2
	424899 436277	AL119387 R88520	Hs.119062		3.2 3.2
	436277	NOWE	Hs.120917	COTO	4.2

	454.455	41007007	Hs.8821	bondidia natimioushial nonfide	3.2
	451455 445078			hepcidin antimicrobial peptide junctophilin 3	3.2
	447746	AW015920	Hs.161359	ESTs	3.2
_	435458		Hs.4892	Homo sepiens clone 24841 mRNA sequence	3.2 3.2
5	427729 417417	AB033100 F05745		KIAA protein (similar to mouse paladin) ATPase, Ca↔ transporting, plasma membra	3.1
	438810	AW897846	Hs.6421	hypothetical protein DKFZp761N09121	3.1
	439570	T79925	Hs.269165	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.1 3.1
10	432527	AW975028	Hs.102754 Hs.79971	ESTs sal (Drosophila)-like 2	3.1
10	416801 421988	X98834 AW450481	Hs.161333	ESTs	3.1
	426509	M31166	Hs.2050	pentaxin-related gene, rapidly induced b	3.1
	408786	AA773187	Hs.294027	ESTs	3.1 3.1
15	433494	AB029396	Hs.3353 Hs.335951	beta-1,3-glucuronyltransferase 1 (glucur hypothetical protein AF301222	3.1
13	412723 418329	AA548459 AW247430	Hs.84152	cystathionine-beta-synthase	3.1
	439456	A1752409	Hs.109314	hypothetical protein FLJ20980	3.1
	428832	AA578229	Hs.324239	ESTs, Moderately similar to ZN91_HUMAN Z	3.1 3.1
20	452780	BE171598	Hs.13522 Hs.337620	ESTs, Weakly similar to I38022 hypotheti Homo sapiens AFG3L1 isoform 1 mRNA, part	3.1
20	438192 424939	A1859065 AK000059	Hs.153881	Homo sapiens NY-REN-62 antigen mRNA, par	3.1
	403053	R58624	Hs.2186	eukaryotic translation elongation factor	3.1
	404299			1	3.1 3.1
25	407864	AF069291 AI468210	Hs.40539 Hs.261285	chromosome 8 open reading frame 1 pleiotropic regulator 1 (PRL1, Arabidops	3.1
23	410181 418852	BE537037	Hs.273294	hypothetical protein FLJ20069	3.1
	449101	AA205847	Hs.23016	G protein-coupled receptor	3.1
	453240	AI969564	Hs.166254	hypothetical protein DKFZp566l133	3.1 3.1
30	440486	BE243513	Hs.7212 Hs.83765	hypothetical protein PP1044 dihydrofolate reductase	3.1
30	408096 439864	BE250162 AI720078	Hs.291997	ESTs, Weakly similar to A47582 B-cell gr	3.1
	414706	AW340125	Hs.76989	KIAA0097 gene product	3.1
	436315	BE390513	Hs.27935	hypothetical protein MGC4837	3.1 3.1
35	426855	AL117427 AB037813	Hs.172778 Hs.159200	Homo sapiens mRNA; cDNA DKFZp566P013 (fr hypothetical protein DKFZp762K222	3.1
22	425683 410126	BE169274	Hs.169387	KIAA0036 gene product	3.1
	435312	AJ243396	Hs.4865	voltage-gated sodium channel beta-3 subu	3.1 3.1
	425491	AA883316	Hs.255221	ESTs	3.1 3.1
40	456273 412140	AF154846 AA219691	Hs.1148 Hs.73625	zinc finger protein RAB6 interacting, kinesin-like (rabkines	3.1
70	445255	NM_014841	Hs.12477	synaptosomal-associated protein, 91 kDa	3.1
	432154	AI701523	Hs.112577	ESTs	3.1
	453128	AW026516	Hs.31791	acylphosphatase 2, muscle type	3.1 3.1
45	438458 448616	AW975186 AF035621	Hs.21611	gb:EST387294 MAGE resequences, MAGN Homo kinesin family member 3C	3.0
43	429281	AA830856	Hs.29808	Homo sapiens cDNA: FLJ21122 fis, clone C	3.0
	443906	AA348031	Hs.7913	ESTs	3.0
	417318	AW953937	Hs.12891	ESTs Homo sapiens, clone IMAGE:4298026, mRNA,	3.0 3.0
50	452619 444153	AW298597 AK001610	Hs.61884 Hs.10414	hypothetical protein FLJ10748	3.0
30	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	3.0
	426327	W03242	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	3.0 3.0
	451468	AW503398	Hs.293663 Hs.284180		3.0
55	422758 421633	AF152329 AF121860	Hs.106260		3.0
55	428361	NM_015905		transcriptional intermediary factor 1	3.0
	418932	L34059	Hs.89484	cadherin 4, type 1, R-cadherin (retinal)	3.0 3.0
	416805	F13271 U79289	Hs.79981 Hs.90798	Human clone 23560 mRNA sequence Human clone 23695 mRNA sequence	3.0
60	419518 422709	0/9269 AA315331	Hs.153485		3.0
	423135	N67655	Hs.26411	ESTs	3.0
	424901	Z11933	Hs.182505		3.0 3.0
	426617 427386	W58006 AW836261	Hs.266258 Hs.337717		3.0
65	429859				3.0
-	435071		Hs.35495	ESTs	3.0
	435092		Hs.4749	Homo sapiens mRNA; cDNA DKFZp761E13121 (hypothetical protein FLJ10719; KIAA1794	3.0 3.0
	436211 436936		Hs.33482 Hs.19747		3.0
70	445855		Hs.14556	9 ESTs	3.0
	452294	AI871925	Hs.11789	5 ESTs, Moderately similar to A47582 B-cel	3.0
	433980		Hs.28604	9 phosphoserine aminotransferase ESTs, Highly similar to T00391 hypotheti	3.0 3.0
	430228 451026		Hs.6382 Hs.15749		3.0
75	435232			cyclin-dependent kinase inhibitor 2C (p1	3.0
	439566			gb:Homo sapiens full length insert cDNA	3.0
	425782	2 U66468	Hs.15952	5 cell growth regulatory with EF-hand doma	3.0 3.0
	416588		Hs.14144		3.0
80	416874 410388		Hs.42568 Hs.3327	Homo sapiens cDNA: FLJ22219 fis, clone H	3.0
	411411		Hs.55950	ESTs, Wealdy similar to KIAA1330 protein	3.0
	424066	5 Z99348	Hs.11246		3.0 3.0
	404041	В			3.0
				220	

	400463	*****		chicagonal of Course MCI. T. CRC St Morros	3.0
	429163 454117	AA884766 BE410100	Hs.40368	gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s adaptor-related protein complex 1, sigma	3.0
	418196	AI745649	Hs.26549	KIAA1708 protein	3.0
_	434131	AI858275	Hs.143659	ESTs	3.0
5	441255	R06350	Hs.171635	ESTs	2.9
	453900	AW003582	Hs.226414	ESTs, Wealthy similar to ALUS_HUMAN ALU S	2.9 2.9
	453905 416602	NM_002314 NM_006159	Hs.36566 Hs.79389	LIM domain kinase 1 nel (chicken)-like 2	2.9
	431173	AW971198	Hs.294068	ESTs	2.9
10	425599	AW366745	Hs.214140	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.9
	436401	AI087958	Hs.29088	ESTs	29
	422960	AW890487	Hs.63984	cadherin 13, H-cadherin (heart)	29 29
	451558 412490	NM_001089 AW803564	Hs.26630 Hs.288850	ATP-binding cassette, sub-family A (ABC1 Homo sepiens cDNA: FLJ22528 fis, clone H	29
15	433149	BE257672	Hs.42949	hypothetical protein HES6	2.9
	434811	AW971205	Hs.114280	ESTs	29
	425897	AA935315	Hs.48965	Homo sapiens cDNA: FLJ21693 fis, clone C	2.9
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210 solute carrier family 2 (facilitated glu	2.9 2.9
20	453496 411124	AA442103 AW196937	Hs.33084 Hs.53929	ESTs, Weakly similar to ALUB_HUMAN !!!!	2.9
20	419227	BE537383	Hs.89739	cholinergic receptor, nicotinic, beta po	2.9
	427651	AW405731	Hs.18498	Homo sapiens cDNA FLJ12277 fis, clone MA	2.9
	441707	R42637	Hs.21963	hypothetical protein DKFZp761B0514	2.9 2.9
25	435741	A1240668	Hs.113099 Hs.120873	ESTs ESTs, Highly similar to T46266 hypotheti	29
25	437273 422939	AL137451 AW394055	Hs.98427	ESTs, Weakly similar to 138022 hypotheti	2.9
	439376	AA883521	Hs.222064	ESTs	2.9
	439935	\$75105	Hs.301676	glutamate receptor, ionotropic, kainate	2.9
20	437267	AW511443	Hs.258110	ESTs	2.9 2.9
30	453740	AL120295	Hs.311809	ESTs, Moderately similar to PC4259 ferri	29
	400250 400992				2.9
	408814	N62499	Hs.176227	hypothetical protein FLJ11155	2.9
	411849	AW964970	Hs.18861	ESTs, Moderately similar to KIAA1276 pro	29
35	414853	U31116	Hs.77501	sarcoglycan, beta (43kD dystrophin-assoc	2.9 2.9
	423751	AW235633 AA470023	Hs.46525 Hs.190089	ESTs ESTs, Moderately similar to ALU1_HUMAN A	2.9
	426910 450203	AF097994	Hs.301528	L-kynurenine/alpha-aminoadipate aminotra	2.9
	459311	R40192	Hs.21527	Human DNA sequence from clone GS1-115M3	2.9
40	425304	AA463844	Hs.31339	fibroblast growth factor 11	2.9
	428500	AIB15395	Hs.184641	fatty acid desaturase 2	2.9 2.9
	421641 421141	AI638184	Hs.106334 Hs.125914	Homo sapiens clone 23836 mRNA sequence ESTs	2.9
	407870	AW117261 AB032990	Hs.40719	hypothetical protein KIAA1164	2.9
45	456723	Z43902	Hs.4748	adenylate cyclase activating polypeptide	2.9
	436456	AW292677	Hs.248122	G protein-coupled receptor 24	2.9
	421483	NM_003388	Hs.104717	hypothetical protein MGC11333	2.9 2.9
	412190 446131	R16180 NM_000929	Hs.274461 Hs.290	ESTs phospholipase A2, group V	29
50	441668	AI611973	Hs.127525	ESTs	2.9
	437387	Al198874	Hs.28847	AD026 protein	2.9
	423420	AI571364	Hs.128382	Homo sapiens mRNA; cDNA DKFZp76111224 (f	2.9
	427958	AA418000	Hs.98280	potassium intermediate/smail conductance splicing factor 3b, subunit 3, 130kD	2.9 2.9
55	429084 447067	AJ001443 R42098	Hs.195614 Hs.21964	ESTs	2.9
	430887	N66801	Hs.260287	KIAA1841 protein	2.9
	441824	AB007871	Hs.7977	KIAA0411 gene product	2.9
	424126	AA335635	Hs.96917	ESTs	2.9 2.9
60	408739 447422	W01556 BE618703	Hs.238797 Hs.98258	ESTs, Moderately similar to 138022 hypot orthopedia (Drosphila) homolog	2.9
O	435615	Y15065	Hs.4975	potassium voltage-gated channel, KQT-lik	2.9
	446997	AA383439	Hs.16758	Spir-1 protein	29
	433573	AF234887	Hs.57652	cadherin, EGF LAG seven-pass G-type rece	2.9
65	408447	AK002089	Hs.45080	Homo sapiens cDNA FLJ11227 fis, clone PL ESTs, Wealdy similar to I38022 hypotheti	2.9 2.8
U)	419586 417022	AI088485 NM_014737	Hs.144759 Hs.80905	Ras association (RalGDS/AF-6) domain fam	2.8
	408432	AW195262	713.00340	gb:xn67b05.x1 NCI_CGAP_CML1 Homo sapiens	2.8
	420320	AB002361	Hs.96633	KIAA0363 protein	2.8
70	425241	AA324624	Hs.155247		2.8 2.8
70	428670	AA431682 NM_001975	Hs.134832 Hs.146580		2.8 2.8
	424415 409185	AW961601	Hs.252406		2.8
	411555	AF113537	Hs.70669	HMP19 protein	2.8
7.	426847	S78723	Hs.298623		2.8
75	458809	AW972512	Hs.20985	sin3-associated polypeptide, 30kD ATP-binding cassette, sub-family A (ABC1	2.8 2.8
	420071 424572	AB028985 M19650	Hs.94806 Hs.150741		2.8
	444670	H58373	Hs.332938		2.8
00	411089	AA456454	Hs.183418	cell division cycle 2-like 1 (PITSLRE pr	2.8
80	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (2.8 2.8
	440637	AW900115 AA836381	Hs.7309 Hs.315111	Homo sapiens clone 23741 mRNA sequence nuclear receptor co-repressor/HDAC3 comp	2.8 2.8
	408554 403056	R58624	Hs.2186	eukaryotic translation elongation factor	2.8
	.50050				

	423449	A1497900	Hs.33067	ESTs	2.8
	423445			zinc finger protein	2.8
	429006			hypothetical protein FLJ13842	2.8
-	434981			ESTs	2.8 2.8
5	437435	AA249439		hypothetical protein DKFZp762H1311	2.8
	442748	AI016713		ESTs ESTs	2.8
	443312 450940	N52025 A1744943		ESTs, Weakly similar to 138022 hypotheti	2.8
	452738	AL133800		hypothetical protein MGC12435	2.8
10	409182	AA064970		ESTs	2.8
	439793	AA018825	Hs.7934	Kruppel-like factor 4 (gut)	2.6 2.8
	432683	AW995441	Hs.10475	ESTs similar to murine leucine-rich repeat pr	2.8
•	434269 429500	AK001991 X78565	Hs.3781 Hs.289114	hexabrachion (tenascin C, cytotactin)	2.8
15	433290	R20077	Hs.302185	Homo sapiens clone 23618 mRNA sequence	2.8
	434276	AF123659	Hs.93605	leucine zipper, putative tumor suppresso	2.8
	435977	AL138079	Hs.5012	brain-specific membrane-anchored protein	2.8 2.8
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4 gb:yq37d04.s1 Soares fetal liver spleen	2.8
20	425168 428180	R96366 AJ129767	Hs.182874	guanine nucleotide binding protein (G pr	2.8
20	409348	A1401535	Hs.146090	ESTs	2.8
	409887	AL137534	Hs.56876	Homo sapiens mRNA; cDNA DKFZp434H1419 (f	2.8
	457211	AW972565	Hs.32399	ESTs, Wealthy similar to S51797 vasodilat	2.8 2.8
25	430039	BE253012	Hs.153400	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.8
25	417642	BE302665	Hs.105461 Hs.262346	hypothetical protein FLJ20357 ESTs, Weakly similar to S72482 hypotheti	2.8
	419169 434008	AW851980 AA740878	Hs.112982	ESTs	2.8
	446776	AW293417	Hs.156455	ESTs	2.8
	408838	AI669535	Hs.40369	ESTs	2.8
30	422565	BE259035	Hs.118400	singed (Drosophila)-like (sea urchin fas	2.8 2.8
	447397	BE247676	Hs.18442	E-1 enzyme hypothetical protein FLJ13346	2.8
	412530 424330	AA766268 AW073953	Hs.266273 Hs.333396	Homo sapiens cDNA FLJ13596 fis, clone PL	2.8
	446377	AW014022	Hs.170953	EST8	2.8
35	458924	BE242158	Hs.24427	DKFZP566O1646 protein	2.8
	447710	Al420523	Hs.328241	ESTs	2.8 2.8
	404049			gb:RC1-DT0001-031299-011-a11 DT0001 Homo	2.8
	416913	AW934714 M78361	Hs.169743	Homo sapiens clone 25121 neuronal olfact	2.8
40	426400 413264	W26456	Hs.134757	hypothetical protein FLJ20033	2.8
40	458997	AW937420	Hs.69662	ESTs	2.7
	422864	AA318323		gb:EST20390 Retina II Homo sapiens cDNA	2.7 2.7
	430526	AF181862	Hs.242407	G protein-coupled receptor, family C, gr	2.7
45	452023	AB032999	Hs.27566	KIAA1173 protein Homo sapiens mRNA; cDNA DKFZp761L1212 (f	27
43	432022 452438	AL162042 BE514230	Hs.272348 Hs.29595	JM4 protein	2.7
	435408	H07897	Hs.4302	ESTs. Weakly similar to T29299 hypotheti	2.7
	418791	AA935633	Hs.194628		2.7
	438821	AA826425	Hs.291829		2.7 2.7
50	423464	NM_016240			2.7
	442091 442242	AW770493 AV647908	Hs.182874 Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	2.7
	412436	AA665089	113.30727	gb:nu76d01.s1 NCI_CGAP_Alv1 Homo sapiens	2.7
	432821	BE170702	Hs.279005	solute carrier family 21 (organic anion	2.7
55	416404	AA180138	Hs.107924	ESTs	2.7 2.7
	441364	AW450466	Hs.126830		2.7
	450202 426304	AW969756 AA374532	Hs.34145 Hs.124673		2.7
	428722	U76456	Hs.190787		2.7
60	449701	AW952323	Hs.129908	R KIAA0591 protein	2.7
	420372	AW960049	Hs.293660	Homo sapiens, clone IMAGE:3535476, mRNA,	2.7 2.7
	410318	AA084050	Hs.269259	ESTs, Weakly similar to S23650 retroviru ESTs, Weakly similar to YEX0_YEAST HYPOT	2.7
	414603 416096	R58394 H18577	Hs.25119 Hs.88974	cytochrome b-245, beta polypeptide (chro	2.7
65	420896			Homo sapiens cDNA: FLJ22165 fis, clone H	2.7
•	424856		Hs.9521	ESTs, Weakly similar to ZN43_HUMAN ZINC	27
	436304		Hs.10888		2.7 2.7
	441027		Hs.12644		2.7
70	452545 454201		Hs.14434 Hs.44131		2.7
70	434201				2.7
	426807		Hs.15668	2 ESTs	2.7
	425825		Hs.15959		2.7 2.7
75	440351			RAD1 (S. pombe) homolog 4 protein tyrosine phosphatase, non-recept	2.7
13	425390 427624		Hs.15611 Hs.24895		2.7
	42/624			gb:EST90805 Synovial sarcoma Homo sapien	2.7
	422491			6 neuronatin	2.7
00	424560	AA158727			2.7 2.7
80	432415		Hs.28901		2.7
	414865 415827		Hs.27441 Hs.23079		2.7
	415827 445568		Hs.26874		2.7

	433315	R96754	Hs.239706	GRB2-associated binding protein 1	27 27
	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	2.7
	447959 426420	AI452784 BE383808	Hs.270270 Hs.322430	ESTs, Wealty similar to 2109260A B cell NDRG family, member 4	2.7
5	436899	AA764852	Hs.291567	ESTs	27
	444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	2.7
	426501	AW043782	Hs.293616	ESTs	2.7
	449092	U91641	Hs.22985	alpha2,8-sialyttransferase	2.7
	427311	AB020672	Hs.175411	KIAA0865 protein	2.7
10	453313	BE005771	Hs.153746	hypothetical protein FLJ22490	2.7
	404029				2.7
	416289	W26333	Hs.337438	ESTs	2.7
	439108	AW163034	Hs.6467	synaptogyrin 3	2.6
1.5	418746	AI955289	Hs.300759	ribosomal protein L36	2.6
15	412046	Y07847	Hs.73088	RAS-related on chromsome 22	2.6 2.6
	435040	AJ932350	Hs.152825	ESTs	2.6
	453083	U87223	Hs.31622 Hs.16332	contactin associated protein 1 ESTs	2.6
	428167 420028	AA770021 AB014680	Hs.8786	carbohydrate (N-acetylglucosamine-6-O) s	2.6
20	443715	AL583187	Hs.9700	cyclin E1	2.6
20	421247	BE391727	Hs.102910	general transcription factor IIH, polype	2.6
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	2.6
	415056	AB004662	Hs.77867	adenosine A1 receptor	2.6
	451697	AW449774	Hs.296380	POM (POM121 rat homolog) and ZP3 fusion	2.6
25	433701	AW445023	Hs.15155	ESTs	2.6
	457358	AJ479755	Hs.129010	ESTs	2.6
	430347	NM_002039	Hs.239706	GRB2-associated binding protein 1	2.6
	418027	AB037807	Hs.83293	hypothetical protein	2.6
20	440491	R35252	Hs.24944	ESTs, Weakly similar to 2109260A B cell	26
30	425171	AW732240	Hs.16365	ESTS	2.6 2.6
	459335	AW298545	Hs.250726	EST ESTs, Wealdy similar to B34323 GTP-bindi	26
	425402 453169	AI215881 AB037815	Hs.24970 Hs.32156	KIAA1394 protein	26
	433647	AA603367	Hs.222294	ESTs	26
35	450414	A1907735	Hs.21446	KIAA1716 protein	2.6
55	446233	AI282028	Hs.25205	ESTs	2.6
	415446	F08898	Hs.66075	ESTs	2.6
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-4	2.6
	413012	D83777	Hs.75137	KIAA0193 gene product	2.6
40	428671	BE297851	Hs.189482	zinc finger protein 179	2.6
	427158	AA935603	Hs.166231	ESTs	2.6
	408988	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	2.6
	459516	A1049662	Hs.246858	EST	2.6
45	402693				2.6
45	408039	AA131424	Hs.50340	ESTs	2.6
	422896	AW961489	Hs.154116	ESTs	2.6
	423130	AW897586	Hs.21213	ESTs	2.6 2.6
	438796	W67821	Hs.109590	genethonin 1 hypothetical protein FLJ23476	2.6
50	439871 440192	R88518 AA872282	Hs.46736 Hs.190596	ESTs	26
30	419708	AK000753	Hs.92374	hypothetical protein	2.6
	449436	AA860329	Hs.279307	hypothetical protein DKFZp434l2117	2.6
	436870	AW204219	Hs.155560	calnexin	2.6
	448424	AW009892	Hs.31924	ESTs	2.6
55	401324				2.6
	414136	AA812434	Hs.119023	SMC2 (structural maintenance of chromoso	2.6
	433943	AA992805	Hs.44865	lymphoid enhancer-binding factor 1	26
	428001	H97428	Hs.219907		26
C O	429139	F09092	Hs.66087	ESTs	2.6
60	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	2.6 2.6
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	
	444001	AI095087	Hs.152299	ESTs, Moderately similar to S65657 alpha	2.6
	412049	N53437	Hs.18268	adenylate kinase 5 Homo sapiens clone 25012 mRNA sequence	2.6 2.6
65	441783	8E313412	Hs.7961 Hs.155524	peanut (Drosophila)-like 2	2.6
05	425287 432149	R88249 AW614326	Hs.157022	ESTs, Weakly similar to T34549 probable	2.6
	452234	AW084176	Hs.223296		. 2.6
	453478	AF083898	Hs.33021	neuro-oncological ventral antigen 2	2.6
	418962	AA714835	Hs.271863		2.6
70	418858	AW961605	Hs.21145	hypothetical protein RG083M05.2	2.6
	443257	AI334040	Hs.11614	HSPC065 protein	2.6
	428748	AW593206	Hs.98785	Ksp37 protein	2.6
	444984	H15474	Hs.132898		2.6
76	433404	T32982	Hs.102720		2.6
75	434779	AF153815	Hs.50151	potassium inwardly-rectifying channel, s	2.6
	420582	BE047878	Hs.99093	Homo sapiens chromosome 19, cosmid R2837	2.6
	452856	AF034799	Hs.30881	protein tyrosine phosphatase, receptor t	26
	436440	AJ471862	Hs.196008		2.6 2.6
80	438527	AI969251	Hs.115325	RAB7, member RAS oncogene family-like 1 neuroligin 3	2.6
50	433216 435380	AF217412 AA679001	Hs.47320 Hs.192221		26
	428966	AF059214	Hs.194687		2.6
	439653	AW021103	Hs.6631	hypothetical protein FLJ20373	2.6
				· ·	

				POT 191 44 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	2.6
	419304		Hs.146101 Hs.48965	ESTs, Wealtly similar to T45070 protein k Homo sapiens cDNA: FLJ21693 fis, clone C	2.6
	422991 448548	R13209	Hs.21413	solute carrier family 12, (potassium-chi	26
_	435370	AJ964074	Hs.225838	ESTs	2.6
5	408875	NM_015434		DKFZP434B168 protein	2.5 2.5
	457005 430154	AJ007421 AW583058	Hs.172597 Hs.234726	sal (Drosophila)-like 3 serine (or cysteine) proteinase inhibito	2.5
	438549	BE386801	Hs.21858	trinucleotide repeat containing 3	2.5
• •	427951	AI826125	Hs.43546	ESTs	2.5 2.5
10	411800	N39342 A1821877	Hs.103042 Hs.140002	microtubule-associated protein 1B ESTs, Moderately similar to ALU7_HUMAN A	2.5
	457683 451422	AB002336	Hs.26395	erythrocyte membrane protein band 4.1-li	2.5
	430713	AA351647	Hs.2642	eukaryotic translation elongation factor	2.5 2.5
1.5	428826	AL048842	Hs.194019	attractin	2.5 2.5
15	428963	AW382682 D50402	Hs.258208 Hs.182611	Homo sapiens, clone MGC:15606, mRNA, com solute carrier family 11 (proton-coupled	2.5
	428141 429550	AW293055	Hs.119357	ESTs	2.5
	438662	AA223599	Hs.6351	cleavage and polyadenylation specific fa	2.5 2.5
20	435760	AF231922	Hs.213004	chromosome 21 open reading frame 62 ESTs	2.5
20	427513 430061	AI476318 AB037817	Hs.192480 Hs.230188	KIAA1396 protein	2.5
	435923	BE301930	Hs.5010	Homo sapiens clone 24672 mRNA sequence	2.5
	417123	BE326521	Hs.159450	ESTS	2.5 2.5
25	439699	AF086534 AI815750	Hs.187561 Hs.20977	ESTs, Moderately similar to ALU1_HUMAN A hypothetical protein MGC3129 similar to	2.5
23	412980 427209	H06509	Hs.92423	KIAA1566 protein	2.5
	424327	AA431707	Hs.31209	ESTs	2.5 2.5
	436340	R42246	Hs.21606	ESTs hypothetical protein MGC3295	2.5
30	450650 439444	T65617 AI277652	Hs.101257 Hs.54578	ESTs, Weakly similar to 138022 hypotheti	2.5
50	400777	METIONE	155.54010		2.5
	439478	AF049460	Hs.6574	deformed epidermal autoregulatory factor	2.5 2.5
	450407	NM_000810	Hs.24969	gamma-aminobutyric acid (GABA) A recepto synuclein, alpha interacting protein (sy	2.5
35	450385 432558	AI631024 R97268	Hs.24948 Hs.177269	ESTs	2.5
<i></i>	400860	1.0.200			2.5
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	2.5 2.5
	416063	BE047699 NM 002543	Hs.93454 Hs.77729	ESTs oxidised low density lipoprotein (lectin	2.5
40	414998 452823	AB012124	Hs.30696	transcription factor-like 5 (basic helix	2.5
	417791	AW965339	Hs.111471	ESTs	2.5 2.5
	418079	R40058	Hs.6911	ESTs ESTs	2.5
	408495 442104	W68796 L20971	Hs.237731 Hs.188	phosphodiesterase 4B, cAMP-specific (dun	2.5
45	437370	AL359567	Hs.161962	Homo sapiens mRNA; cDNA DKFZp547D023 (fr	2.5
	429803	W81489	Hs.223025	RAB31, member RAS oncogene family	2.5 2.5
	424959	NM_005781 BE547647	Hs.153937 Hs.177781	activated p21cdc42Hs kinase hypothetical protein MGC5618	2.5
	427413 408955	BE315170	Hs.8087	NAG-5 protein	2.5
50	415261	T40928	Hs.8346	ESTs	2.5 2.5
	415716	N59294	Hs.179662		2.5
	417873 418388	BE266659 R72332	Hs.293659 Hs.29258	Homo sapiens cDNA FLJ11364 fis, clone HE	2.5
	421002	AF116030	Hs.100932	transcription factor 17	2.5
55	423244	AL039379	Hs.209602	ESTs, Weakly similar to ubiquitous TPR m ESTs, Weakly similar to DYLX_HUMAN CYTOP	2.5 2.5
	423553 427961	AA405635 AW293165	Hs.96854 Hs.143134		2.5
	428301	AW628666		ESTs, Weakly similar to 138022 hypotheti	2.5
۲۵	428508	BE252383	Hs.184668	SBBI31 protein	2.5 2.5
60	428858		Hs.37636	gb:zv67d11.r1 Soares_total_fetus_Nb2HF8_ ESTs, Wealdy similar to KIAA1392 protein	2.5
	428943 432427		Hs.6638	Homo sapiens cDNA FLJ11602 fis, clone HE	2.5
	435347			3 ESTs	2.5
65	437949		Hs.41654	ESTs, Wealdy similar to A46010 X-linked	2.5 2.5
65	438208 440286		Hs.65379 Hs.7138	ESTs cholinergic receptor, muscarinic 3	2.5
	441523			1 ESTs, Weakly similar to ALUF_HUMAN !!!!	2.5
	441805	AA285136	Hs.30191		2.5 2.5
70	442337		Hs.12925		2.5
70	442789 445556		Hs.13119 Hs.12887		2.5
	449088		Hs.20803	7 ESTs	2.5
	459583			gb:IL-BT152-080399-004 BT152 Homo sapien	2.5
75	TADIC	24D-			
, 5	TABLE Pkey:	; 240. U	nique Eos prot	eset identifier number	
	CAT n	umber: G	ene cluster nu	mber	
	Access	sion: G	ienbank access	SION NUMBERS	
80	Pkey	CAT Num	ber Accessio	n	
	40843	2 1058667_	1 AW1952	62 R27868 AW811262	
	41222	5 1284108_	1 AW9020	42 N77591 19 AA135130 AA484059 AA102419 AW877765	
	41243	6 129439_1	MADOJUE	2.2.2	

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H46739 H51513 H19779
           416120
                       1571266_1
                                      H98716 N90792 N24283
                       1626761_1
           416871
                                      AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499
           416913
                       163001_1
                                      AA318323 H11145 R15289 AA451945 AA476690 AA436954 Z43802 F11753 T65491 D81821
                       222336 1
           422864
  5
           422949
                       223184_1
                                      AA319435 N56456 AA319377 AW961532 T48452 AA894424
                                      AA631498 AI017191 AA491211 AA761823 AA714555 AA768099 AA808286 AI934069 AA570223 AA574389 AA582438 AI745346 AW964510 AA319642
           422977
                       223410_1
                                      AW853758 H56414
                                      AA828125 AA834883 AA330555
                       231725 1
           423756
                                      R96366 AL133929 AA351636 H78818 AA477084 Z28957 H80194
           425168
                       247552 1
10
                                      AF121179 BE162736 AA358827
           425517
                       252729_1
                                      AA377823 AW954494 Al022688
AA418703 AA418711 BE071915 BE071920 BE071912
           426413
                       266650_1
           428002
                       285602_1
                       294049 1
                                      AA431765 AA432015
           428679
                       296453_1
                                      AA436760 AW237453 BE327496 N47347 N56967
           428858
                                      D80642 AA443145 AL 119015 AW904500
AA884766 AW974271 AA592975 AA447312
AW975367 AA598607 AA742735
15
           429007
                       298301_1
           429163
                       300543_1
                       368950_1
           433532
                                      AK001059 AA633055
                       41555_1
           436190
           437034
                       431713_1
                                      AA742643 AA808575 AW976668
20
                                      AW975186 AA807807 D29548
AA828995 AA834879 AI926361
AF086387 W77884 W72711
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438993
                       457837_1
                       467651_1
                       47387_1
           439566
                                      AA879430 BE070262 BE070493 BE070272 BE070484 BE070397 BE070395 BE070201 BE070198 BE070404 BE070270 BE070400
                       491965_1
            440322
                                      Al168422 D80113 T59074
R36075 Al366546 R36167
           444584
                       611496_1
25
           447197
                       711623 1
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           448451
                       764066 1
           450625
                       84032_1
                                      AW970107 AA513951 AA010406
            452453
                       918300_1
                                       AI902519 AI902518 AI902516
            454996
                       1248640 1
                                      AW850180 AW850326
30
                                      AW901809 AW901787 AW901795 AW901792 AW901744 AW901753 AW901807 AW901798
                       1283853_1
           455350
            TABLE 24C:
                                Unique number corresponding to an Eos probeset
Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA
            Pkey:
            Ref-
35
                                sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
                                Indicates DNA strand from which exons were predicted.
            Strand:
            Nt_position:
                                Indicates nucleotide positions of predicted exons.
                                                     Nt_position
                                       Strand
 40
                                                     70745-71121
            400777
                        8131663
                                       Plus
             400780
                        8131663
                                                     118372-118619
                                       Minus
                                                     91888-92018,98131-98294,99474-99570
            400859
                        9757499
                                       Minus
                                                     151830-152104,152649-152744
                        9757499
                                       Minus
            400860
                        8096828
                                       Plus
                                                     140390-140822
            400992
 45
                        9863791
                                                     234057-234174
            401324
                                       Plus
                                                     110326-110491
20393-20767
47680-47973
             402408
                        9796239
                                       Minus
            402604
402605
                        9909420
                                       Plus
                        9909420
                                       Minus
            402693
                        8569863
                                       Minus
                                                     82366-82515
 50
                                                     59763-59909
108716-111112
             402855
                        9662953
                                       Minus
             404029
                        7671252
                                       Plus
             ANANAR
                        3688074
                                       Minus
                                                      54421-56808
                                                      75765-78155
             404049
                        3688074
                                       Minus
                                                      99460-99564
             404283
                        2276311
                                        Minus
 55
             404299
                        5738652
                                        Minus
                                                      3826-4025
                                                      103456-103664
             404541
                        8318559
                                       Plus
             404584
                        9857511
                                                      138651-139153
                                        Plus
             404593
                         9944086
                                                      74922-75788
                                        Minus
             404721
                         9856648
                                        Minus
                                                      173763-174294
 60
                                                      16223-16319,16427-16513,16736-16859,16941-17075,17170-17287,17389-17529,18261-18357,18443-18578
                        4678240
             404819
                                        Plus
             405238
                        7249119
                                                      51728-51836
                                        Minus
                                                      91191-91254,91510-91589
             405771
                         7018349
                                        Ptus
             405819
                         4007557
                                        Plus
                                                      2830-2967
                                                      137114-139033
             406311
                        9211559
                                        Minus
 65
             TABLE 25A: ABOUT 1202 GENES UP-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT CENTRAL NERVOUS SYSTEM (CNS)
             Table 25A lists about 1202 genes up-regulated in glioblastoma compared to normal adult central nervous system (CNS). These were selected from 59680 probesets on the AffyrmetrivEos Hu03 GeneChip array such that the ratio of "average" glioblastoma to "average" normal adult CNS tissues was greater than or equal to 2.0. The "average"
             glioblastoma level was set to the 75th percentile amongst various glioblastoma tumors. The "average" normal adult CNS tissue level was set to the 95th percentile amongst various
  70
             non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was
             subtracted from both the numerator and the denominator before the ratio was evaluated.
                                 Unique Eos probeset identifier number
             Pkey:
                                 Exemplar Accession number, Genbank accession number
             ExAccn:
  75
             UnigenetD:
                                  Unigene number
                                 Unigene gene title
Ratio of 75<sup>th</sup> percentile tumor to 95<sup>th</sup> percentile normal adult nervous system tissue
             Unigene Title:
             RI:
                                        UnigeneID
Hs.108106
                                                      Unigene Title
                         ExAcon
  80
             452461
                         N78223
                                                      transcription (actor
                                                      carbonic antivorase XII
                                         Hs.5338
             435895
                         AF037335
                                         Hs.36820
                         U39817
                                                      Bloom syndrome
             453941
             443247
                         BE614387
                                         Hs.333893
                                                      c-Myc target JPO1
                                                                                                                          12.4
```

					12.0
			Hs.2256 r	natrix metalloproteinase 7 (matrilysin,	11.7
	447342			torno sapiens, Similar to RIKEN cDNA 2010	11.4
	422163			prominin (mouse)-like 1 neterochromatin-like protein 1	11.2
5	439451			MyoD family inhibitor	10.2
,	424800 416111			chromatin assembly factor 1, subunit A (10.0
	444190			cysteine and glycine-rich protein 2	9.9
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	9.9
	449340	AW235786	Hs.195359	hypothetical protein MGC10954	9.8
10	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	9.4
	439978	BE139460	Hs.124673	Homo sapiens cDNA FLJ11477 fis, clone HE	8.9 8.9
	411411	AA345241		ESTs, Weakly similar to KIAA1330 protein	8.2
	456516	BE172704		KIAA1610 protein	7.9
1.5	420092	AA814043		ESTs	7.9
15	422631	BE218919		hypothetical protein FLJ10688 SRY (sex determining region Y)-box 11	7.9
	453392	U23752	Hs.32964 Hs.115325	RAB7, member RAS oncogene family-like 1	7.9
	438527	A1969251 NM_014788		KIAA0129 gene product	7.8
	427581 418661	NM_001949	Hs.1189	E2F transcription factor 3	7.8
20	440684	AI253123	Hs.127356	ESTs, Highly similar to S21424 nestin [H	7.8
20	429643	AA455889	Hs.167279	FYVE-finger-containing Rab5 effector pro	7.7
	409638	AW450420	Hs.21335	ESTs	7.5
	444665	BE613126	Hs.47783	8 aggressive lymphoma gene	7.5
	456759	BE259150	Hs.127792	delta (Drosophila)-like 3	7.5
25	412777	Al335773	Hs.270123	ESTs	7.4
	436607	AW661783	Hs.211061	ESTs	7.3 7.3
	432058	AW665996	Hs.130729	ESTs, Weakly similar to ALU1_HUMAN ALU S	7.3 7.3
	417061	A1675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, done HE	7.2
20	428976	AL037824	Hs.194695	ras homolog gene family, member i	7.1
30	433244	AB040943	Hs.271285	KIAA1510 protein ESTs, Weakly similar to T00079 hypotheti	7.1
	436726	AA324975	Hs.128993	gb:xn67b05.x1 NCI_CGAP_CML1 Homo sapiens	7.1
	408432	AW195262	Hs.148135	serine/threonine kinase 33	7.0
	434164 445873	AW207019 AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-l	7.0
35	439726	AW449893	Hs.293707	ESTs, Weakly similar to 138598 zinc fing	7.0
55	432656	NM_000246	Hs.3076	MHC class II transactivator	6.8
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	6.8
	453387	AI990741	Hs.252809	ESTs	6.8
	418821	AA436002	Hs.183161	ESTs	6.6
40	437034	AA742643		gb:ny91c01.s1 NCI_CGAP_GCB1 Homo sapiens	6.6
	411252	AB018549	Hs.69328	MD-2 protein	6.5
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	6.4
	452953	AI932884	Hs.271741	ESTs, Wealty similar to A46010 X-linked	6.3 6.3
4.5	433532	AW975367		gb:EST387475 MAGE resequences, MAGN Homo	6.3
45	420311	AW445044	Hs.38207	Human DNA sequence from clone RP4-530115	6.2
	418097	R45137	Hs,21868	ESTS	6.2
	407304	AA565832	11- 42072	gb:nj32b03.s1 NCI_CGAP_AA1 Homo sapiens	6.1
	435256	AF193766	Hs.13872	cytokine-like protein C17 ESTs	6.1
50	449448	D60730	Hs.57471	E313	6.0
50	403790 425517	AF121179		gb:AF121179 Horno sapiens liver (Chang L-	6.0
	420674	NM_000055	Hs.1327	butyrylcholinesterase	6.0
	435542	AA687376	Hs.269533	ESTs	5.9
	418216	AA662240	Hs.283099	AF15q14 protein	5.8
55	439086	AF085947		gb:Homo sapiens full length insert cDNA	5.8
	408037	AW271720	Hs.42233	hypothetical protein FLJ10300	5.7
	412225	AW902042		gb:QV0-NN1022-170400-193-c02 NN1022 Homo	5.7 5.7
	436109	AA922153	Hs.132760		5.7 5.7
~ ^	435005	U80743	Hs.306094	trinucleotide repeat containing 12	5.7 5.7
60	429149	AW193360	Hs.197962	ESTs, Weakly similar to I38022 hypotheti SRY (sex determining region Y)-box 4	5.6
	418113	AJ272141	Hs.83484	SRY (sex determining region 1 poux 4	5.6
	405558		Un 2017B	hypothetical protein FLJ23468	5.6
	442432		Hs.38178 Hs.217484		5.6
65	442547 413063		Hs.75184	chitinase 3-like 1 (cartilage glycoprote	5.5
UJ	420560			ESTs	5.5
	408096		Hs.83765	dihydrofolate reductase	5.5
	443539		Hs.134074		5.4
	426318		Hs.147112		5.4
70	429115		Hs.289020) Homo sapiens cDNA FLJ14098 fis, clone MA	5.3
	453900			ESTs, Weakly similar to ALU8_HUMAN ALU S	5.3
	444168			gb:RC1-HT0256-081199-011-f01 HT0256 Homo	5.3
	432789	D26361	Hs.3104	KIAA0042 gene product	5.3
	437036	AI571514	Hs.13302		5.2 5.2
75	421247				5.2 5.2
	441523				5.2 5.1
	451108				5.1
	457211				5.1
80	454157			1 3127	5.1
٥v	42334				5.1
	425291 406671			gb:zm66b07.r1 Stratagene neuroepithelium	5.1
	44267		Hs.13477		5.1
	* *4.44				

	433001	AF217513	Hs.279905	clone HQ0310 PR00310p1	5.0
	418819	AA228776	Hs.191721	ESTs	5.0
	432946	U60899	Hs.279854	mannosidase, alpha, class 28, member 1	4.9
_	420730	NM_002691	Hs.99890	polymerase (DNA directed), delta 1, cata	4.9
5	441217	AI922183	Hs.213246	ESTs	4.9
	453385	AW296101	Hs.252806	ESTs	4.8 4.7
	418203 450813	X54942 A1739625	Hs.83758 Hs.203376	CDC28 protein kinase 2 ESTs	4.7
	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	4.7
10	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	4.7
	431070	AW408164	Hs.249184	transcription factor 19 (SC1)	4.7
	429786	AL080232	Hs.220696	Homo sapiens mRNA; cDNA DKFZp586A061 (fr	4.7
	405771			for	4.6
15	457065	AJ476318	Hs.192480	ESTS	4.6 4.6
13	436190 400859	AK001059		gb:Homo sapiens cDNA FLJ10197 fis, clone	4.6
	435267	N23797	Hs.110114	ESTs	4.6
	443454	AI057494	Hs.133421	ESTs	4.5
	452811	AA937079	Hs.118983	hypothetical protein FLJ12150	4.5
20	437267	AW511443	Hs.258110	ESTs	4.5
	435020	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8	4.5
	454269 422106	Al961060 D84239	Hs.129908 Hs.111732	KIAA0591 protein Fc fragment of IgG binding protein	4.5 4.5
	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	4.5
25	456534	X91195	Hs.100623	phospholipase C, beta 3, neighbor pseudo	4.5
	423756	AA828125		gb:od71a09.s1 NCI_CGAP_Ov2 Homo sapiens	4.5
	417308	H60720	Hs.81892	KIAA0101 gene product	4.5
	422170	Al791949	Hs.112432	anti-Mullerian hormona	4.4
20	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotactin)	4.4
30	406568	AF088886	Hs.11590	cathepsin F	4.4 4.4
	426812 402516	AF105365	Hs.172613	solute carrier family 12 (potassium/chlo	4.4
	432865	Al753709	Hs.152484	ESTs, Weakly similar to I38022 hypotheti	4.4
	413625	AW451103	Hs.71371	ESTs	4.4
35	436098	R20597	Hs.9739	glycerol-3-phosphate dehydrogenase 1 (so	4.4
	418333	W92113		gb:zh48e01.r1 Soares_fetal_liver_spleen_	4.4
	416933	BE561850	Hs.80506	small nuclear ribonucleoprotein polypept	4.4
	438192	AI859065	Hs.337620	Homo sapiens AFG3L1 isoform 1 mRNA, part	4.3
40	457374	AA493662	Un 150507	gb:nh05d12.s1 NCI_CGAP_Thy1 Homo sapiens	4.3 4.3
40	433159 444386	AB035898 BE065183	Hs.150587	kinesin-like protein 2 gb:RC1-BT0314-020200-012-c04 BT0314 Homo	4.3
	453202	AW085781	Hs.26270	hypothetical protein FLJ11588	4.3
	441020	W79283	Hs.35962	ESTs	4.3
	414733	BE514535	Hs.77171	minichromosome maintenance deficient (S.	4.3.
45	407902	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	4.3
	405701				4.3
	451659	BE379761	Hs.14248	ESTs	4.3
	418845	AA852985	Hs.89232	chromobox homolog 5 (Drosophila HP1 alph	4.2 4.2
50	433323 439811	AA805132 AA135332	Hs.30701 Hs.71608	ESTs ESTs	4.2
30	415406	T26510	HS.1 1000	gb:AB282F8R Infant brain, LLNL array of	4.2
	436282	R91913	Hs.272104	ESTs, Moderately similar to ALU1_HUMAN A	4.1
	441269	AW015206	Hs.178784	ESTs	4.1
	418727	AA227609	Hs.94834	ESTs	4.1
55	433006	8E242758	Hs.190223	ESTs, Moderately similar to T29285 hypot	4.1
	436480	AJ271643	Hs.87469	putative acid-sensing ion channel	4.1 4.1
	430786 445372	AA486144 N36417	Hs.31293 Hs.144928	ESTs ESTs	4.1
	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	4.0
60	457465	AW301344	Hs.122908	DNA replication factor	4.0
	422094	AF129535	Hs.272027	F-box only protein 5	4.0
	442029	AW956698	Hs.14456	neural precursor cell expressed, develop	4.0
	459321	AW044477	Hs.299538	ESTs	4.0
65	421308 420567	AA687322 AK000812	Hs.192843 Hs.98874	leucine zipper protein FKSG14 similar to proline-rich protein 48	4.0 4.0
05	447004	AW296968	Hs. 157539	ESTs	4.0
	448295	AI381911	Hs.334859	KIAA 1814 protein	3.9
	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	3.9
	440704	M69241	Hs.162	insufin-like growth factor binding prote	3.9
70	453096	AW294631	Hs.11325	ESTs	3.9
	457026	AA397620	Hs.48692	ESTs	3.9
	404642	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	3.9 3.9
	450375 430132	AA204686	Hs.234149		3.9
75	430132	AI927288	Hs.196779		3.9
. •	438490	AW593272	Hs.301299		3.9
	429919	AA460692	Hs.278945	hypothetical protein FLJ23024	3.9
	413604	R51767		gb:yg73g11.r1 Soares infant brain 1NIB H	3.9
80	425599	AW366745	Hs.214140		3.9
οU	448796	AA147829	Hs.301431 Hs.222165		3.9 3.8
	449300 452203	A1656959 X57522	Hs.158164		3.8
	425769	U72513	Hs.159486		3.8
				•	

			•		
	404295			a constant control de la terralisma	3.8 3.8
	410361	BE391804		guanylate binding protein 1, interferon-	3.8
	428728 409142	NM_016625 AL136877		hypothetical protein SMC4 (structural maintenance of chromoso	3.8
5	430172	AA468591		ESTs	3.8
•	447499	AW262580		protocadherin beta 16	3.8
	405884				3.8
	437236	AW137817	Hs.244353	ESTs	3.7 3.7
10	418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	3.7
10	444143	AW747996	Hs.160999 Hs.158282	ESTs, Moderately similar to A56194 throm KIAA0040 gene product	3.7
	425529 425502	NM_014656 R98895	Hs.125823	ESTs	3.7
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	3.7
	402424			•	3.7
15	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	3.7
	434072	H70854	Hs.283059	Homo sapiens PRO1082 mRNA, complete cds	3.7 3.7
	414872	U82010	Hs.77513	COX10 (yeast) homolog, cytochrome c oxid	3.7
	426071	AW138057	Hs.163835	ESTs insulinoma-associated 1	3.7
20	419078	M93119 N47474	Hs.89584 Hs.89230	potassium intermediate/small conductance	3.7
20	428037 416547	H62914	Hs.268946	ESTs, Weakly similar to PC4259 ferritin	3.7
	436899	AA764852	Hs.291567	ESTs	3.6
	436722	AW975977		gb:EST388086 MAGE resequences, MAGN Homo	3.6
	440652	A1216751	Hs.143977	ESTs	3.6 3.6
25	428450	NM_014791	Hs.184339	KIAA0175 gene product	3.6 3.6
	452103	R42764	Hs.339654	ESTs, Weakly similar to 138022 hypotheti	3.6
	409048	H59990	Hs.37699	ESTs ab:Homo sapiens full length insert cDNA	3.6
	439546 443544	AF088056 AI076315	Hs.16359	ESTs	3.6
30	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	3.6
-	435889	AI249107	Hs.269901	ESTs	3.6
	420301	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	3.6
	438078	AI016377	Hs.131693	ESTS	3.6 3.6
25	408420	NM_006915	Hs.44766	retinitis pigmentosa 2 (X-linked recessi	3.5
35	416871	H98716	Un 120226	gb:yx13d08.s1 Soares melanocyte 2NbHM Ho replication factor C (activator 1) 2 (40	3.5
	424085 446291	NM_002914 BE397753	Hs.139226 Hs.14623	interferon, garma-inducible protein 30	3.5
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	3.5
	436123	AA057484	Hs.35406	ESTs, Highly similar to unnamed protein	3.5
40	411256	AW834039		gb:QV0-TT0010-091199-053-e09 TT0010 Homo	3.5
	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	3.5
	435065	BE064391	447005	gb:RC4-BT0310-110300-015-b08 BT0310 Homo	3.5 3.5
	435532	AW291488	Hs.117305 Hs.44189	Homo sapiens, clone IMAGE:3682908, mRNA ESTs	3.5
45	447101 410530	N72185 M25809	Hs.64173	ATPase, H+ transporting, lysosomal (vacu	3.5
73	422156	N34524	113,04110	gb:yy56d10.s1 Soares_multiple_sclerosis_	3.5
	453616	NM_003462	Hs.33846	dynein, axonemal, light intermediate pol	3.5
	439743	AL389956	Hs.283858	Homo sapiens mRNA full length insert cDN	3.5
60	453884	AA355925	Hs.36232	KIAA0186 gene product	3.5 3.5
50	424954	NM_000546		turnor protein p53 (Li-Fraumeni syndrome)	3.5
	420721 426764	AA927802 AA732524	Hs.159471 Hs.151464	ZAP3 protein ESTs, Weakly similar to ALUC_HUMAN !!!!	3.4
	420649	AJ866964	Hs.124704		3.4
	448831	AL080123	Hs.22182	zinc finger protein 23 (KOX 16)	3.4
55	444371	BE540274	Hs.239	forkhead box M1	3.4
	402604				3.4
	442407	AW469584	Hs.32353	mitogen-activated protein kinase kinase	3.4 3.4
	414300	AL304870	Hs.188680		3.4
60	444670 414550	H58373 BE379808	Hs.332938	gb:601159567T1 NIH_MGC_53 Homo sapiens c	3.4
00	452211	Af985513	Hs.233420		3.4
	414416	AW409985	Hs.76084	hypothetical protein MGC2721	3.4
	449961	AW265634	Hs.133100	ESTs	3.4
65	413257	BE075035		gb:PM3-BT0584-260300-002-g05 BT0584 Homo	3,4 3,4
65	453857	AL080235	Hs.35861	DKFZP586E1621 protein	3.4
	417404 422846	NM_007350 BE513934	Hs.82101 Hs.1583	pteckstrin homology-like domain, family neutrophil cytosolic factor 1 (47kD, chr	3,4
	446189		Hs.214013		3.4
	437385		Hs.164060) ESTs	3.4
70	453652			ESTs, Moderately similar to \$65657 alpha	3.4
	408298		Hs.27192	Homo sapiens cDNA: FLJ22785 fis, clone K	3.4 3.3
	455778		U= 400/F	gb:CM2-8T0693-210300-123-d09 BT0693 Homo	3.3 3.3
	417546		Hs.18845 Hs.73946		33
75	412471 454631			gb:ti_3-ST0141-131099-017-A02 ST0141 Homo	3.3
,,	454294		Hs.50640	JAK binding protein	3.3
	457131			3 Human Chromosome 16 BAC clone CIT987SK-A	3.3
	410102	AW248508	Hs.27972	7 Homo sapiens cDNA FLJ14035 fis, clone HE	3.3
90	449676				3.3
80	436211		Hs.33482	8 hypothetical protein FLJ10719; KIAA1794 gb:DKFZp761H119_r1 761 (synonym: hamy2)	3.3 3.3
	453746 452799		Hs.21378		3.3
	435380				3.3
	,				

	426746	J03626 H14988	Hs.2057	uridine monophosphate synthetase (orotat	3.3 3.3
	453362		Hs.107375 Hs.25682	ESTS	3.3
	456473 416426	AI202788 AA180256	Hs.210473	Homo sapiens mRNA for KIAA1863 protein. Homo sapiens cDNA FLJ14872 fis, clone PL	3.3
5	445777	A1580371	Hs.145384	ESTs	3.3
,	423757	AL049337	Hs.132571	Homo sapiens mRNA; cDNA DXFZp564P016 (fr	3.3
	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone CO	3.3
	404299	7000.00			3.3
	404108				3.3
10	425189	H16622		gb:ym26c07.r1 Soares infant brain 1NIB H	3.3
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cONA 5730	3.3
	450193	AI916071	Hs. 15607	Homo sapiens Fanconi anemia complementat	3.2
	427725	U56839	Hs.180533	mitogen-activated protein kinase kinase	3.2
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	3.2
15	418968	NM_000078	Hs.89538	cholesteryl ester transfer protein, plas	3.2
	449248	M33782	Hs.23391	Homo sapiens, Similar to transcription f	3.2
	439416	W58294	Hs.56254	ESTs	3.2
	401596	AA172106	Hs.110950	Rag C protein	3.2
20	408380	AF123050	Hs.44532	diubiquitin	3.2
20	450325	AJ935962	Hs.26289	ESTs	3.2
	428730	AA625947	Hs.25750	ESTs	3.2
	457536	AA305233	Hs.278712	eukaryotic translation initiation factor	3.2
	426836	N41720	Hs.172684	vesicle-associated membrane protein 8 (e	3.2 3.2
25	442710	AI015631	Hs.23210 Hs.4854	ESTs	3.2
23	435232	NM_001262	Hs.144083	cyclin-dependent kinase inhibitor 2C (p1 ESTs	3.2
	430970 416192	AI018210 NM_005036	Hs.998	peroxisome proliferative activated recep	3.2
	446676	H09380	Hs.300965	ESTs	3.2
	451459	Al797515	Hs.270560	ESTs, Moderately similar to ALU7_HUMAN A	3.2
30	407603	AW955705	Hs.62604	Homo sapiens, clone IMAGE:4299322, mRNA,	3.2
50	413840	Al301558	Hs.145381	RNA binding motif protein, X chromosome	3.2
	448751	BE551203	Hs.201792	ESTs	3.2
	432593	AW301003	Hs.51483	ESTs, Wealthy similar to hypothetical pro	3.2
	458786	Al457098	Hs.280848	ESTs	3.2
35	455909	BE156417	Hs.278798	ESTs	3.2
	419311	AA689591		gb:nv66a12.s1 NCI_CGAP_GCB1 Homo sapiens	3.2
	439710	AF086543		gb:Horno sapiens full length insert cDNA	3.2
	434559	AF147315		gb:Homo sapiens full length insert cDNA	. 3.1
	455800	R22479	Hs.167073	Homo sapiens cDNA FLJ13047 fis, clone NT	3.1
40	436703	AW880614	Hs.146381	RNA binding motif protein, X chromosome	3.1
	414799	AI752416	Hs.77326	insulin-like growth factor binding prote	3.1
	437860	AA333063	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	3.1
	434182	W20309	Hs.118520	G-protein gamma-12 subunit	3.1
4.5	417900	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevi	3.1
45	434769	AA648884	Hs.134278	Homo sapiens cDNA FLJ12676 fis, clone NT	3.1
	414825	X06370	Hs.77432	epidermal growth factor receptor (avian	3.1
	426413	AA377823		gb:EST90805 Synovial sarcoma Homo sapien	3.1
	447959	AI452784	Hs.270270	ESTs, Wealthy similar to 2109260A B cell	3.1
50	404589	11004505	11- 440435		3.1 3.1
30	421764	AI681535	Hs.148135	serine/threonine kinase 33	3.1
	419986	AI345455	Hs.78915	GA-binding protein transcription factor,	3.1
	416941	BE000150 AU077228	Hs.48778 Hs.77256	niban protein enhancer of zeste (Drosophila) homolog 2	3.1
	414761 449611	AI970394	Hs.197075	ESTs	3.1
55	434746	AA648368	Hs.295368	ESTs	3.1
"	434274	AA628539	Hs.116252	ESTs, Moderately similar to ALU1_HUMAN A	3.1
	427899	AA829286	Hs.332053	serum emyloid A1	3.1
	417642	BE302665	Hs.105461	hypothetical protein FLJ20357	3.1
	452472	AW957300	Hs.294142	ESTs, Wealty similar to C55663 oligodend	3.1
60	446131	NM_000929	Hs.290	phospholipase A2, group V	3.1
	440052	A1633744	Hs 195648	ESTs, Weakly similar to I38022 hypotheti	3.1
	426531	AA381071		gb:EST94100 Activated T-cells XII Homo s	3.1
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	3.1
15	406267				3.1
65	447039	AV661798	Hs.282915	ESTs	3.1
	404802				3.1
	406927	M26460		gb:Homo sapiens (clone 104) retinoblasto	3.1
	419314	AW971924	Hs.87280	ESTs	3.0
70	435894	AJ076667	Hs.188011	ESTs	3.0 3.0
70	432140	AK000404	Hs.272688	hypothetical protein FLJ20397	3.0
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1 ESTs, Wealdy similar to 138022 hypotheti	3.0
	425202	AW962282	Hs.152049	gb:H.sapiens SOD-2 gene for manganese su	3.0
	407047	X65965 M26682	Hs.1149	UM domain only 1 (rhombotin 1)	3.0
75	418241 446599	M20082 Z97832	Hs.15476	differentially expressed in FDCP (mouse	3.0
, ,	412950	BE018581	Hs.245342		3.0
	428670	AA431682	Hs.134832		3.0
	446975	BE246446	Hs.16695	ubiquitin-activating enzyme E1-like	3.0
	437756	AA767537	Hs.197096		3.0
80	416084	L16991	Hs.79006	deoxythymidylate kinase (thymidylate kin	3.0
	402374	AL135225	Hs.301865		3.0
	443885	H91806	Hs.15284	ESTs	3.0
	434008	AA740878	Hs.112982	ESTs	3.0

		44000004	LL 200070	Home agricus PAIA, aCAIA DVE70547M072 (fr	3.0
	452568 414239	AA805634 AI288330		Homo sapiens mRNA; cDNA DKFZp547M072 (fr ESTs	3.0
	421013	M62397	Hs.1345	mutated in colorectal cancers	3.0
_	424635	AA420687		Homo sapiens cDNA FLJ14259 fis, clone PL	3.0 3.0
5	410276	AJ554545		ESTs ESTs	3.0
	433865 406028	N29862	Hs.44104	Cois	3.0
	401626				3.0
10	415949	H10562		ESTs	3.0 3.0
10	418583	AA604379 X02308	Hs.86211 Hs.82962	hypothetical protein thymidylate synthetase	3.0
	417933 4 34577	R37316	Hs.179769	Homo sapiens cDNA: FLJ22487 fis, clone H	3.0
	430437	Al768801	Hs.169943	Homo sapiens cDNA FLJ13569 fis, clone PL	3.0
1.5	427940	AA417812	Hs.38775	ESTS	2.9 2.9
15	456060	C14904	Hs.45184 Hs.161333	Homo sapiens cDNA FLJ12284 fis, clone MA ESTs	2.9
	421988 448775	AW450481 AB025237	Hs.388	nudix (nucleoside diphosphate linked moi	2.9
	438598	AI805943	Hs.326067	hypothetical protein MGC5178	2.9
••	429612	AF062649	Hs.252587	pituitary tumor-transforming 1	2.9 2.9
20	451189	AA016019	Hs.40905	ESTs	2.9
	401558 426207	BE390657	Hs.30026	HSPC182 protein	2.9
	404721	0200001	· 10.000-0	,	2.9
0.0	401384				2.9 2.9
25	417288	A1984792	Hs.108812	hypothetical protein FLJ22004 proteasome (prosome, macropain) subunit,	2.9
	427648 435928	Al376722 H64345	Hs.180062 Hs.183961	ESTs	2.9
	431740	N75450	Hs.183412	ESTs, Moderately similar to AF116721 67	2.9
••	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	2.9
30	439972	Al348100	Hs.124662	ESTs ESTs, Weakly similar to unnamed protein	2.9 2.9
	433112 423751	AA973801 AW235633	Hs.144553 Hs.46525	ESTs. Weardy Similar to distributed protess.	2.9
	406748	AW339106	Hs.217493	annexin A2	2.9
	422154	T79045	Hs.126927	ESTs	2.9 2.9
35	405588		11- 112553	ESTs	2.9
	440911 412420	AA909536 AL035668	Hs.143562 Hs.73853	bone morphogenetic protein 2	2.9
	445043	AW014413	Hs.196066	ESTs	2.9
	410114	AW590540	Hs.271280	ESTs	2.9
40	419217	AA504571		gb:aa60e12.r1 NCI_CGAP_GCB1 Homo sapiens	2.9 2.9
	415849	R20529 AF146761	Hs.6806 Hs.20450	ESTs BCM-like membrane protein precursor	2.9
	448140 453331	AI240665	Hs.8895	ESTs	2.9
	432065	AA401039	Hs.2903	protein phosphatase 4 (formerly X), cata	2.9
45	438380	T06430	Hs.6194	chondroitin sulfate proteoglycan BEHAB/b	2.9 2.9
	454377	AA076811 H99999	Hs.42736	gb:7803C12 Chromosome 7 Fetal Brain cDNA ESTs	2.9
	421491 452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	28
	415446	F08898	Hs.66075	ESTs	2.8
50	43951B	W76326	474007	gb:zd60d04.r1 Soares_fetal_heart_NbHH19W	2.8 2.8
	427221 422493	L15409 AW474183	Hs.174007 Hs.250173	von Hippel-Lindau syndrome hypothetical protein FLJ13158	2.8
	419451	AI907117	Hs.90535	syntaxin binding protein 2	2.8
	448789	BE539108	Hs.22051	hypothetical protein MGC15548	2.8
55	424126	AA335635	Hs.96917	ESTs	2.8 2.8
	458695	AV660159 AA233056	Hs.282284 Hs.191518		2.8
	418973 440471	AA886146	Hs.307944		2.8
	421016	AA504583	Hs.101047	transcription factor 3 (E2A immunoglobul	2.8
60	433647	AA603367	Hs.222294		2.8 2.8
	415817	U88967	Hs.78867 Hs.300717	protein tyrosine phosphalase, receptor-t sodium channel, voltage-gated, type III,	2.8
	421723 434964	AA620400 AI638850	Hs.130746		2.8
	432022	AL162042	Hs.272348	Homo sapiens mRNA; cDNA DKFZp761L1212 (f	2.8
65	400517	AF242388	Hs.149585		2.8 2.8
	433023				2.8
	448734 406736		Hs.326416 Hs.182426		2.8
	409207				2.8
70	440196	N72847	Hs.12522		2.8
	403961		II. nnenn	ECT.	2.8 2.8
	425193 425268		Hs.22509 Hs.18005		2.8
	440483		Hs.15038	6 ESTs	2.8
75	412391)	gb:RC0-MT0004-130300-011-e07 MT0004 Homo	2.8
	448769	N66037	Hs.38173	ESTs	2.8 2.8
	411632) Hs.12222	gb:QV2-CT0261-201099-011-f01 CT0261 Homo 4 ESTs, Wealdy similar to ALU5_HUMAN ALU S	2.0 2.8
	438221 457578			gb:nf20h01.s1 NCI_CGAP_HSC1 Homo sapiens	2.8
80	455510		Hs.14364	0 ESTs, Weakly similar to hyperpolarizatio	2.8
	447769	AW873704			2.8 2.8
	427701		Hs.24388 Hs.13515		2.8
	433800	, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	110,10010		

	420552	MOTORS	11- 200000	ECT	2.8
	439662 425694	H97552 U51333	Hs.269060 Hs.159237	ESTs hexokinase 3 (white cell)	2.8
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitosin	2.8
_	414598	AI094221	Hs.135150	lung type-I cell membrane-associated gly	2.8
5	447752	M73700	Hs.105938	lactotransferrin	2.8
	408761	AA057264	Hs.238936	ESTs, Wealdy similar to (define not ava	2.8 2.7
	453350 456629	AJ917771 AW891965	Hs.61790 Hs.279789	hypothetical protein FLJ23338 histone deacetylase 3	27
	439538	AA837323	Hs.164047	ESTs	2.7
10	458814	AJ498957	Hs.170861	ESTs, Wealty similar to Z195_HUMAN ZINC	2.7
	456029	8E255990	Hs.218329	hypothetical protein	2.7
	451129	BE072881		gb:RC2-8T0548-200300-012-e09 BT0548 Homo	27
	456412 453536	AW749617 AA137000	Hs.280776 Hs.62578	tankyrase, TRF1-interacting enkyrin-rela ESTs	2.7 2.7
15	438378	AW970529	Hs.86434	hypothetical protein FLJ21816	27
	425745	U44060	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	2.7
	446322	N23033	Hs.155814	ESTs	2.7
	451592	AI805416	Hs.213897	ESTs	2.7
20	429466	M85835	Hs.12827	ESTs	2.7 2.7
20	429747 455514	M87507 AW983871	Hs.2490	caspase 1, apoptosis-retated cysteine pr gb:RC1-HN0003-220300-021-h07 HN0003 Homo	2.7
	414732	AW410976	Hs.77152	minichromosome maintenance deficient (S.	2.7
	444207	AI565004	Hs.79572	cathepsin D (lysosomal aspartyl protease	2.7
25	427421	AA402414	Hs.3059	coatomer protein complex, subunit beta	2.7
25	449655	Al021987	Hs.59970	ESTs	2.7 2.7
	422648 428494	D86983 AA233439	Hs.118893 Hs.184634	Melanoma associated gene hypothetical protein FLJ20005	2.7
	406895	X60648	Hs.172550	polypyrimidine tract binding protein (he	2.7
	453255	AA278167	Hs.19215	Homo sapiens, clone IMAGE:3605822, mRNA	2.7
30	427348	NM_014137	Hs.177258	PRO0650 protein	2.7
	435370	AI964074	Hs.225838	ESTs	2.7
	407862	BE548267	Hs.50724	Homo sapiens cDNA FLJ10934 fis, done OV ESTs	2.7 2.7
	411874 421192	AA096106 AA833718	Hs.20403 Hs.204529	KIAA1806 protein	2.7
35	435899	W89093	Hs.189914	ESTs	2.7
	414603	R58394	Hs.25119	ESTs, Weakly similar to YEXO_YEAST HYPOT	2.7
	453462	AL037291	Hs.236605	ESTs, Moderately similar to ALU4_HUMAN A	2.7
	436554	AI985810	Hs.301173	ESTs	2.7 2.7
40	427528 403881	AU077143	Hs.179565	minichromosome maintenance deficient (S.	2.7
40	431779	AW971178	Hs.268571	apolipoprotein C-I	2.7
	404984			4	2.7
	448275	BE514434	Hs.20830	kinesin-like 2	2.7
15	445839	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	2.7
45	411927	BE274009	Hs.772	glycogen synthase 1 (muscle)	. 2.7 2.7
	404756 447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	2.7
	422176	H80977	115.172.0	gb:yu89a11.s1 Soares fetal fiver spleen	2.7
	439627	BE621702	Hs.29076	hypothetical protein FLJ21841	2.7
50	436532	AA721522		gb:nv54h12.r1 NCI_CGAP_Ew1 Homo sapiens	2.7
	412833	AW960547	Hs.298262	ribosomal protein S19	2.7 2.7
	457245 446861	A1745498 A1696519	Hs.204579 Hs.14427	ESTs Homo sapiens cDNA: FLJ21800 fis, clone H	2.7
	453263	R91778	Hs.99369	ESTs	2.7
55	459385	BE380047		gb:601159362F2 NIH_MGC_53 Homo sapiens c	2.7
	438764	AA824524	Hs.336452	ESTs	2.7
	429285	Ai971081	Hs.20432	ESTs, Wealdy similar to 138022 hypotheti	2.7 2.7
	424853 430037	BE549737 BE409649	Hs.132967 Hs.227789	Human EST clone 122887 mariner transposo mitogen-activated protein kinase-activat	2.7
60	449892	N73608	Hs.50309	ESTs	2.7
	454201	AB023191	Hs.44131	KIAA0974 protein	2.7
	452279	AA286844	Hs.61260	hypothetical protein FLJ13164	27
	427954	J03060	Hs.247551	metaxin 1	2.7 2.7
65	400371 452449	U80740 AW068658	Hs.20943	ESTs	2.7
03	431114	AA492400	Hs.291015	ESTs	2.7
	417088	M54915	Hs.81170	pim-1 oncogene	2.7
	447674	8E270640	Hs.19192	cyclin-dependent kinase 2	2.7
70	403680				27
70	454679 411968	AW813110 AI207410	Hs.69280	gb:CM4-ST0189-051099-021-f05 ST0189 Homo Homo sapiens, clone IMAGE:3636299, mRNA,	2.7 2.6
	422240	R60594	Hs.29002	KIAA1706 protein	2.6
	424368	AB037766	Hs.146085	KIAA1345 protein	2.6
75	405808				2.6
75	419700	AF084935	Hs.92357	galactokinase 1	2.6
	435972 453568	W95088 S70782	Hs.114198 Hs.557	ESTs adrenergic, alpha-10-, receptor	2.6 2.6
	443725	AW245680	Hs.9701	growth arrest and DNA-damage-inducible,	2.6
	444156	AW500059	Hs.86437	ESTs, Highly similar to AF219140 1 gastr	2.6
80	428209	AA424197	Hs.98947	ESTs. Weakly similar to S33496 trypsin	2.6
	437640	AA764893	Hs.272155		2.6 2.6
	453948 415402	AJ970797 AA154687	Hs.64859 Hs.177576	ESTs mannosyl (alpha-1,3-)-glycoprotein beta-	2.6
				· · · · · · · · · · · · · · · · · · ·	

	425397 418228	J04088 AA962181	Hs.156346 Hs.111219	topoisomerase (DNA) II alpha (170kD) ESTs, Moderately similar to ALU1_HUMAN A	2.6 2.6
	401324				26 26
5	425234	AW152225	Hs.165909	ESTs, Wealdy similar to 138022 hypotheti hypothetical protein MGC13168	26
5	443210 457244	AI692649 AA581385	Hs.9451 Hs.162473	ESTs, Weakly similar to I38022 hypotheti	2.6
	417144	AA382104	Hs.81337	tectin, galactoside-binding, soluble, 9	2.6
	433933	A1754389	Hs.133494	Homo sapiens clone TCCCIA00164 mRNA sequ	26
• •	437437	AA226869	Hs.16520	hypothetical protein DKFZp762L0311	2.6 2.6
10	434206	AW136973	Hs.288516	ESTs, Weakly similar to S69890 mitogen i	26
	400992	414004744		gb:RC1-HN0015-040400-011-d03 HN0015 Homo	2.6
	455530 436139	AW984744 AA765786	Hs.120936	ESTs	2.6
	448330	AL036449	Hs.207163	ESTs	26
15	412942	AL120344	Hs.75074	mitogen-activated protein kinase-actival	2.6
	432753	NM_014075	Hs.336938	Homo sapiens PRO0593 mRNA, complete cds	2.6 2.6
	433430	AI863735	Hs.186755	ESTs B-cell CLL/lymphoma 7C	2.6
	436693 429482	AW973223 AF076974	Hs.303197 Hs.203952	transformation/transcription domain-asso	2.6
20	432715	AA247152	Hs.200483	ESTs, Wealty similar to KIAA1074 protein	2.6
20	414217	Al309298	Hs.279898	Horno sapiens cDNA: FLJ23165 fis, clone L	26
	434165	AA971328	Hs.95361	myosin VIIA (Usher syndrome 1B (autosoma	2.6 2.6
	414835	AA156720	Hs.185342	ESTs	2.6
25	424489	T48851 AA281959	Hs.149250 Hs.5210	D-siglec precursor, glia maturation factor, gamma	2.6
23	436496 403797	MAZ01939	115.5210	And married and a series	2.6
	434573	AW372340	Hs.159717	ESTs	2.6
	418841	NM_002332	Hs.89137	low density lipoprotein-related protein	2.6
20	415785	R82419	Hs.23603	ESTs, Moderately similar to ALUB_HUMAN A	2.6 2.6
30	450608	AA010365	Hs.193229	ESTs fibroblast growth factor 11	2.6
	425304 432268	AA463844 BE311856	Hs.31339 Hs.274230	3-phosphoadenosine 5'-phosphosulfate sy	2.6
	410507	AA355288	Hs.40834	transitional epithelia response protein	2.6
	427343	A1880044	Hs.176977	protein kinase C binding protein 2	2.6
35	420917	AW135716	Hs.117330	ESTs	2.6 2.6
	414399	L47345	Hs.155202	transcription elongation factor B (StII) ESTs, Moderately similar to A47582 B-cel	2.6
	446089	AI860021	Hs.270651 Hs.7446	chromosome 6 open reading frame 5	2.6
	440829 408475	AF136407 AA315514	Hs.47986	hypothetical protein MGC10940	2.6
40	450946	AA374569	Hs.127698	ESTs, Moderately similar to 2109260A B c	2.6
. •	421462	AF016495	Hs.104624	aquaporin 9	2.6 2.6
	434846	AW295389	Hs.119768	ESTs	2.6
	422887	AI751848	Hs.49215	ESTs carbonic anhydrase III, muscle specific	2.6
45	417435	NM_005181 AL359587	Hs.82129 Hs.271586		2.5
43	437389 408981	AW500797	Hs.49427	Gem-interacting protein	2.5
	432180	Y18418	Hs.272822		2.5
	418079	R40058	Hs.6911	ESTs	2.5 2.5
50	437820	AA769062	Hs.323836		2.5
50	439685 425681	AW956781 AB018297	Hs.293937 Hs.159183		2.5
	435177	AI018174	Hs.42936	ESTs	2.5
	437323	AA371145	Hs. 226627		2.5
	422114	AW194851	Hs.111801		2.5 2.5
55	448478	AI523218	Hs.203456 Hs.132793		2.5
	426623 448764	AA382826 AI568607	Hs.18211		2.5
	458385	AI051489	Hs.246214	ESTs	2.5
	403726	N28939	Hs.13434	Homo sapiens clone 24418 mRNA sequence	2.5 2.5
60	444888	AI651039	Hs.14855		2.5
	456179	H75490	Hs.27193		2.5
	424840 406273		Hs.15347 Hs.83920		2.5
	418054				2.5
65	445936		Hs.61478	hypothetical protein FLJ22329	2.5
	454967			gb:IL3-CT0214-150200-074-E06 CT0214 Homo	2.5 2.5
	442303		Hs.12916		2.5
	456583 434263		Hs.10410 Hs.44648		2.5
70	416892		Hs.80409	growth arrest and DNA-damage-inducible.	2.5
	424528			4 ESTs, Wealthy similar to KIAA1204 protein	2.5
	406038		Hs.88219	zinc finger protein 200	2.5 2.5
	413495		Hs.31517		2.5 2.5
75	423098		Hs.20468 Hs.93659		2.5
13	410817 439841		Hs.6710	mannose-P-dolichol utilization defect 1	2.5
	453828			ests	2.5
	445034	AW293376	Hs.1436	9 ESTs	2.5
00	449620				2.5 2.5
80	406876		Hs.1808	12 ribosomal protein L13 gb:RC2-ET0021-280400-011-c05 ET0021 Homo	2.5
	412370 423642				2.5
	43035				2.5

					26
	414853	U31116	Hs.77501	sarcoglycan, beta (43kD dystrophin-assoc	2.5 2.5
	416097	BE387371	Hs.118964	hypothetical protein FLJ20085	2.5 2.5
	428619	AK002140	Hs.187378	hypothetical protein FLJ11278	
5	413976	BE295452	Hs.75655	procollagen-profine, 2-oxoglutarate 4-di	2.5
)	445223	AW291553	Hs.254983	ESTs	2.5 2.5
	423926	X03833	Hs.1722	interleukin 1, alpha	25
	410165	BE560228	Hs.71869	apoptosis-associated speck-like protein	25
	406474	A145000144	Un 467076	FOT-	25
10	433908	AW298141	Hs.157975	ESTs	2.5
10	439755	AW748482	Hs.77873	87 homolog 3	2.5
	437528	N59645	Hs.169745	crumbs (Drosophila) homolog 1	2.5
	420734	AW972872	Hs.293736	gb:HSC13E071 normatized infant brain cDN	2.5
	415346	Z43108	Hs.209978		2.5
15	419337 444606	AW291112 R09478	Hs.18041	ESTs ESTs	25
13					2.5
	430061	AB037817	Hs.230188	KIAA1396 protein	2.5
	413407	AI356293 BE467339	Hs.75339 Hs.280115	inositol polyphosphate phosphatase-like	25
	411965 409278	AA346683	Hs.52763	ESTs anaphase-promoting complex subunit 7	25
20	403142	777340003	115.52105	mightigge-brothomis complex separation	2.5
20	401714				25
	425081	X74794	Hs.154443	minichromosome maintenance deficient (S.	2.5
	416505	H66470	Hs.16004	ESTs	2.5
	431518	AA743462	Hs.165337	EST8	2.5
25	448623	BE613468	Hs.107515	ESTs, Weakly similar to T00329 hypotheti	2.5
20	428301	AW628666	Hs.98440	ESTs, Weakly similar to 138022 hypotheti	2.5
	404366	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	10.50110	2010, 1120, 2112	2.5
	449733	R74546	Hs.29438	Homo sagiens cDNA FLJ12094 fis, clone HE	2.5
	459583	AI907673		gb:IL-BT152-080399-004 BT152 Homo sapien	2.5
30	402856	AW939659		gb:RC0-DT0076-110100-031-c09 DT0076 Homo	2.5
	420751	J03019	Hs.99913	adrenergic, beta-1-, receptor	24
	436805	AA731533	Hs.270751	ESTs	2.4
	420285	AA258124	Hs.293878	ESTs, Moderately similar to ZN91_HUMAN Z	2.4
	453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	2.4
35	453853	AL040600	Hs.188083	ESTs	2.4
-	407909	AW103986		qb:xd63e06.x1 NCI_CGAP_Ov23 Homo sapiens	2.4
	454630	BE142075		gb:CM3-HT0137-170999-012-f02 HT0137 Homo	2.4
	451026	AA013218	Hs.157492	cer-d4 (mouse) homolog	2.4
	420779	L12398	Hs.99922	doparnine receptor D4	2.4
40	438322	AA804170	Hs.221349	ESTs	2.4
	455908	BE156306		gb:QV0-HT0367-150200-114-h04 HT0367 Homo	2.4
	419625	U91616	Hs.91640	nuclear factor of kappa light polypeptid	2.4
	440773	AA352702	Hs.332541	Homo sapiens, Similar to RIKEN cDNA 2700	2.4
	450823	T81223	Hs.22011	complement-c1q tumor necrosis factor-ref	2.4
45	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	2.4
-	429109	AL008637	Hs.196352	neutrophil cytosolic factor 4 (40kD)	2.4
	451802	AI817711	Hs.209374	ESTs	24
	419417	R92491	Hs.39429	ESTs	2.4
	407094	AF000574	Hs.22405	leukocyte immunogłobulin-tike receptor,	2.4
50	423567	BE252949	Hs.69331	hypothetical protein FLJ13633	2.4
	427501	A1369280	Hs.131743	ESTs	2.4
	451773	Z42044	Hs.26996	KIAA1278 protein	2,4
	436845	AA732297	Hs.113928	ESTs	2.4
<i></i>	431584	AW296121	Hs.266263	Homo sapiens cDNA FLJ14115 fis, clone MA	2.4
55	440514	AA781530	Hs.127236	hypothetical protein FLJ12879	2.4
	423721	AF176911	Hs.132004	cardiotrophin-like cytokine; neurotrophi	2.4
	452125	BE312642	Hs.28077	GDP-mannose pyrophosphorylase 8	2.4
	419508	AW997938	Hs.90786	ATP-binding cassette, sub-family C (CFTR	2.4 · 2.4
60	453446	BE299996	14. 400007	gb:600944574F1 NIH_MGC_17 Homo sapiens c	2.4
JU	419792	AA250890	Hs.190037 Hs.106642	ESTs ESTs. Weakly similar to T09052 hypotheti	2.4
	452786	R61362	ns. 106642	gb:MR3-ST0220-290100-016-e04 ST0220 Homo	24
	410447	AW816134	He Cate		24
	438662	AA223599	Hs.6351	cleavage and polyadenylation specific fa	2.4
65	402408	MH 001105	He noon	epithefial membrane protein 3	2.4
05	443950 414625	NM_001425 AA335738		glutathione peroxidase 1	2.4
		AA333136	Hs.76686	Biographone beroxioese i	2.4
	403048	AA525454		gb:ni85c09.s1 NCI_CGAP_Pr20 Homo sapiens	2.4
	432088		Hs.267749		2.4
70	431692	AL021331 AW850907	rts.201143	gb:tL3-CT0220-310100-065-H11 CT0220 Homo	24
, 0	455023 426249	F05422	Hs. 168352		2.4
	446795	AI797713	Hs.156471	`	2.4
	414774	X02419	Hs.77274	plasminogen activator, urokinase	2.4
	414252	AA346483	Hs.126191		2.4
75	417918	AA209205	Hs.163754		24
	427550		Hs.179606		2.4
	404020	222 -2010			2.4
	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	2.4
	417222		Hs.42053	hypothetical protein MGC2383	2.4
80	443639		Hs.9661	proteasome (prosome, macropain) subunit,	2.4
	452706	AW449390	Hs.257150		2.4
	401676			·	2.4
	428882		Hs.131748	ESTs, Moderately similar to ALU7_HUMAN A	2.4

					2.4
	436277	R88520		ESTS	2.4
	426271	AF026547	Hs.169047	chondroitin sulfate proteoglycan 3 (neur	2.4
	405353 409193	AA131483		gb:zo08e05.r1 Stratagene neuroepithefium	2.4
5	431431	AL096711	Hs.252953	Human DNA sequence from clone RP3-403A15	2.4
,	407889	R34556	Hs.30800	ESTs, Weakly similar to S65657 alpha-1C-	2.4
	453335	AW857376	Hs.169238	fucosyltransferase 3 (galactoside 3(4)-L	2.4
	450621	AW297288	Hs.55918	hypothetical protein FLJ11354	24
	419652	AL157485	Hs.91973	hypothetical protein	2.4
10	421151	BE174431		ESTs	2.4
	437846	AA773866	Hs.244569	esophagus cancer-related gene-2	2.4 2.4
	420681	AA847602	Hs.106510	ESTs, Moderately similar to ALU2_HUMAN A	2.4
	405288				2.4
1.5	453527	R49570	Hs.180236	ESTS	2.4
15	429875	AI091815	U- 400754	gb:qa58b06.s1 Soares_NhHMPu_S1 Homo sapi	2.4
	436360	Al962796	Hs.136754 Hs.284153	ESTs Fanconi anemia, complementation group A	2.4
	418592	X99226 AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	2.4
	419991 449539	W80363	Hs.58446	ESTs	2.4
20	419870	AW403911	Hs.266175	phosphoprotein associated with GEMs	2.4
20	404584	717400511	1.0.200110		2.4
	454276	AW294996	Hs.255374	ESTs	2.4
	423746	AW361817	Hs.132370	NADPH oxidase 1	2.4
	415558	AA885143	Hs.125719	ESTs	2.4
25	428141	D50402	Hs.182611	solute carrier family 11 (proton-coupled	2.4
	406953	L36847		gb:Hurnan (clone p17/90) rearranged iduro	2.4 2.4
	444471	AB020684	Hs.11217	KIAA0877 protein	2.4 2.4
	451031	Al360187	Hs.4254	ESTs	2.4
	455302	AW997641		gb:RC6-BN0052-170200-011-D06 BN0052 Homo	2.4
30	449063	AI627352	Hs.236547	Homo sapiens, clone IMAGE:2905978, mRNA,	2.4
	401048		11- 40 4004	hypothetical protein FLJ22578	2.4
	434420	AA688278	Hs.194864		2.4
	425848	BE242709	Hs.159637 Hs.208037	valyt-tRNA synthetase 2 ESTs	2.4
35	449086	Al628357 R37780	Hs.200037 Hs.21422	ESTs	2.4
22	415238		Hs.3782	ESTs	2.4
	448337 416991	AW206453 N36389	Hs.141296	KIAA0226 gene product	2.3
	412600	L28824	Hs.74101	spleen lyrosine kinase	2.3
	418385	AW590613	Hs.301040	Homo sapiens, clone IMAGE:3357127, mRNA,	2.3
40	440769	BE561793	Hs.21446	KIAA1716 protein	2.3
40	450437	X13956	Hs.24998	hypothetical protein MGC10471	2.3
	412035	N78559	Hs.293629	hypothetical protein MGC3121	2.3
	406739	AI566709	Hs.182426	ribosomal protein S2	2.3
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	2.3
45	410286	AI739159	Hs.61898	DKFZP586N2124 protein	2.3
	443740	R56434	Hs.21062	ESTs	2.3
	405605				2.3 2.3
	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	2.3
50	426509	M31166	Hs.2050	pentaxin-related gene, rapidly induced b	2.3
50	445828	F05802	Hs.81907	ESTs	2.3
	457195	AB011099	Hs.196647	KIAA0527 protein Homo sapiens, clone IMAGE:3535476, mRNA,	2.3
	420372	AW960049	Hs.293660 Hs.1634	cell division cycle 25A	2.3
	423198	M81933 AW753613	HS. 1034	gb:RC1-CT0268-060100-013-e01 CT0268 Homo	2.3
55	457730 412014	A1620650	Hs.43761	ESTs, Weakly similar to A46010 X-linked	2.3
33	447131	NM_004585		retinoic acid receptor responder (tazaro	2.3
	446288	AW189209	Hs.149708		2.3
	436954	AA740151	Hs.130425	ESTs	2.3
	411658	AW855598		gb:CM1-CT0278-031199-032-e08 CT0278 Homo	2.3
60	404240				2.3
	456094	H95091		gb:yw57a09.r1 Soares_placenta_8to9weeks_	2.3
	416951	AA190926	Hs.190785	ESTs, Moderately similar to \$65657 alpha	2.3 2.3
	406737	AI356586		gb:qy15h09.x1 NCI_CGAP_Brn23 Homo sapien	2.3
	458453		Hs.135095		2.3
65	452330		Hs.191979		2.3
	408523			PESTs gb:PM0-MT0011-240300-001-c09 MT0011 Hama	2.3
	455470				2.3
	436323		Hs.140963		2.3
70	450000		Hs.10888 Hs.125790		2.3
70	416171		HS.123794 Hs.22177	· · · · · · · · · · · · · · · · · · ·	2.3
	419134 445933		Hs.29386		2.3
	422089		Hs.10313		2.3
	449911		Hs.12653		2.3
75	417079		Hs.81134		2.3
	411742				2.3
	43561		Hs.4975	potassium voltage-gated channel, KQT-lik	2.3
	42349		Hs.12967		2.3
~~	40718	2 AA312551	Hs.23015		23
80	41144				23
	43864		Hs.12903	7 ESTS	2.3 2.3
	43269		Hs.3080	mitogen-activated protein kinase 7	23 23
	45219	8 A1097560	Hs.61210	ESTs, Wealdy similar to I38022 hypotheti	دع

					• • •
	411125 404054	AA151647	Hs.68877	cytochrome b-245, alpha polypeptide	2.3 2.3
	430458	AA479300	Hs.225706	ESTs, Weakly similar to 138022 hypotheti	2.3
_	440210	AW674562	Hs.125296	ESTs	2.3
5	446727	AB011095	Hs. 16032	KIAA0523 protein	2.3
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	23
	438379	N23018	Hs.171391 Hs.200141	C-terminal binding protein 2 ESTs	2.3 2.3
	449919 415293	A1574685 R49462	Hs.106541	ESTs .	2.3
10	441126	NM_000429	Hs.323715	methionine adenosyltransferase I, alpha	2.3
	408203	AA053137	Hs.42390	nasopharyngeal carcinoma susceptibility	2.3
	434941	AW073202	Hs.334825	Homo sapiens cDNA FLJ14752 fis, clone NT	23
	450748	A1733093	Hs.130016	ESTs	2.3
15	404185	1170270	U- 04420	paired-like homeodomain transcription fa	23 23
13	418327 451370	U70370 AI791929	Hs.84136 Hs.300782	ESTs	23
	400034	74751323	15.300/02	2013	23
	407723	AW071161	Hs.252873	ESTs	2.3
~~	431320	AW969474	Hs.183070	ESTs	2.3
20	429271	AF039850	Hs.198515	dead ringer (Drosophila)-like 1	2.3
	453707	AW003879	Hs.126522	Homo sapiens, clone MGC:16722, mRNA, com	2.3 2.3
	419225 444656	U70073 AI277924	Hs.145199	gb:HSU70073 Human Homo saplens cDNA clon ESTs	23
	405741	PME11324	10.140.00		2.3
25	400917				2.3
	432567	AA736777	Hs.293770	ESTs	2.3
	437949	U78519	Hs.41654	ESTs, Wealdy similar to A45010 X-linked	2.3
	450514	AC005785	Hs.25059	A kinase (PRKA) anchor protein 8	2.3 2.3
30	418400 444019	BE243026 BE173977	Hs.301989 Hs.10098	KIAA0246 protein putative nucleolar RNA helicase	2.3 2.3
50	406326	DC113311	15.10030	potatre moccola reer nements	2.3
	412077	N51107	Hs.47199	ESTs, Wealthy Similar to FLJ00004 protein	2.3
	427647	W19744	Hs.180059	Homo sapiens cDNA FLJ20653 fis, clone KA	2.3
25	414528	AA148950	Hs.188836	ESTs	2.3
35	414854	BE546797	Hs.51483	ESTs, Weakly similar to hypothetical pro	2.3 2.3
	420352 439467	BE258835 AW292275	Hs.158365	gb:601117374F1 NIH_MGC_16 Homo sapiens c ESTs	2.3
	402627	MILESELIS	115, 150000	2013	23
	451711	AK000461	Hs.26890	cat eye syndrome chromosome region, cand	2.3
40	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	2.3
	423869	BE409301	Hs.134012	C1q-related factor	2.3
	405915			-1- #- 40	2.3
	431503	NM_012129	Hs.258576 Hs.108198	claudin 12 ESTs	2.3 2.3
45	423306 443232	W88562 AF161521	Hs.9081	phenylalanyl-IRNA synthetase beta-subuni	2.3
43	433064	D79991	Hs.30002	SH3-containing protein SH3GLB2; KIAA1848	2.3
	434437	Al912566	Hs.187813	ESTs	2.3
	436191	BE407866	Hs.170253	hypothetical protein FLJ23282	2.3
50	420006	H14429	Hs.94300	serologically defined colon cancer antig	23
50	447942	F12628	Hs.334786	hypothetical protein MGC16040	2.3 2.3
	403166 422119	AI277829	Hs.111862	KIAA0590 gene product	2.3
	403751	74211023	113.111002	Tara according to the procession	2.3
	426451	Al908165	Hs.169946	GATA-binding protein 3	2.3
55	427413	BE547647	Hs.177781	hypothetical protein MGC5618	2.3
	409091	AW970386	Hs.269423	ESTS	2.3
	440491 427722	R35252 AK000123	Hs.24944 Hs.180479	ESTs, Weakly similar to 2109260A B cell hypothetical protein FLJ20116	2.3 2.3
	405747	AN000123	115.100473	hypotheseas protestive area vio	2.3
60	438210	AA780519	Hs.311601	EST	2.3
	404652				2.3
	423524	AF055989	Hs.129738	potassium voltage-gated channel, Shaw-re	2.2
	426793	X89887	Hs.172350	HIR (histone cell cycle regulation defec	2.2
65	444424	A1654684	Hs.196377	ESTs pseudouridylate synthase 1	2.2 2.2
03	434031 427650	BE384165 AW501245	Hs.23723 Hs.252259	ribosomal protein S3	2.2
	435220	050030	Hs.104	HGF activator	2.2
	438279	AA805166	Hs.154762	HIV-1 rev binding protein 2	2.2
70	424668	D83702	Hs.151573	cryptochrome 1 (photolyase-like)	2.2
70	429961	BE246829	Hs.226770	DXF2P566C0424 protein	2.2
	442065	AJ831229 AW009480	Hs.128417	hypothetical protein FLJ14009 natural killer cell transcript 4	2.2 2.2
	415198 420536	AUU3460 AL117455	Hs.943 Hs.275438	histone deacetylase 7A	2.2
	411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-assoc	2.2
75	443753	AW367578	Hs.134749	ESTs .	2.2
	423243	AA351938	Hs.23964	sin3-essociated polypeptide, 18kD	2.2
	446572	AV659151	Hs.282961	ESTs	2.2
	412247	AF022375 AA715026	Hs.73793 Hs.135280	vascular endothelial growth factor ESTs	2.2 2.2
80	421040 426212	S71824	Hs.167988		2.2
-0	455584	BE007420	101 000	gb:PM3-BN0142-200300-001-c04 BN0142 Homo	2.2
	406851	AA609784	Hs. 180255	major histocompatibility complex, class	2.2
	444153	AK001610	Hs.10414	hypothetical protein FLJ 10748	2.2

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					2.2
				opoisomerase (DNA) III alpha	2.2 2.2
			Hs.159743 (Hs.104157 (ESTs ESTs, Weakly similar to KIAA0694 protein	2.2
	456261 415737		Hs.118743	ESTs	2.2
5	447554		Hs.36119	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.2 2.2
	405159		044443	F0T-	2.2
	442177			ESTs ESTs	2.2
	446139 458339	H77395 AW976853		ESTs	2.2
10	401876	711131 0000		•	2.2 2.2
	439566	AF086387		gb:Homo sapiens full length insert cDNA	2.2
	425079	H09963		vitronectin (serum spreading factor, som core-binding factor, beta subunit	2.2
	441837	AA361743 AB015419	Hs.179881 Hs.247710	preproprolactin-releasing peptide	2.2
15	430644 431474	AL133990	Hs.190642	ESTs	2.2
13	407739	NM_002285	Hs.38070	lymphoid nuclear protein related to AF4	2.2 2.2
	424244	AV647184	Hs.143601	hypothetical protein hCLA-iso	2.2
	438057	AW294544	Hs.125785	ESTs, Wealdy similar to CORB MOUSE CORNI primase, polypeptide 2A (58kD)	2.2
20	412715	NM_000947	Hs.74519 Hs.115521	REV3 (yeast homolog)-like, catalytic sub	2.2
20	422365 404170	AF035537	10.110021		2.2
	406902	M32074		gb:Hurnan retinoic acid receptor gamma 2	2.2 2.2
	437902	AA770599	Hs.144055	ESTs	2.2
25	401012		11- 200024	ESTs	2.2
25	446502	A1302654 AW467376	Hs.208024 Hs.129640	ESTS	2.2
	442554 443021	AA368546	Hs.8904	lg superfamily protein	2.2
	421141	AW117261	Hs.125914	FSTs	2.2 2.2
	443070	BE388662	Hs.8984	Homo sapiens chromosome 14 BAC 98L12	2.2
30	446566	H95741	Hs.17914	membrane-spanning 4-domains, subfamily A	2.2
	427695	R88483	Hs.172862	ESTs gb:EST93093 Skin tumor I Homo sapiens cD	2.2
	426503 431468	AA380153 AW248431	Hs.256526	nuclear prelamin A recognition factor	2.2
	416185	AW975861	Hs.47367	KIAA 1785 protein	2.2 2.2
35	437319	BE410958	Hs.56406	Homo sapiens cDNA FLJ13549 fis, clone PL	2.2
	402064			ret-	2.2
	413335	AI613318 AA297567	Hs.48442 Hs.43728	ESTs hypothetical protein	2.2
	408212 406169	PAZ31301	16,45720	ii)pooloonii pioniii	2.2
40	451099	R52795	Hs.25954	interteukin 13 receptor, alpha 2	2.2 2.2
	407335	AA631047	Hs.158761	Homo sapiens cDNA FLJ13054 fis, clone NT	2.2
	409715	W42591	Hs.23892	ESTs	2.2
	431921	N46466	Hs.58879 Hs.9877	ESTs hypothetical protein	2.2
45	443823 432458	BE089782 AI968598	Hs.78768	malignant cell expression-enhanced gene/	2.2
73	419726	U50330	Hs.1274	hone morphogenetic protein 1	2.2 2.2
	423178	Al033140	Hs.124983	Homo sapiens mRNA; cDNA DKFZp564C142 (fr	2.2
	451089	AA903705	Hs.4190	Homo sapiens cDNA: FLJ23269 fis, clone C Homo sapiens cDNA FLJ11421 fis, clone HE	2.2
50	415216	AI825905 AV647908	Hs.193211 Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	2.2
50	442242 441830	AA383104	Hs.42954	hypothetical protein DKFZp564D0372	2.2
	406660	X65371	Hs.172550	polypyrimidine tract binding protein (he	2.2 2.2
	443378	AW392550	Hs.9280	proteasome (prosome, macropain) subunit,	2.2
55	432558	R97268	Hs.177269 Hs.81057	hypothetical protein MGC2718	2.2
22	408146 419865			U1-snRNP binding protein homolog (70kD)	2.2
	439444		Hs.54578	ESTs, Wealdy similar to 138022 hypotheti	2.2 2.2
	438407		Hs.12967.		2.2
۲0	450184		Hs.237617		2.2
60	409130	*********	Hs.75658 Hs.30190		2.2
	428844 429489		Hs.20403	o aristalessilike homeobox 3	2.2
	433042			5 Homo sapiens cDNA FLJ11660 fis, clone HE	2.2 2.2
	440658		Hs.14303		2.2
65	408204		Hs.43666		2.2
	427491 408001		6 Hs.17872 Hs.30334		2.2
	44570			olycine dehydrogenase (decarboxylating;	2.2
	43144		Hs.25536		2.2 2.2
70	45666			solute carrier family 30 (zinc transport nuclear transcription factor, X-box bind	2.2
	43309				2.2
	41585 41524		Hs.12779 Hs.27252		2.2
	44365			gb:yf42f10.s1 Soares fetal fiver spleen	2.2
75	40252				2.2 2.2
	41481	9 BE177320			22
	44653				2.2
	41579 41481		Hs.7736		2.2
80	45302		2 Hs.3144	2 RecQ protein-fike 4	2.2
	41213	3 U83460	Hs.7361		2.2 2.2
	40788				2.2
	4370	33 AW24836	34 Hs.5409	Little Politica con a paparati	

	400722	A A E77 A E E	Hs.24937	transformer 2 eleba (htm. 2 alaha)	2.2
	422732 416388	AA577455 AI417358	Hs.73677	transformer-2 alpha (htra-2 alpha) ESTs	2.2
	452849	AF044924	Hs.30792	hook2 protein	2.2
	446615	BE513202	Hs.15589	PPAR binding protein	2.2
5	428361	NM_015905	Hs.183858	transcriptional intermediary factor 1	2.2
	446279	AA490770	Hs.182382	ESTs .	2.2
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	2.2 2.2
	403969	418//02/22	U- 63490	mentals have in a shorthestorn one monet	2.2
10	410423	AW402432 AF125304	Hs.63489 Hs.212680	protein tyrosine phosphatase, non-recept tumor necrosis factor receptor superfami	2.2
10	429736 447091	AW089648	Hs.157779	ESTs, Wealthy similar to CA17_HUMAN COLLA	2.2
	422017	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	2.2
	426728	NM_007118	Hs.171957	triple functional domain (PTPRF interact	2.2
	438726	AB033103	Hs.6385	KIAA1277 protein	2.2
15	453315	BE544203	Hs.24831	ESTs	2.2
	423244	AL039379	Hs.209602	ESTs, Wealthy similar to ubiquitous TPR m	2.2
	433610	AA806822	Hs.112547	ESTs	2.2
	429451	BE409861	Hs.202833	herne oxygenase (decycling) 1	2.2 2.2
20	417980	R32235		gb:yh67f08.r1 Soares placenta Nb2HP Homo	2.2
20	406347	DC202004		gb:601177814F1 NIH_MGC_17 Homo sapiens c	22
	414406 401827	BE297904		(D.001117014F11011_mOC_11110110 adjusted to	2.2
	446913	AA430650	Hs.16529	transmembrane 4 superfamily member (tetr	2.2
	452294	AI871925	Hs.117895	ESTs, Moderately similar to A47582 B-cel	2.2
25	404084			•	2.2
-	456786	AK002084	Hs.132851	hypothetical protein FLJ11222	2.2
	435031	AI632091	Hs.116877	ESTs	2.2
	442609	AL020996	Hs.8518	selenoprotein N	2.1
20	439732	AW529604	Hs.167641	hypothetical protein from EUROIMAGE 1703	2.1 2.1
30	421506	BE302796	Hs. 105097	thymidine kinase 1, soluble	21
	439253	AF086064 AW177551	Hs.332252 Hs.220255	ESTs hypothetical protein MGC13098	2.1
	409669 429574	BE268321	Hs.208912	hypothetical protein MGC861	2.1
	437470	AL390147	Hs.134742	hypothetical protein DKFZp547D065	2.1
35	408945	AW015089	Hs.4964	DKFZP586J1624 protein	2.1
<i></i>	447687	AI627947	Hs.150186	hypothetical protein DKFZp566K1946	2.1
	459584	Al910884	Hs.207898	ESTs	21
	439130	AA306090	Hs.124707	ESTs	2.1
40	428180	AI129767	Hs.182874	guanine nucleotide binding protein (G pr	2.1
40	442028	AJ239437	Hs.48945	ESTS	2.1 2.1
	430968	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	21
	443609	AV650231	Hs.282941	ESTs, Highly similar to A Chain A, Human heterogeneous nuclear ribonucleoprotein	21
	417164 444534	AA338283 AW271626	Hs.81361 Hs.42294	ESTs	2.1
45	438391	AI262248	Hs.25027	ESTs	21
43	442003	AW297497	Hs.201891	ESTs	2.1
	456278	BE300369	Hs.289038	hypothetical protein MGC4126	2.1
	416976	BE243985	Hs.80680	major vault protein	2.1
	417810	D28419	Hs.82609	hydroxymethylbilane synthase	2.1
50	445242	BE156478	Hs.21108	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.1 2.1
	452712	AW838616		gb:RC5-LT0054-140200-013-001 LT0054 Homo mitochondrial ribosomal protein L32	21
	434926	BE543269 AB007854	Hs.50252 Hs.105850	KIAA0404 protein	2.1
	421564 424927	AW973666	Hs.153850	hypothetical protein C321D2.4	2.1
55	432742	AA564453	Hs.162339	ESTs	2.1
	435958	H98180	Hs.117975	ESTs	2.1
	421531	AA713505	Hs.291769	ESTs	21
	410431	BE261320	Hs.158196	transcriptional adaptor 3 (ADA3, yeast h	2.1
60	420503	AI570943	Hs.337546	ESTS	2.1 2.1
60	448127	AI478416	Hs.282883	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.1
	452897	BE066058	Hs.269233 Hs.7154	ESTs, Moderately similar to 178885 serin ESTs	2.1
	447112 406577	H17800	ns./ 139	LUIS	2.1
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	21
65	451460	AI797550	Hs.209652		2.1
• • •	447402	H54520	Hs.18490	hypothetical protein FLJ20452	2.1
	435828	AA700705	Hs.13852	ESTs	2.1
	436396	AI683487	Hs.152213		2.1
70	420582		Hs.99093	Homo sepiens chromosome 19, cosmid R2837	2.1
70	452020		Hs.255757		2.1 2.1
	415586		He 410300	gb:HSC2QE041 normalized infant brain cDN ESTs	2.1
	452620 457066		Hs.119286 Hs.158272		2.1
	435472		Hs.283022		2.1
75	431741		Hs.191701		2.1
	446840		Hs.209203		2.1
	440818		Hs.146726		2.1
	410174	AA306007	Hs.59461	DKFZP434C245 protein	2.1
00	400822			507-	21
80	412760		Hs.41324	ESTs 95 kDa retinoblastoma protein binding pr	2.1 2.1
	410653		Hs.65238 Hs.315689		21
	426925 424242		Hs.293984		2.1
	7E7E76				

					2.1
	452560			ESTs ESTs - No decately similar to PC4259 forti	2.1
	456437	AI924228 BE501831		ESTs, Moderately simitar to PC4259 ferri ESTs	2.1
	458922 439231	AW581935	Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	2.1
5	419488	AA316241	Hs.90691	nucleophosmin/nucleoplasmin 3	2.1
_	411829	AW865749		gb:QV3-SN0021-100500-185-c03 SN0021 Homo	2.1
	457192	AL135682	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	2.1 2.1
	422128	AW881145		gb:QV0-ÖT0033-010400-182-a07 OT0033 Homo	2.1
10	452571	W31518		ESTs PCAF associated factor 65 alpha	2,1
10	423699 406610	H41850	NS.131040	CAL SOCIETY INCOME OF SPIN	2.1
	453638	AW814996		gb:MR1-ST0206-170400-024-h09 ST0206 Homo	2.1
	418856	AA362858		gb:EST72900 Ovary II Homo sapiens cDNA 5	2.1
	437623	D63880	Hs.5719	chromosome condensation-related SMC-asso	2.1 2.1
15	410908	AA121686	Hs.10592	ESTs	21
	420221	N25991	Hs.43725 Hs.221610	ESTs ESTs	21
	424739	AA346108 AL049689	Hs.156369	hypothetical protein similar to tenascin	- 21
	425398 424901	Z11933	Hs.182505	POU domain, class 3, transcription facto	2.1
20	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	2.1
	415635	F13168		gb:HSC3JF101 normalized infant brain cDN	2.1 2.1
	418181	U37012	Hs.83727	cleavage and polyadenylation specific fa	2.1
	407103	AA424881	Hs.256301	hypothetical protein MGC13170 gb:lL3-CT0213-170100-055-F02 CT0213 Homo	2.1
25	454389	AW752571		80:112-010212-110100-000-02-0102-01-01-01	21
25	400021 439228	N51700		gb:yy72d01.s1 Soares_multiple_sclerosis_	2.1
	456505	AA504595	Hs.111418	ESTs .	2.1
	405258				2.1
	444645	A1184564	Hs.101654	ESTs	2.1 2.1
30	430246	AI269069	Hs.109268	hypothetical protein FLJ12552 GLUT4 enhancer factor	2.1
	458687	AW024815	Hs.170088	GLU14 ennancer factor	2.1
	403857 400258				2.1
	422221	AA306649	Hs.169370	FYN oncogene related to SRC, FGR, YES	2.1
35	441054	AA913591	Hs.126480	ESTs	2.1
	452700	Al859390	Hs.288940	five-span transmembrane protein M83	2.1 2.1
	454606	AW809752		gb:MR4-ST0124-181299-020-b06 ST0124 Homo	2.1
	448954	AB014564	Hs.22616	KIAA0664 protein ESTs, Wealdy similar to ALU8_HUMAN ALU S	21
40	443148	A1034357 AL039201	Hs.211194 Hs.173554	ubiquinol-cytochrome c reductase core pr	2.1
40	453486 437695	AA769202	Hs.192142	ESTs	21
	425449	X52056	Hs.157441	spleen focus forming virus (SFFV) provir	2.1
	447270	AC002551	Hs.331	general transcription factor IIIC, polyp	2.1
4.5	435677	AA594142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	2.1 2.1
45	436382	AW977063	Hs.250181	ESTs Homo sapiens cDNA FLJ11431 fis, clone HE	2.1
	435837	AI689210	Hs.187276 Hs.12867	ESTs	2.1
	458287 423794	AA987556 BE551781	Hs.231895	ESTs	2.1
	408049	AW076098	Hs.74316	desmoplakin (DPI, DPII)	2.1
50	402721				2.1
	451999	AW176401	Hs.27424	DEAD/H (Asp-Gtu-Ala-Asp/His) box polypep	2.1 2.1
	417541	AI992191	Hs.180040	hypothetical protein FLJ22439 modulator recognition factor !	2.1
	414857 435760	AW402389 AF231922	Hs.920 Hs.213004		2.1
55	428086	AL110193	Hs.224137	hypothetical protein	2.1
"	447853		Hs.164285	THE THE PERSON NEARLY AFRA	21
	419034			hemopoietic cell kinase	21 21
	431019			forkhead box G1B	21
60	421064		Hs.101382 Hs.179703		21
UU	416435 437014		Hs.222531	and the same of th	2.1
	459369	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	I D. LELOO	gb:yd40e03.r1 Soares fetal liver spleen	2.1
	402239			• .	21
	412280	AW205116			2.1 2.1
65	426012		Hs.75874		2.1
	438885		Hs.18498	7 ESTs gb:EST374787 MAGE resequences, MAGG Horno	2.1
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	442932		Hs.8858	bromodomain adjacent to zinc finger doma	2.1
70	408175		Hs.19066	hypothetical protein DKFZp667O2416	2.1
• -	423867			gb:EST35757 Embryo, 8 week I Homo sapien	2.1
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13	433679 45674		Hs.75518 Hs.18449		21
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00	43926	2 AA832333	Hs.33304	5 ESTs	21 21
80	40310		7 11 0000	53 hypothetical protein FLJ14733	21 21
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	424441 422726	X14850 U11690	Hs.147097 Hs.1572	H2A histone family, member X faciogenital dysplasia (Aarskog-Scott sy	2.1 2.1
	424576	BE154142	Hs.96833	ESTs	2.1
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	441940 439190	AW298115 AW978693	Hs.128152 Hs.293811	ESTS ESTS	21
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	459642 450385	AI631024	Hs.24948	synuclain, alpha interacting protein (sy	21
	425159	NM_004341	Hs.154868	carbamoyl-phosphate synthetase 2, aspart	21
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20	445101 412811	T75202 H06382	Hs.12314 Hs.21400	Homo sapiens mRNA; cDNA DKFZp586C1019 (f ESTs	21 21
	426369	AF134157	Hs.169487	Kreisler (mouse) maf-related leucine zip	21
	435924	AW029203	Hs.191952	ESTs	2.1
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	427539	AA405205	Hs.97960	ESTs, Wealty similar to T51146 ring-box	2.1
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	436588	AA759233	Hs.126506	ESTs	2.0
	452487	AW207659	Hs.6630	Homo sapiens cDNA FLJ13329 fis, clone OV	2.0
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                                sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
                                Indicates DNA strand from which exons were predicted. Indicates nucleotide positions of predicted exons.
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PCT/US02/29560 WO 03/025138

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              406610
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TABLE 26A: ABOUT 582 GENES SIGNIFICANTLY DOWN-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT CNS TISSUES
Table 26A lists about 582 genes significantly down-regulated in glioblastoma compared to normal adult CNS tissues. These were selected from 59680 probesets on the
Alfymetrix/Eos Huú3 GeneChip array such that the ratio of "average" normal CNS to "average" glioblastoma was greater than or equal to 3. The "average" normal CNS level was set
to the 75" percentile amongst various normal CNS tissues. The "average" glioblastoma level was set to the 85° percentile amongst various tumor samples. In order to remove genespecific background levels of non-specific hybridization, the 10° percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator
before the ratio was evaluated. 70

Unique Eos probeset identifier number Pkey:

Exemplar Accession number, Genbank accession number ExAcon: 75 Unigene number

UnigenelD: Unigene Titla:

Ratio of 75th percentile normal central nervous system (issue to 85th percentile tumor

Pkey 453655 417275 430829	ExAccn AW960427 X63578 AW451999	Hs.295449 Hs.194024	parvalbumin ESTs	136.7 29.0 25.7 22.6
	453655 417275	453655 AW960427 417275 X63578 430829 AW451999	453655 AW960427 Hs.79059 417275 X63578 Hs.295449 430829 AW451999 Hs.194024	453655 AW960427 Hs. 79659 transforming growth factor, beta recepto 417275 X63578 Hs. 295449 parvalbumin 430829 AW451999 Hs. 194024 ESTs

	410054	D14720	U- 02002	music making and 10h and 1 hade Tooth	21.2
	419954 459247	D14720 N46243	Hs.93883 Hs.110373	myelin protein zero (Charcot-Marie-Tooth ESTs, Highly similar to Y42626 secreted	18.5
	416133	NM_001683	Hs.89512	ATPase, Ca→ transporting, plasma membra	15.5
	416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin t	15.2
5	417167	AW206437	Hs.4290	ESTs	14.8
	433940	H05129	Hs.7459	cyclic AMP-regulated phosphoprotein, 21	13.4
	413324	V00571	Hs.75294	conticutropin releasing hormone	13.1
	439830	AA846666	Hs.151489	ESTs, Wealthy similar to XE7_HUMAN PROTEI	12.6
10	408068	AW148652	Hs.167398	ESTs	12.6 12.5
IU	412636 429096	NM_004415 AB011106	Hs.74316 Hs.196012	desmoplakin (DPI, DPII) KIAA0534 protein	12.2
	412638	AA910199	Hs.203838	ESTs	12.2
	423690	AA329648	Hs.23804	ESTs, Wealdy similar to PN0099 son3 prot	12.1
	456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosphatida	11.9
15	418318	U47732	Hs.84072	transmembrane 4 superfamily member 3	10.9
	442593	R39804	Hs.31961	ESTs	10.8
	446353	Al290919	Hs. 153661	ESTs	10.4
	420290	AW977318	Hs.194480	ESTs	10.3
20	414220	BE298094	Un 71701	gb:601118231F1 NIH_MGC_17 Homo sapiens c	10.3 10.2
20	414290 426365	AI568801 AA376667	Hs.71721 Hs.10283	ESTs RNA binding motif protein 8B	10.0
	414937	R38698	Hs.12382	ESTs	10.0
	419643	F06066	Hs.91791	chromosome 11 open reading frame 25	9.5
	407173	T64349		gb:yc10d08.s1 Stratagene lung (937210) H	9.5
25	412454	R55745	Hs.167330	ESTs	9.5
	439366	AF100143	Hs.6540	fibroblast growth factor 13	9.4
	415315	F12240	Hs.250655	prothymosin, atpha (gene sequence 28)	9.3
	441790	AW294909	Hs.132208	ESTs	9.2 9.1
30	448117 400661	H49129	Hs.172982	ESTs	9.0
50	433558	AA833757	Hs.201769	ESTs, Weakly similar to T24435 hypotheti	9.0
	412453	R20205	Hs.167330	ESTs	9.0
	408920	AL120071	Hs.48998	fibronectin leucine rich transmembrane p	8.9
	409031	AA376836	Hs.76728	ESTs	8.7
35	428106	BE620016	Hs. 182470	PTD010 protein	8.3
	446544	AI631932	Hs.7047	ESTs, Weakly similar to Unknown (H.sapie	8.2
	423479	NM_014326	Hs.129208	death-associated protein kinase 2	8.2 8.2
	439480	AL038511 Z37976	Hs.125316 Hs.83337	ESTs, Wealdy similar to S33990 finger pr latent transforming growth factor beta b	8.0
40	418036 456490	U83171	Hs.97203	small inducible cytokine subfamily A (Cy	8.0
40	410200	AA082557	Hs.101915	Stargardt disease 3 (autosomal dominant)	8.0
	414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	8.0
	408428	NM_014787	Hs.44896	DnaJ (Hsp40) homolog, subfamily B, membe	7.9
	437073	AI885608	Hs.94122	ESTs	7.9
45	408434	AW195317	Hs.107716	hypothetical protein FLJ22344	7.9
	438150	AA037534	Hs.79059	transforming growth factor, beta recepto	7.9
	440209	H05049	Hs.22269	neurexin 3	7.8 7.8
	408119 417421	W26213 AL138201	Hs.101672 Hs.82120	ESTs, Weakly similar to T00331 hypotheti nuclear receptor subfamily 4, group A, m	7.8 7.8
50	410587	AA370706	Hs.86412	chromosome 9 open reading frame 5	7.8
-	429611	AI889077	Hs.211388	Homo sapiens BAC clone CTB-60N22 from 7q	7.7
	405800		*	,	7.7
	421750	AK000768	Hs.107872	hypothetical protein FLJ20761	7.7
66	426356	BE536836	Hs.98682	hypothetical protein FKSG32	7.7
55	423440	R25234	Hs.143434	contactin 1	7.7
	445148	AI214510	Hs.146304	ESTs	7.6 7.6
	416294 424087	D86980 N69333	Hs.79170 Hs.143434	KIAA0227 protein contactin 1	7.6
	437479	R61866	Hs.101277	ESTs	7.5
60	405071				7.5
	421224	AW402154	Hs.125812	== :	7.4
	442025	AW887434	Hs.11810	CDA11 protein	7.4
	459476	BE185844		gb:IL5-HT0731-110500-087-c08 HT0731 Homo	7.2 7.1
65	430573	AA744550	Hs.136345	ESTs	7.1
U.J	401836 448958	AB020651	Hs.22653	KIAA0844 protein	7.1
	430152	AB001325	Hs.234642	aguaporin 3	7.1
	419474	AW968619	Hs.155849	ESTs	7.1
	401780	-		-	7.1
70	446052	AA358760		gb:EST67699 Fetal tung II Homo sapiens c	7.0
	423605	AF047826	Hs.129887	cadherin 19, type 2	7.0
	433098	AW190593	Hs.151143		7.0 6.9
	449511	AI436187 AW137912	Hs.296261 Hs.227583		6.9 6.8
75	451285 428414	AL049980	Hs.184216		6.8
, 5	419273	BE271180	Hs.293490		6.8
	443155	R54485	Hs.23772	ESTs	6.8
	450561	R49674	Hs.25909	ESTs	6.8
00	433058	NM_006456			6.8
80	440729	AA904739	Hs.128204		6.8 6.7
	448426 423589	BE018315 AA328082	Hs.280776 Hs.209569		6.6
	423569 415681	AJ379882	Hs.72630	ESTs	6.5
	710001	5002		 -	5.0

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	413510	F13044		gb:HSC3HH101 normalized infant brain cDN	6.4
	427992	Y15014	Hs.181353	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	6.4
	453344	BE349075	Hs.44571	ESTs	6.4
_	450642	R39773		copine IV	6.4
5	432251	AW972983	Hs.232165	polycythemia rubra vera 1; cell surface	6.4
	429322	D86984	Hs.199243	KIAA0231 protein	6.4 6.4
	444927	AW016637	Hs.199425	ESTs	6.4
	447482	AB033059	Hs.18705	KIAA1233 protein FLT4	6.3
10	400332	S66407	Hs.248032 Hs.7378	Homo sapiens mRNA; cDNA DKFZp434G227 (fr	6.3
10	440703 446129	AL137663 AW244073	Hs.145946	ESTs	6.3
	454076	AW204712	Hs.61957	ESTs	6.3
	425526	AA359933	110.01301	gb:EST69040 Fetal lung II Homo sapiens c	6.3
	421913	A1934365	Hs.109439	osteoglycin (osteoinductive factor, mime	6.3
15	434273	AA913143	Hs.26303	ESTs	6.2
	408480	AJ350337	Hs.164568	fibroblast growth factor 7 (keratinocyte	6.2
	451301	Al769514	Hs.209890	EST	6.2
	430754	AW862610	Hs.157068	ESTs	6.2
	438356	AA805530	Hs.48527	ESTs	6.2
20	422743	BE304678	Hs.119598	ribosomal protein L3	6.2
	453355	AW295374	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	6.2
	426388	AW081394	Hs.97103	ESTs	6.2
	452502	Al904296		gb:PM-BT046-220199-286_1 BT046 Homo sapi	6.1
	402546				6.1
25	457534	AI761307	Hs.232226	ESTs	6.1
	408165	AL137573	Hs.43143	Homo sapiens mRNA; cDNA DKFZp564A2463 (f	6.1
	404958				6.1
	432501	BE546532	Hs.25682	Homo sapiens mRNA for KIAA1863 protein,	6.1
20	442979	AW440782	Hs.174743	ESTs	6.1 6.0
30	422262	AL022315	Hs.113987	lectin, galactoside-binding, soluble, 2	6.0
	408713	NM_001248	Hs.47042	ectonucleoside triphosphate diphosphohyd	6.0
	454065	BE394588		gb:601311808F1 NIH_MGC_44 Homo sapiens c	5.9
	430004	U27768	Hs.227571	regutator of G-protein signalling 4	5.9
25	401521	000404	U- 4000E0	ECT.	5.9
35	425087	R62424	Hs.126059	ESTs	5.9
	446298	AF187813	Hs.14637	kidney- and liver-specific gene ESTs	5.9
	417761	R13727	Hs.21435 Hs.105689	MSTP031 protein	5.9
	424806	AA382523	Hs. 183745	hypothetical protein FLJ13456	5.9
40	441695	T12411	Hs.272558	endomucin-1	5.9
40	457483 417175	AB034694 R44558	Hs.94002	ESTs	5.8
	437483	AL390174	15.54002	gb:Homo sapiens mRNA; cDNA DKFZp547J184	5.8
	436427	Al344378	Hs.143399	ESTs	5.8
	411939	Al365585	Hs.146246	ESTs	5.8
45	459053	AI807052	Hs.210361	ESTs	5.7
13	411052	AW814950	15.210501	gb:MR1-ST0206-130400-023-d06 ST0206 Homo	5.7
	431063	Z98949	Hs.326843		5.7
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	5.7
	408478	NM_000806		gamma-aminobutyric acid (GABA) A recepto	5.7
50	442676	A1733585	Hs.130897	ESTs	5.7
	446443	AV659082	Hs.134228	ESTs	5.7
	400865				5.7
	459080	AW192083	Hs.290855		5.6
	407952	Al215902	Hs.88845	ESTs, Highly similar to T50835 hypotheti	5.6
55	431984	AL080239	Hs.272284		5.6
	425705	AF007833	Hs.159265		5.6
	442238	AW135374	Hs.270949		5.6 5.6
	422994	AW891802	Hs.296276		5.6
60	457148	AF091035	Hs.184627		5.6
UU	428356	AL046991	Hs.10338	ESTs	5.5
	415927 402092	AL120168	Hs.78919	Kell blood group precursor (McLeod pheno	5.5
		A1027242	Hs.211471	ESTs	5.5
	440526 444409	AI832243 AI792140	Hs.49265	ESTs	5.5
65	417877	AI025829	Hs.86320	ESTs	5.4
05	458238	AW071521	Hs.333541		5.4
	430702	U56979	Hs.250651		5.4
	456189	H91010	Hs.44940	ESTs	5.4
	427424	AA402453	Hs.113011		5.4
70	437354	AA749215	Hs.291886	5 ESTs	5.4
	455617	BE078070		gb:CM1-BT0614-160300-149-f02 BT0614 Homo	5.4
	429290	AF203032	Hs.198760		5.3
	427861	AA813185	Hs.98183	ESTs	5.3
	408556	U49516	Hs.46362		5.3
75	444209	A1753134	Hs.14649	4 ESTs	5.3
	422831	R02504	Hs.33294	3 ESTs	5.3
	403180				5.3
	418026		Hs.83213		5.3
0.0	430339		Hs.23962		5.2
80	431596		Hs.27292		5.2
	431930		Hs.27221		5.2 5.2
	437403		Hs.12119		5.2 5.2
	438285	AA782845	Hs.22790	ESTs	3.2

	420004	M7209E	No 124160	COT.	5.2
	439901	N73885 AA809052	Hs.124169 Hs.211275	ESTs ESTs	5.2
	438507 449222	AW293984	Hs.197621	ESTs ESTS	5.2
	402834	AK001507	Hs.306084	Homo sapiens clone FLB6914 PRO1821 mRNA,	5.2
5	419042	T81429	Hs.221065	ESTs	5.2
-	436777	AA731199	Hs.293130	ESTs	5.2
	445071	AI280246	Hs.149504	ESTs	5.1
	408016	AW136827	Hs.256096	ESTs	5.1
	412047	AA934589	Hs.49696	ESTs	5.1
10	436953	AW959074	Hs.23648	Homo sapiens cDNA FLJ13097 fis, clone NT	5.1
	436773	AW078629	Hs.82110	PC4 and SFRS1 interacting protein 1	5.1
	409263	AA069573	Hs.50319	ESTs	5.1
	453830	AA534296	Hs.20953	ESTs	5.1
15	459580	AA022888	Hs.176065	ESTs	5.1
15	417616	R07728	Hs.268668	ESTs	5.1 5.1
	423457 441535	F08208	Hs.283844 Hs.7885	similar to rat tricarboxylate carrier-li phosphatidylinositol binding clathrin as	5.0
	416490	AL135735 AF090116	Hs.79348	regulator of G-protein signalling 7	5.0
	417284	N62889	Hs.107242	Homo sapiens cDNA FLJ12965 fis, clone NT	5.0
20	447135	T58148	113.107272	gb:yb98g06.s1 Stratagene lung (937210) H	5.0
	448605	AL109678	Hs.21597	Homo sapiens mRNA full length insert cDN	5.0
	442240	AJ791883	Hs.292719	ESTs	4.9
	459399	BE407712	Hs.153998	creatine kinase, mitochondrial 1 (ubiqui	4.9
~ -	427972	AA864870	Hs.181304	putative gene product	4.9
25	432944	AA570687	Hs.38512	ESTs	4.9
	440198	BE560093		gb:601345159F1 NIH_MGC_8 Homo sapiens cD	4.9
	444047	AI097452	Hs.135095	ESTs	4.9
	416040	AW819158	Hs.289044	Homo sapiens cDNA FLJ12048 fis, clone HE	4.9
20	444922	AJ921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	4.8
30	436670	AI690021	Hs.201536	ESTs .	4.8 4.8
	448072	AI459306	Hs.24908 Hs.293549	ESTs ESTs	4.8
	408936 412622	AL138043 AW664708	Hs.171959	ESTs	4.8
	414943	D80647	Hs.124193	ESTs	4.8
35	429254	H10133	Hs.91846	hypothetical protein DKFZp761C121	4.8
-	453567	AI742835	Hs.33368	hypothetical protein FLJ11175	4.8
	407906	AA369665	Hs.41185	Homo sapiens mRNA; cDNA DKFZp564O1262 (f	4.8
	441028	AI333660	Hs.17558	Homo sapiens cDNA FLJ14446 fis, clone HE	4.7
40	405130				4.7
40	455225	AW996689		gb:QV3-BN0046-150400-151-g09 BN0046 Homo	4.7
	446218	AV657159		gb:AV657159 GLC Homo sapiens cDNA clone	4,7
	443347	A1052543	Hs.133244	metanoma-derived teucine zipper, extra-n	4.7
	402176				4.7
45	416577	BE063207	Hs.79381	grancalcin	4.7
43	436221	AK001781	Hs.296543	Homo sapiens cDNA FLJ10919 fis, clone OV	4.7 4.7
	420480	AL137361	Hs.98173 Hs.46925	hypothetical protein eyes absent (Drosophila) homotog 3	4.6
	400800	Y10262 AF124150	Hs.272091	ESTs	4.6
	435161 404793	AF 124130	115.272031	LOIS	4.6
50	430895	U66581	Hs.248121	G protein-coupled receptor 22	4.6
-	438571	AW020775	Hs.56022	ESTs	4.6
	445924	AI264671	Hs.164166	ESTs	4.6
	444585	AW170015	Hs.6594	ESTs	· 4.6
	421044	AF061871	Hs.311736	Human DNA sequence from clone RP1-238D15	4.6
55	418274	AI458587	Hs.128677	Human DNA sequence from clone RP1-50O24	4.6
	425475	W56339	Hs.107057	ESTs	4.6
	434311	BE543469	Hs.266263	Homo sapiens cDNA FLJ14115 fis, clone MA	4.5
	414272	AI651603	Hs.46988	ESTS	4.5 4.5
60	445235	AI564022	Hs.138207	ESTs Missish similar in 124435 humathadi	4.5 4.5
00	414327 414630	BE408145 BE410857	Hs.185254	ESTs, Wealdy similar to T24435 hypotheti gb:601301177F1 NIH_MGC_21 Horno sapiens c	4.5
	414456	H74314		gb:yu56e10.r1 Soares fetal liver spleen	4.5
	401024	114514		go.youde rour r doares retained speech	4.5
	414699	AIB15523	Hs.76930	synuclein, alpha (non A4 component of am	4.5
65	423449	AJ497900	Hs.33067	ESTs	4.5
	405138				4.5
	413544	BE147225		gb:PM2-HT0225-031299-003-f11 HT0225 Homo	4.5
	453880	AI803166	Hs.28462	ESTs, Weakly similar to 138022 hypotheti	4.5
	433521	T66087	Hs.112482	Homo sapiens unknown mRNA sequence	4.4
70	441184	AA922009	Hs.150269		4.4
	429876	AB028977	Hs.225974		4.4
	445481	AW661846	Hs.148836		4.4
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	4.4
75	404769	4141400015	13. 04444	CCT-	4.4
75	444331	AW193342	Hs.24144	ESTs	4.4
	429726	AW628326	Hs.27151 Hs.22998	ESTs neurexin 1	4.4 4.4
	449093 451959	AB035356 AA056203	Hs.27337	hypothetical protein FLJ20623	4.4
	451959 415716	N59294	Hs.179662		4.4
80	417888	R23053	15.173002	gb:yh31a05.r1 Soares placenta Nb2HP Homo	4.4
	419656	AB002314	Hs.92025	KIAA0316 gene product	4.4
	425864	U56420	Hs.159903		4.4
	435078	AW518888	Hs.40937	ESTs	4.4

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					43
	413493	BE144444		gb:MR0-HT0168-141199-002-f09 HT0168 Homo sterol-C5-desaturase (fungal ERG3, delta	4.3 4.3
	432712 459650	AB016247 R25754		SECTI-CO-COSS atorics of francial Encode, General ESTs	4.3
_	404828	120.0.			4.3
5	423782	AI472209		ESTs	4.3 4.3
	426867 426802	AA460967 AA385182	Hs.22668 Hs.46699	ESTs ESTs	4.3
	457353	X65633	Hs.248144	melanocortin 2 receptor (adrenocorticotr	4.3
10	412112	BE180342		gb:RC3-HT0622-130400-012-a07 HT0622 Homo	4,3 4.3
10	401522	N47812 Al365384	Hs.306198 Hs.11571	CGI-35 protein Homo sapiens cDNA FLJ11570 fis, clone HE	4.3
	419055 410171	H07892	Hs.12431	ESTs	4.3
	419564	U08989	Hs.91139	solute carrier family 1 (neuronal/epithe	4.3
1.5	458789	AL157468	Hs.325825	Homo sapiens cDNA FLJ20848 fis, clone AD gb:QV0-CT0225-100400-187-d08 CT0225 Homo	4.3 4.3
15	455040 438533	AW852286 AM40266	Hs.170673	ESTs, Weakly similar to T24832 hypotheti	4.3
	459005	AA447679	Hs.144558	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.2
	418489	U76421	Hs.85302	adenosine deaminase, RNA-specific, B1 (h	4.2 4.2
20	433389 454356	AF038171 AW390363	Hs.11522	gb:Homo sapiens clone 23671 mRNA sequenc hypothetical protein from Xq28	4.2
20	442339	BE299668	Hs.227591	ESTs, Weakly similar to 1901303A Leu zip	4.2
	421249	AA285362		gb:HTH277 HTCDL1 Homo sapiens cDNA 5/3	4.2 4.2
	443998	A1620661	Hs.296276 Hs.232048	ESTs ESTs	4.2
25	452197 451117	AW023595 AA015752	Hs.205173	ESTs	4.2
	404501	AW247252	Hs.75514	nucleoside phosphorylase	4.2
	410378	R23324	Hs.41693	DnaJ (Hsp40) homolog, subfamily 8, membe	4.2 4.2
	422528 440323	AB011182 AA970614	Hs.118087 Hs.127992	KIAA0610 protein ESTs	4.1
30	425767	AF054176	Hs.159483	chromosome 1 open reading frame 7	4.1
• •	434460	AA478486	Hs.3852	KIAA0368 protein	4.1 4.1
	410362	H04811 T96090	Hs.93164 Hs.142678	proprotein convertase subtilisin/kexin t ESTs	4.1
	413121 409403	AA668224	Hs.6634	Homo sapiens cDNA: FLJ22547 fis, clone H	4.1
35	450235	AA007512	Hs.17538	ESTs	4.1
	449754	H00820	Hs.30977	ESTs, Weakly similar to B34087 hypotheti gb:tz49b05.y1 NCI_CGAP_Bm52 Homo sapien	4.1 4.1
	421813 408496	BE048255 AI683802	Hs.136182	ESTs	4.1
	430261	AA305127	Hs.237225	hypothetical protein HT023	4.1
40	434101	AA625205	Hs.259599	KIAA1622 protein	4.1 4.1
	451837 411772	T92157 BE170301	Hs.16970	ESTs ab:QV4-HT0536-040500-193-f05 HT0536 Homo	4.1
	437630	AI252782	Hs.153026	SWAP-70 protein	4.1
4.5	430212	AA469153		gb:nc67f04.s1 NCI_CGAP_Pr1 Homo sapiens	4.0 4.0
45	400216 429830	AI537278	Hs.225841	DKFZP434D193 protein	4.0
	453155	S74727	Hs.32042	aspartoacytase (aminoacytase 2, Canavan	4.0
	418047	R37633	Hs.4847	ESTs	4.0 4.0
50	405354	AW206512	Hs.186996	ESTs	4.0
50	427931 428775	AA434579	Hs.143691	ESTs	4.0
	449422	AA001373	Hs.59821	ESTs	4.0 4.0
	453864 456407	AW021407 AW968614	Hs.21068	hypothetical protein gb:EST380690 MAGE resequences, MAGJ Horno	4.0
55	441869	NM_003947	Hs.8004	huntingtin-associated protein interactin	4.0
	420784	T65158	Hs.102399	ESTs, Moderately similar to \$65657 alpha	4.0
	425195	AA352026	Hs.94319 Hs.13268	VPS10 domain receptor protein ESTs	4.0 4.0
	429628 410087	H09604 F12079	Hs.332579		4.0
60	409840	AW502122		gb:UI-HF-BR0p-air-c-08-0-UI.r1 NIH_MGC_5	4.0
	452854	AA437061	Hs.14060	prokineticin 1 precursor BESTs, Wealdy similar to A46010 X-finked	4.0 4.0
	419910 427443	AA662913 AA402713	Hs.190173 Hs.97872	ESTs	4.0
	414990	C17758	Hs.221652		3.9
65	412678		Hs.114914	ESTs	3.9 3.9
	405629 420299		Hs.15276	ESTs	3.9
	453098		Hs.86379	ESTs	3.9
70	435752	AF230801		gb:Homo sapiens growth hormone receptor	3.9 3.9
70	441005 414516		Hs.30317 Hs.13556		3.9
	442257	AW503831			3.9
	422563	BE299342	Hs.19348	hypothetical protein FLJ13119	3.9
75	406697		Hs.12301 Hs.33461		3.9 3.9
13	443850 412677			ESTs	3.9
	422788	AL117352	Hs.12082		3.9
	405377		He conte	ESTs, Weakly similar to 16.7Kd protein [3.9 3.9
80	414376 453341		Hs.66915 Hs.29634		3.9
~ ~	431960	AW241821	Hs.30192	7 c6.1A	3.9
	416854		Hs.80296		3.9 3.9
	427264	I AA400117	Hs.12574	7 ESTs	43

	422746	NM_004484	Hs.119651	glypican 3	3.9
	452346	BE243534		gb:TCBAP1D0885 Pediatric pre-B cell acut	3.9
	414666	NM_004466	Hs.76828	glypican 5	3.8
5	418217	AI910647	Hs.13442 Hs.139204	ESTs ESTs	3.8 3.8
,	419118 445017	AA234223 AI205493	Hs.176860	ESTS	3.8
	405867				3.8
	422760	BE409561		gb:601299865F1 NIH_MGC_21 Homo sapiens c	3.8
10	453863	X02544	Hs.572	orosomucoid 1	3.8 3.8
10	457821 457330	H47166 AB013818	Hs.124322 Hs.247220	ESTs, Weakly similar to A47582 B-cell gr peroxisome biogenesis factor 10	3.8
	435600	AL047034	Hs.119747	ESTs	3.8
	456083	U46922	Hs.77252	fragile histidine triad gene	3.8
1.	413341	H78472	Hs.191325	ESTs, Weakly similar to T18967 hypotheti	3.8
15	449057	AB037784	Hs.22941	KIAA1363 protein	3.8 3.8
	421855 414764	F06504 AW013887	Hs.27384 Hs.72047	ESTs, Moderately similar to ALU4_HUMAN A ESTs	3.8
	404391	A11013001	16.72047	2013	3.7
	433629	R13140	Hs.13359	ESTs	3.7
20	424738	AI963740	Hs.46826	ESTs	3.7
	401315	A 4 4 D 4 D 0 E	Un 20012	ECTs. Mandacatable similar to C23650 satro	3.7 3.7
	407706 440530	AA191085 AA888646	Hs.26612 Hs.174187	ESTs, Moderately similar to S23650 retro ESTs	3.7
	433930	AA620338	Hs.273781	ESTs	3.7
25	409662	AW452320	Hs.279726	ESTs	3.7
	437268	AJ754847	Hs.227571	regulator of G-protein signalling 4	3.7
	445688	A1248205	Hs.153244 Hs.197617	ESTs ESTs	3.7 3.7
	408593 417091	R19566 AA193283	Hs.291990	ESTS	3.7
30	448556	AW885606	Hs.5064	ESTs	3.7
-	423135	N67655	Hs.26411	ESTs	3.7
	400135				3.7 3.7
	459150	BE155356 AW383197	Hs.218260	gb:PM1-HT0350-160300-009-d06 HT0350 Homo ESTs	3.7
35	457221 451660	A1807927	Hs.249601	ESTS	3.7
-	401600	BE247275	Hs.151787	U5 snRNP-specific protein, 116 kD	3.7
	446818	AJ342668	Hs.279765	ESTs	3.7
	447795	AW295151	Hs.163612	ESTs	3.7 3.6
40	427562 412258	R56424 AA376768	Hs.26534 Hs.324841	ESTs hypothetical protein FLJ22622	3.6
70	454339	AW381980	115.527071	gb:QV4-HT0316-091199-028-d05 HT0316 Homo	3.6
	439274	AF086092	Hs.48372	ESTs	3.6
	452381	H23329	Hs.290880	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.6
45	422897	AA679784	Hs.4290	ESTs	3.6 3.6
43	429656 421908	X05608 AW935200	Hs.211584 Hs.285814	neurofilament, light polypeptide (68kD) sprouty (Drosophila) homolog 4	3.6
	407978	AW385129	Hs.41717	phosphodiesterase 1A, calmodulin-depende	3.6
	426452	AW614271	Hs.121647	ESTs, Highly similar to AC0060148 simil	3.6
50	400685				3.6
50	417154 447176	A1674701 Z42549	Hs.21388 Hs.160893	ESTs ·	3.6 3.6
	423893	AL031709	Hs.134846	Human DNA sequence from clone 316G12 on	3.6
	449231	BE410360	Hs.298573	KIAA1720 protein	3.6
<i></i>	411607	AW853498		gb:RC1-CT0252-170200-025-h02 CT0252 Homo	3.6
55	405977	DE 500074	11- 201000	ESTs	3.6 3.6
	441470 - 423568	BE503874 NM_005256	Hs.301986 Hs.129818	growth arrest-specific 2	3.6
	441235	AI884586	Hs.135570	Homo sapiens cDNA: FLJ21268 fis, clone C	3.6
	450236	AW162998	Hs.24684	KIAA1376 protein	3.6
60	425364	AF052150	Hs.155959	Homo sapians clone 24533 mRNA sequence	3.6
	426775	AA384564 M31158	Hs.108829 Hs.77439	ESTs protein kinase, cAMP-dependent, regulato	3.6 3.6
	414831 416876	AW501916	Hs.117897	ESTs	3.6
	400878	,			3.6
65	425153	AW023193	Hs.27046	ESTs	3.6
	432222	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	3.5 3.5
	415047 401532	F13142		gb:HSC3JD031 normalized infant brain cDN	3.5
	446495	D60923	Hs.153460	ESTs	3.5
70	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	3.5
	445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	3.5
	455901	BE155527	LL- 2020C	gb:PM1-HT0350-190400-013-b08 HT0350 Homo eukaryotic translation initiation factor	3.5 3.5
	416421 455697	AA134006 BE067952	Hs.79306	gb:CM0-8T0365-061299-122-g09-8T0365 Homo	3.5
75	405678	DC-001 332		Garania arrana arrana respilara arrana respe	3.5
	418207	C14685	Hs.34772	ESTs	3.5
	425383	D83407	Hs.156007		3.5
	417027	AA192306	Hs.23926	triadin homolog of rat orphan transporter v7-3	3.5 3.5
80	408367 417702		Hs.44424 Hs.191146		3.5
	445687	W80382	Hs.149297	ESTs	3.5
	408776	AA057365	Hs.63356	ESTs, Wealdy similar to 138022 hypotheti	3.5
	413164	BE068494		gb:MR1-BT0371-050500-009-a12 BT0371 Homo	3.5

					3.5
	414593	BE386764 AB033089	Hs.32452	gb:601273249F1 NIH_MGC_20 Homo sapiens c Homo sapiens mRNA for KIAA1263 protein,	3.5
•	453220 415621			ESTs	3.5
_	454437	AI248173		hypothetical protein MGC12936	3.5 3.5
5	446066			ESTs KIAA1349 protein	3.5 3.5
	423374 419347	AB037770 C15944		superiorcervical ganglia, neural specifi	3.5
	418516	NM_006218	Hs.85701	phosphoinositide-3-kinase, catalytic, at	3.5
10	451776	W45679		hypothetical protein SP192	3.5 3.5
10	432305	M62402 T89832		insulin-like growth factor binding prote ESTs	3.5
	456995 403323	103032	113.1102.0	20.0	3.5
	425022	M95724		centromere protein C 1	3.5 3.4
15	439394	AA149250	Hs.56105	ESTs ESTs	3.4
15	433803 450715	AI823593 AI266484	Hs.27688 Hs.31570	ESTs, Weakly similar to KIAA1324 protein	3.4
	411474	AW848427	110.01010	gb:IL3-CT0214-150200-075-H10 CT0214 Homo	3.4
	415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	3.4 3.4
20	423826	U20325	Hs.1707	cocaine- and amphetamine-regulated trans gb:601076707F1 NIH_MGC_12 Homo sapiens c	3.4
20	459495 427173	BE544158 BE255017	Hs.97540	ESTs	3.4
	408112	AW451982	Hs.248613	ESTs	3.4
	446092	N33522	Hs.145894	ESTs	3.4 3.4
25	416868	AI656856 BE551408	Hs.292597 Hs.127196	ESTs ESTs	3.4
23	458234 419555	AA244416	HS. 127 130	gb:nc07d11.s1 NCI_CGAP_Pr1 Homo sapiens	3.4
	414314	BE312991		gb:601150275F1 NIH_MGC_19 Homo sapiens c	3.4
	400425	AY004252	Hs.287385	PR domain containing 12	3.4 3.4
30	414366	BE549143 AW445136	Hs.134946	gb:601076456F1 NIH_MGC_12 Homo sapiens c ESTs	3.4
30	434053 449997	A1683052	Hs.201577	KIAA1829 protein	3.4
	433461	AI636047	Hs.197623	ESTs	3.4
	428006	AA418743	Hs.98306	KIAA1862 protein	3.4 3.4
35	424695	U58331 A1733625	Hs.151899 Hs.133053	sarcoglycan, delta (35kD dystrophin-asso ESTs	3.4
33	443294 428212	AV733025 AW444451	Hs.134812	ESTs	3,4
	457673	AASS1569	Hs.272034	hypothetical protein PRO2822	3.4
	446390	AA233393	Hs.14992	hypothetical protein FLJ11151	3.3 3.3
40	428536 426597	A1143139 AA382250	Hs.2288 Hs.145601	visinin-like 1 ESTs	3.3
40	410366	A1267589	Hs.302689	hypothetical protein	3.3
	458258	AW406546	Hs.127971	ESTs	3.3 3.3
	401738			and indusible exterior subfemily & ICV	3.3 3.3
45	409038 425785	T97490 T27017	Hs.50002 Hs.159528	smati inducible cytokine subfamily A (Cy Homo sapiens clone 24400 mRNA sequence	3.3
43	433328	AW298159	Hs.23644	ESTs, Weakly similar to \$65824 reverse t	3.3
	414541	BE293116	Hs.76392	aldehyde dehydrogenase 1 family, member	3.3 3.3
	434998	AW975157	Hs.26037	ESTs	3.3
50	456359 426527	AI967991 NM_001037	Hs.93574 - Hs.170238	homeo box D3 sodium channel, voltage-gated, type I, b	3.3
50	454267	AA437199	Hs.656	cell division cycle 25C	3.3
	400302	N48056	Hs.1915	folate hydrolase (prostate-specific memb	3.3 3.3
	434077	AF116659	Hs.321151	Homo sapiens PRO1412 mRNA, complete cds ESTs	3.3
55	436602 449204	AJ793222 AB000099	Hs.166817 Hs.23251	Down syndrome critical region gene 4	3.3
"	417935	R53697	Hs.170044	ESTs	3.3
	423310	AA325225	Hs.124023		3.3 3.3
	436624	T64297 Al 192987	Hs.5241 Hs.61784	fatty acid binding protein 1, liver hypothetical protein FLJ14451	3.3
60	453406 420164	AW339037	Hs.24908	ESTs	3.3
	447826	AW779317	Hs.258556	ESTs	3.3
	419875		Hs.93557	proenkephalin	3.3 3.3
	444512 418504		Hs.22902 Hs.85335	ESTs Homo sapiens mRNA; cDNA DKFZp564D1462 (I	3.2
65	415242		Hs.295014	'	3.2
	418188	AW139413	Hs.151880		3.2 3.2
	430355			3 phosphoinositide-3-kinase, catalytic, be qb:EST378726 MAGE resequences, MAGI Homo	3.2
	421640 432359		Hs.27441		3.2
70	408806			5 Homo sapiens cDNA: FLJ21532 fis, clone C	3.2
	400409	AF153341	Hs.28395		3.2 3.2
	446015		Hs.13531		3.2 3.2
	425495 403092		Hs.78026	E3 (5, 11¢ard) Stilles to stilles to city)	3.2
75	452971		Hs.91789	ESTs	3.2
	454186	BE141030		gb:MR0-HT0067-201099-002-h11 HT0067 Homo	3.2 3.2
	401489				3.2
	401949 457452		5	gb:EST384766 MAGE resequences, MAGL Horno	3.2
80	454100		Ks.12604	3 chromosome 21 open reading frame 51	3.2
	448440	AA173467			3.2 3.2
	42120				3.2 3.2
	43014	2 RM_000=0	, is.es	257	

	433197	AB040889	Hs.281022	KIAA1456 protein	3.2
	443509	AV645470	Un 120120	gb:AV645470 GLC Homo sapiens cDNA clone	3.2 3.2
	440827 432799	AI733110 NM_016161	Hs.128128 Hs.278960	ESTs alpha-1,4-N-acetylglucosaminyltransferas	3.2
5	409257	AW370362	113.270300	gb:RC1-BT0255-181099-012-607 BT0255 Homo	3.2
-	459235	BE246010	Hs.271468	Homo sapiens mRNA for FLJ00038 protein,	3.2
	416789	AA223439	Hs.79933	cyclin I	3.2
	429809	AL162010	Hs.223603	Homo sapiens mRNA; cDNA DKFZp761D09121 (3.2
10	420156	AW449258	Hs.6187	ESTs	3.2
10	455577	BE006341		gb:RC2-BN0127-240300-011-b05 BN0127 Homo	3.2
	400617	AF151064	Hs.36069	hypothetical protein	3.2 3.2
	437129 451820	AL049327 AW058357	Hs.302057 Hs.337353	Homo sapiens mRNA; cDNA DKFZp564E016 (fr ESTs	3.2
	457535	AA609685	Hs.278672	membrane component, chromosome 11, surfa	3.2
15	419956	AL137939	Hs.40096	ESTs	3.1
	456235	AA203637		gb:zx58b12.r1 Soares_fetal_liver_spleen_	3.1
	423930	AA332697	Hs.42721	ESTs	3.1
	403796				3.1
~~	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	3.1
20	445886	AI793176	Hs.145596	ESTs	3.1
	414401		Hs.124833	ESTs	3.1
	441573	BE563966	Hs.6529	ESTs, Weakly similar to 178885 serine/th	3.1 3.1
	450725	R71389 AI282933	Hs.175951 Hs.23294	ESTs	3.1
25	458805 417868	AI202555 AI078534	Hs.122592	hypothetical protein FLJ14393 ESTs	3.1
LJ	458391	A1792628	Hs.133273	ESTs	3.1
	423346	AI267677	Hs.127416	synaptojanin 1	3.1
	454486	AW857077		gb:RC1-CT0302-140300-016-f04 CT0302 Homo	3.1
	408341	AW182952	Hs.249957	EST8	3.1
30	410669	AW805749	Hs.318885	superoxide dismutase 2, mitochondrial	3.1
	404907			TOTAL ALLE ALLE ALLE AND	3.1
	434910	AI333863	Hs.215474	ESTs, Moderately similar to alternativel	3.1
	436990	AI149729	Hs.120557	ESTs hypothetical protein FLJ21939 similar to	3.1 3.1
35	441921 454673	A1733376 AW812807	Hs.164478	gb:RC3-ST0186-070100-016-c04 ST0186 Homo	3.1
55	429470	AI878901	Hs.203862	guanine nucleotide binding protein (G pr	3.1
	404345	AA730407	Hs.159156	protocadherin 11	3.1
	408217	AI433201	Hs.279860	tumor protein, translationally-controlle	3.1
	417313	AA195602		gb:zr32f09.r1 Soares_NhHMPu_S1 Homo sapi	3.1
40	427322	AK002017	Hs.176227	hypothetical protein FLJ11155	3.1
	411003	AA181018	Hs.13056	hypothetical protein FLJ13920	3.1
	425339	AA936330	Hs.198113	ESTs	3.1
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (lg),	3.1 3.1
45	449078 429608	AK001256 U49250	Hs.22975 Hs.210862	KIAA1576 protein T-box, brain, 1	3.1
73	442308	AA989402	Hs.111	fibroblast growth factor 9 (glia-activat	3.1
	428465	AW970976	Hs.293653	ESTs	3.1
	411666	AF106564	Hs.71346	neurofilament 3 (150kD medium)	3.1
	447965	AW292577	Hs.94445	ESTs	3.1
50	413918	AW015898	Hs.71245	ESTs	3.1
	419682	H13139	Hs.92282	paired-like homeodomain transcription fa	3.1
	425810 427000	AI923627	Hs.31903	ESTs	3.1 3.1
	427865 429060	AA416931 AW139155	Hs.126065 Hs.194995	ESTs hypothetical protein DKFZp43400320	3.1
55	430708	U78308	Hs.278485	offactory receptor, family 1, subfamily	3.1
-	448084	AI467800	Hs.271000	ESTs, Weakly similar to I38022 hypotheti	3.1
	454506	AW847346		gb:RC0-CT0205-240999-021-e01 CT0205 Homo	3.1
	414629	AA345824	Hs.76688	carboxylesterase 1 (monocyte/macrophage	3.0
60	422963	M79141	Hs.13234	ESTs	3.0
60	417696	BE241624	Hs.82401	CD69 antigen (p60, early T-cell activati	3.0
	448175	BE296174	Hs.225160	hypothetical protein FLJ13102 ESTs, Moderately similar to TBB2_HUMAN T	3.0 3.0
	414686 458360	BE 409757 AI027207	Hs.23189 Hs.132253	ESTs	3.0
	451829	AW964081	Hs.247377		3.0
65	445179	AI949743	Hs.224768		3.0
	433090	A1720050	Hs.145362		3.0
	432018	AA524447	Hs.152377		3.0
	407988	N47760	Hs.285107	hypothetical protein FLJ13397	3.0
70	405911	41004000	11- 10000	567-	3.0
70	418808	AI821836	Hs.10359	ESTs ESTs	3.0 3.0
	431900 452893	AW972048 H18017	Hs.192534 Hs.22869	ESTs, Moderately similar to KIAA1395 pro	3.0
	423952	AW877787	Hs.136102	·· · · · · · · · · · · · · · · · · ·	3.0
	412000	AW576555	Hs.15780	ATP-binding cassette, sub-family A (ABC1	3.0
75	405793				3.0
	410711	AB002316	Hs.65746	KIAA0318 protein	3.0
	411279	AW884776		gb:QV4-OT0067-010300-121-d01 OT0067 Homo	3.0
	423957	AW978309	Hs.136235		3.0
80	427071	AA397958	Hs.192719	ESTs gb:EST387061 MAGE resequences, MAGN Homo	3.0 3.0
50	434961	AW974956		Service reduced inspection desired asset titillo	3.0
	T				

TABLE 268: Pkey:

Unique Eos probeset identifier number

		•	tt	
	CAT numbe Accession:		e cluster number bank accession numb	ners
		04741h	Accession	
5	Pkey 409257	1112994_1	Accession AW370362 AW80	9101
•	409840	1156071_1		2125 AW501663 AW501720
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	411279 411474	1247047_2	AWB48427 AW84	8890 AW848159 AW848118 AW848534 AW848285 AW848086 AW648465 AW646265 AW646265
10	411607	1251251_1		3442 AW853590 AW853433 AW853592 1539 AW904851 BE154336 BE154090 BE154275
	411772 412112	1257386_1 1277883_1	IO DE 400	343 AMBA4666 DE466999 DE466999 DE186796 RE18647 RE18641 RE18636 BE160226 ATTO 1037 DE100227 ATTO 1030
	412112	1211000_1	BE180223 BE180	219 BE180346 BE180343 BE180418 BE180Z25 BE180Z27 BE180341 AW901694 BE160Z27 BE160Z27 AV1301631 BE160Z27
15	******	4254400 4		3615 H85799 H83501 BE180220 414 BE068332 BE068347 BE068706 BE068623 BE068450 BE068480 BE068350 BE068255 BE068498 BE068765 BE068328
15	413164	1351422_1	BE068778 BE068	1671 BE068526 BE068493 BE068433 BE068740 BE068306 BE068631 BE068591 BE068745 BE068745 BE068759 BE068628
				1744 AFACACOA AFACACOA DEACAINA DEAGRAIN REINKAIN REINKAIN REINALIA DEUDOI 40 DEUDOI 40 DEUDOU DEUDOU DEUDOU DE
^^				15:29 BE066839 BE068625 BE068596 BE068663 BE0686429 BE068605 BE068633 BE068672 BE068401 BE068579 BE068329 BE068329 BE068329 BE068324 BE06875 BE068329 BE068324 BE06875 BE068324 BE06875 BE068341 BE068548 BE06875 BE068548 BE068575 BE068548 BE06875 BE068548 BE068548 BE06875 BE06855 BE0685 B
20				
			DEGERSOS REGE	RA18 RE068552 RE068598 BE068327 BE068550 BE068712 BE060001 BE060133 BE060123 BE060132 BE060337
				8538 BE068340 BE068537 BE068761 BE068632 BE068758
25	413493 413510	1373555_1 1374377_1	BE144444 BE14	9430 BE145525 BE145493
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	414314 414366	1435028_1 1438636_1		
30	414456	1447655_1		
	414593	1464909_1		
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35	417888	1706092_1		
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40	421813	207654_1		13083 AA298419 52756 AW732798
40	422760 425526	221034_1 252776_1	AA359933 AA3	58889 AW955306 AW962995 AW837746 AW837755 AW837697
	430212	314437_1	AA469153 AI71	8503 AA469225
	432222	343347_1	AI204995 AW8 AF038171 Z43	27539 AW969908 AW440776 AA528756
45	433389 434961	36497_1 396357_1	AW974956 AA	781075 AA654944
13	435752	41050_1	AF230801 AF2	30800 AA401795 AA398260
	437483	43756_1 488242	AL390174 AW8 BE560093	198817
	440198 443509	57199_1	AV645470 T84	636 T82805
50	446052	65988_1	AA358760 AA1	58850 AW062737 AW062738 AV656291
	446218 447135	66686_1 70963_1		145509 BE145512 BE145505 BE145507 5579 AW059603
	452346	912206_	BE243534 BE	243752 AI880228 L44326
55	452502	919733_		48484 BE4884CC BE4884C7
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	40 (100	10 10 10 1	BE141477 BE	141520 BE141456 BE141492 BE141028 BE141775 BE141489 BE141751 AW177399 BE141750 AW177397 BE141312 BE141750
	454220	1122972	BE141749 AV	1177598 1152244 BE152235 BE152238 BE152232
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	454506	1219857	_1 AW847346 AV	V861295 AW847395 AW847385 AW847342 AW847396 AW847339 AW801718 AW801787
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	455225		_1 AW996689 AV	wg96380 AW996453 BE085650 AW868687 BE085595
65	455577		- 05070070 DF	006307 BE006311 061030 BE077927
	455617 455697			067945 BE067942 BE067943 BE067949 BE067954 BE067944 BE067953 BE067956 BE057946
	455901	1381569	_1 BE155527 BE	:155503 BE155188 BE155126
70	456235			832266 H67452 A243209 AA281411
70	456407 457452			A C A 4 7 C C A A E 7 2 M 2 M
	459150			5541368 ANS23003 5153488 BE153461 BE155059 BE155210 BE155413 BE153577 BE153688 BE155063 BE155347 AI903640 BE155492
	TABLE	36C-		
75	Pkey:	200.	Unique number com	esponding to an Eos probeset
	Ref:		Convenes course 1	esponding to an Eus process. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
	Strand		Indicates DNA stran	d from which exons were predicted.
	Nt por		Indicates nucleotide	positions of predicted exons.
80				NL position
	Pkey 40066	Ref 1 811847	Strand '4 Ptus	84912-85187
	40068			72969-73050,73713-73800
				350

PCT/US02/29560 WO 03/025138

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Ptus
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                                   Minus
                                                 135548-136177
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TABLE 27A: ABOUT 533 CNS-ENRICHED GENES SIGNIFICANTLY DOWN-REGULATED IN GUOBLASTOMA COMPARED TO NORMAL ADULT CNS TISSUES Table 27A lists about 533 CNS-enriched genes significantly down-regulated in glioblastoma compared to normal adult CNS tissues. These were selected from 59680 probesels on the Affyrmetrix/Eos Hu/03 GeneChip array such that the ratio of "everage" normal CNS to "everage" glioblastoma was greater than or equal to 2. The "everage" normal CNS lovel was 40 the Anymetruxics Hudu GeneChip array such that the ratio or average normal CNS to average globastoma was greater than or equal to 2. The average normal CNS towards set to the 75° percentite amongst various normal CNS tissues. The "average" globastoma level was set to the 85° percentite amongst various tumor samples. To enrich for CNS specific genes, the ratio of "average" CNS level was set to the 85° percentite amongst various CNS tissues. The "average" normal non-CNS adult tissue level was set to the 85° percentite amongst various CNS tissues. The "average" normal non-CNS adult tissue level was set to the 85° percentite amongst various non-CNS normal tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10° percentite value amongst various non-malignant tissues was subtracted from both the numerator and 45

the denominator before the ratios were evaluated. Unique Eos probeset identifier number

Pkey: Exemplar Accession number, Genbank accession number ExAccn:

Unigene1D: Unigene number Unigene Title:

50

Unigene gene title
Ratio of 75th percentile normal central nervous system tissue to 85th percentile tumor R1: Ratio of 85th percentile central nervous system tissue to 85th percentile normal body fissue

	Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
55	417275	X63578	Hs.295449	parvalbumin	29.0	30.0
	430829	AW451999	Hs.194024	ESTs	25.7	6.2
	410657	AF063228	Hs.65248	dynein, cytoplasmic, intermediate polype	22.6	25.8
	419954	D14720	Hs.93883	myelin protein zero (Charcot-Marie-Tooth	21.2	30.3
	416133	NM_001683	Hs.89512	ATPase, Ca++ transporting, plasma membra	15.5	16.8
60	416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin t	15.2	18.0
	417167	AW206437	Hs.4290	ESTs	14.8	17.7
	433940	H05129	Hs.7459	cyclic AMP-regulated phosphoprotein, 21	13.4	18.1
	413324	V00571	Hs.75294	corticotropin releasing hormone	13.1	18.0
	439830	AA846666	Hs.151489	ESTs, Weakly similar to XE7_HUMAN PROTEI	12.6	16.5
65	408068	AW148652	Hs.167398	ESTs	12.6	16.9
	429096	AB011106	Hs.196012	KIAA0534 protein	12.2	21.1
	412638	AA910199	Hs.203838	ESTs	12.2	16.0
	442593	R39804	Hs.31961	ESTs	10.8	15.0
	446353	AI290919	Hs.153661	ESTs	10.4	13.2
70	426365	AA376667	Hs.10283	RNA binding motif protein 8B	10.0	5.9
	414937	R38698	Hs.12382	ESTs	10.0	10.8
	419643	F06066	Hs.91791	chromosome 11 open reading frame 25	9.5	10.9
	412454	R55745	Hs.167330	ESTs	9.5	14.1
_	439366	AF100143	Hs.6540	fibroblast growth factor 13	9.4	12.3
75	441790	AW294909	Hs.132208	ESTs	9.2	3.2
	448117	H49129	Hs.172982	ESTs	9.1	12.8
	433558	AA833757	Hs.201769	ESTs, Weakly similar to T24435 hypotheti	9.0	14.7
	412453	R20205	Hs.167330	ESTs	9.0	13.7
	408920	AL120071	Hs.48998	fibronectin leucine rich transmembrane p	8.9	17.3
80	409031	AA376836	Hs.76728	ESTs	8.7	8.6
	446544	AI631932	Hs.7047	ESTs, Weakly similar to Unknown [H.sapie	8.2	20.0
	439480	AL038511	Hs.125316	ESTs, Wealdy similar to S33990 finger pr	8.2	8.3
	410200	AA082557	Hs.101915	Stargardt disease 3 (autosomal dominant)	8.0	8.9

	400400	NA 044707	Un 4400C	One I (Head (1)) harmalage subfamily D. membe	7.9	9.6
	408428 437073	NM_014787 AI885608	Hs.44896 Hs.94122	OnaJ (Hsp40) homolog, subfamily B, membe ESTs	7.9	11.3
	408434	AW195317	Hs.107716	hypothetical protein FLJ22344	7.9	16.4
_	440209	H05049	Hs.22269	neurexin 3	7.8	34.3
5	408119	W26213	Hs.101672	ESTs, Weakly similar to T00331 hypotheti Homo sapiens BAC clone CTB-60N22 from 7q	7.8 7.7	9.0 5.0
	429611 423440	AI889077 R25234	Hs.211388 Hs.143434	contactin 1	7.7	9.9
	445148	AI214510	Hs.146304	ESTs	7.6	9.1
••	416294	D86980	Hs.79170	KIAA0227 protein	7.6	7.6
10	424087	N69333	Hs.143434	contactin 1	7.6 7.5	10.3 9.3
	437479 430573	R61866 AA744550	Hs.101277 Hs.136345	ESTs ESTs	7:1	2.8
	448958	AB020651	Hs.22653	KIAA0844 protein	7.1	10.4
	419474	AW968619	Hs.155849	ESTs	7.1	3.0
15	423605	AF047826	Hs.129887	cadherin 19, type 2	7.0 7.0	6.9 9.2
	433098	AW190593	Hs.151143	ESTs guanine nucleotide binding protein (G pr	6.9	3.1
	449511 428414	AI436187 AL049980	Hs.296261 Hs.184216	DKFZP564C152 protein	6.8	5.0
	443155	R54485	Hs.23772	ESTs	6.8	3.5
20	450561	R49674	Hs.25909	ESTs	6.8	8.1
	433068	NM_006456	Hs.288215	sialytransferase	6.8 6.6	2.0 10.5
	423589	AA328082 AI379882	Hs.209569 Hs.72630	ESTs ESTs	6.5	9.0
	415681 413510	F13044	115.7 2000	gb:HSC3HH101 normalized infant brain cDN	6.4	7.1
25	427992	Y15014	Hs.181353	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	6.4	9.5
	450642	R39773	Hs.7130	copine IV	6.4	5.7
	429322	D86984	Hs.199243	KIAA0231 protein	6.4 6.4	8.2 2.3
	447482 446129	AB033059 AW244073	Hs.18705 Hs.145946	KIAA1233 protein ESTs	6.3	B.3
30	421913	A1934365	Hs.109439	osteoglycin (osteoinductive factor, mime	6.3	2.1
50	434273	AA913143	Hs.26303	ESTs	6.2	10.3
	408480	AI350337	Hs.164568	fibroblast growth factor 7 (keratinocyte	6.2 6.2	3.5 12.4
	451301	AJ769514	Hs.209890 Hs.48527	EST	6.2	8.1
35	438356 426388	AA805530 AW081394	Hs.97103	ESTs ESTs	6.2	8.6
55	452502	AI904296	10.01100	gb:PM-BT046-220199-286_1 BT046 Homo sapi	6.1	2.8
	408165	AL137573	Hs.43143	Homo sapiens mRNA; cDNA DKFZp564A2463 (f	6.1	6.3
	442979	AW440782	Hs.174743	ESTs	6.1 6.0	6.3 3.8
40	408713	NM_001248	Hs.47042 Hs.227571	ectonucleoside triphosphate diphosphohyd regulator of G-protein signalling 4	5.9	21.4
40	430004 425087	U27768 R62424	Hs.126059	ESTs	5.9	8.1
	441695	T12411	Hs.183745	hypothetical protein FLJ13456	5.9	3.1
	417175	R44558	Hs.94002	ESTs	5.8	12.5
15	437483	AL390174		gb:Homo sapiens mRNA; cDNA DKFZp547J184	5.8 5.8	2.2 13.8
45	436427 450382	A1344378 AA397658	Hs.143399 Hs.60257	ESTs Homo sapiens cDNA FLJ13598 fis, clone PL	5.7	4.4
	408478	NM_000806	Hs.45740	gamma-aminobutyric acid (GABA) A recepto	5.7	12.5
	442676	AI733585	Hs.130897	ESTs	5.7	6.8
50	446443	AV659082	Hs.134228	ESTs	5.7 5.6	6.4 15.6
50	459080	AW192083	Hs.290855 Hs.272284	ESTs Human DNA sequence from clone GS1-256022	5.6	8.2
	431984 428356	AL080239 AL046991	Hs.10338	ESTs	5.6	6.2
	417877	AI025829	Hs.86320	ESTs	5.4	4.9
	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	5.3	13.1 6.6
55	408556	U49516	Hs.46362	5-hydroxytryptamine (serotonin) receptor cadherin 7, type 2	5.3 5.2	6.0
	431930 438285	AB035301 AA782845	Hs.272211 Hs.22790	ESTs	5.2	7.3
	439901	N73885	Hs.124169		5.2	2.7
	449222	AW293984	Hs.197621		5.2	8.1
60	408016	AW136827	Hs.256096		5.1 5.1	2.5 3.0
	436953 436773	AW959074 AW078629	Hs.23648 Hs.82110	Homo sapiens cDNA FLJ13097 fis, clone NT PC4 and SFRS1 interacting protein 1	5.1	7.3
	409263	AA069573	Hs.50319	ESTs	5.1	12.9
	453830	AA534296	Hs.20953	ESTs	5.1	3.4
65	441535	AL135735	Hs.7885	phosphatidylinositol binding clathrin as	5.0	4.8 20.1
	416490	AF090116	Hs.79348 Hs.107242	regulator of G-protein signaffing 7 Homo sapiens cDNA FLJ12965 fis, clone NT	5.0 5.0	3.9
	417284 448605	N62889 AL109678	Hs.21597	Homo sapiens mRNA full length insert cDN	5.0	6.1
	442240	AI791883	Hs.292719		4.9	6.7
70	427972	AA864870	Hs.18130	putative gene product	4.9	5.2
	416040		Hs.28904 Hs.14487		4.9 4.8	2.8 3.7
	444922 408936		Hs.29354		4.8	6.6
	414943		Hs.12419		4.8	3.1
75	429254	H10133	Hs.91846	hypothetical protein DKFZp761C121	4.8	2.3
	407906		Hs.41185		4.8 4.7	9.1 2.2
	416577 420480		Hs.79381 Hs.98173		4.7	2.8
	404793		140.30110	A Common to a common	4.6	2.2
80	430695	U66581	Hs.24812		4.6	7.4
	438571			ESTS	4.6 4.6	5.4 6.0
	444585 414272		Hs.6594 Hs.46988	ESTs ESTs	4.5	2.2
	4142/2		113.70300		***	

	414699	AI815523	Hs.76930	synuclein, atpha (non A4 component of am	4.5	30.9
	423449	A1497900	Hs.33067	ESTs	4.5 4.4	20.8 2.0
	433521 429876	T66087 AB028977	Hs.112482 Hs.225974	Homo sapiens unknown mRNA sequence KIAA1054 protein	4.4	19.2
5	429726	AW628326	Hs.27151	ESTs	4.4	10.2
•	449093	AB035356	Hs.22998	neurexin 1	4.4	9.4
	415716	N59294	Hs.179662	nucleosome assembly protein 1-like 1	4.4 4.4	15.1 8.2
	419656 425864	AB002314 U56420	Hs.92025 Hs.159903	KIAA0316 gene product offactory receptor, family 5, subfamily	4.4	2.4
10	435078	AW518888	Hs.40937	ESTs	4.4	5.7
	432712	AB016247	Hs.288031	sterol-C5-desaturase (fungal ERG3, delta	4.3	5.9
	426867	AA460967	Hs.22668	ESTs gb:RC3-HT0622-130400-012-a07 HT0622 Homo	4.3 4.3	6.0 3.2
	412112 410171	BE180342 H07892	Hs.12431	ESTs	4.3	5.3
15	442339	BE299668	Hs.227591	ESTs, Wealdy similar to 1901303A Leu zip	4.2	5.0
	421249	AA285362		gb:HTH277 HTCDL1 Homo sapiens cDNA 5/3	4.2	3.5 3.9
	422528	AB011182 AA478486	Hs.118087 Hs.3852	KIAA0610 protein KIAA0368 protein	4.2 4.1	3.9 8.3
	434460 410362	H04811	Hs.93164	proprotein convertase subtilisin/kexin t	4.1	7.0
20	449754	H00820	Hs.30977	ESTs, Wealdy similar to B34087 hypotheti	4.1	3.9
	408496	A1683802	Hs.136182	ESTs	4.1 4.1	4.7 6.3
	434101 430212	AA625205 AA469153	Hs.259599	KIAA1622 protein gb:nc67f04.s1 NCI_CGAP_Pr1 Homo sapiens	4.0	2.5
	453165	S74727	Hs.32042	aspartoacytase (aminoacytase 2, Canavan	4.0	7.4
25	456407	AW968614		gb:EST380690 MAGE resequences, MAGJ Homo	4.0	5.1
	441869	NM_003947	Hs.8004	huntingtin-associated protein interactin	4.0 4.0	32.3 4.5
	429628 410087	H09604 F12079	Hs.13268 Hs.332579	ESTs ESTs	4.0	6.9
	419910	AA662913	Hs.190173	ESTs. Weakly similar to A46010 X-linked	4.0	2.6
30	441005	Z41305	Hs.303172	Homo sapiens mRNA; cDNA DKFZp547G133 (fr	3.9	21.7
	412677	AW029608	Hs.17384 Hs.296341	ESTs adenytyl cyclase-associated protein 2	3.9 3.9	2.2 7.2
	453341 416854	AI758912 H40164	Hs.80296	Purtinje cell protein 4	3.9	2.2
	414666	NM_004466	Hs.76828	glypican 5	3.8	6.2
35	418217	AI910547	Hs.13442	ESTs	3.8	3.2
	421855	F06504	Hs.27384 Hs.72047	ESTs, Moderately similar to ALU4_HUMAN A ESTs	3.8 3.8	2.2 10.7
	414764 433629	AW013887 R13140	Hs.13359	ESTS	3.7	2.7
	424738	AI963740	Hs.46826	ESTs	3.7	2.1
40	407706	AA191085	Hs.26612	ESTs, Moderately similar to S23650 retro	3.7 3.7	5.3 53.7
	437268 423135	A1754847 N67655	Hs.227571 Hs.26411	regulator of G-protein signalling 4 ESTs	3.7	21.7
	446818	AI342668	Hs.279765	ESTS	3.7	2.6
	427562	R56424	Hs.26534	ESTs	3.6	3.6
45	439274	AF086092	Hs.48372	ESTS	3.6 3.6	34.5 6.0
	452381 422897	H23329 AA679784	Hs.290880 Hs.4290	ESTs, Weakly similar to ALU1_HUMAN ALU S ESTs	3.6	5.1
	429656	X05608	Hs.211584	neurofilament, light polypeptide (68kD)	3.6	24.6
	417154	AI674701	Hs.21388	ESTs	3.6	5.8
50	447176	Z42549	Hs.160893	ESTs	3.6 3.6	6.4 3.9
	405977 423568	NM_005256	Hs.129818	growth arrest-specific 2	3.6	2.5
	441235	AI884586	Hs.135570		3.6	5.4
	426775	AA384564	Hs.108829	ESTs	3.6	3.4 2.8
55	414831	M31158	Hs.77439 Hs.27046	protein kinase, cAMP-dependent, regulato ESTs	3.6 3.6	4.9
	425153 446495	AW023193 D60923	Hs.153460		3.5	9.8
	445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	3.5	16.6
60	416421	AA134006	Hs.79306	eukaryotic translation initiation factor	3.5 3.5	5.0 16.0
00	418207 425383	C14685 D83407	Hs.34772 Hs.156007	ESTs Down syndrome critical region gene 1-lik	3.5	6.2
	417027	AA192306	Hs.23926	triadin	3.5	2.5
	408367	AK001178	Hs.44424	homotog of rat orphan transporter v7-3	3.5	5.3
65	408776	AA057365	Hs.63356 Hs.32452	ESTs, Weakly similar to I38022 hypotheti Homo sapiens mRNA for KIAA1263 protein,	3.5 3.5	5.5 23.6
05	453220 419347	AB033089 C15944	Hs.90005	superiorcervical ganglia, neural specifi	3.5	42.3
	433803	AI823593	Hs.27688	ESTs	3.4	3.6
	450715	AJ266484	Hs.31570	ESTs. Weakly similar to KIAA1324 protein	3.4 3.4	4,1 9.8
70	415076 423826	NM_000857 U20325	Hs.77890 Hs.1707	guanylate cyclase 1, soluble, beta 3 cocaine- and amphetamine-regulated trans	3.4 3.4	4.7
70	427173	BE255017	Hs.97540	ESTs	3.4	2.4
	446092	N33522	Hs.145894		3.4	3.5
	416868	AI656856	Hs.292597		3.4 3.4	4.5 4.5
75	458234 434053	BE551408 AW445136	Hs.127196 Hs.134946		3.4	3.9
, ,	428536	Al143139	Hs.2288	visinin-like 1	3.3	42.3
	410366	AI267589	Hs.302689		3.3	14.4 4.6
	425785		Hs.15952 Hs.26037		3.3 3.3	4.7
80	434998 456359		Hs.93574		3.3	4.4
	426527	NM_001037	7 Hs.17023	sodium channet, voltage-gated, type I, b	3.3	5.2
	400302		Hs.1915	folate hydrolase (prostata-specific memb proenkephalin	3.3 3.3	9.0 3.6
	419875	AA853410	Hs.93557	brogivehiam	3.3	3.5

					3.3	3.0
					3.2	2.2
	415242 421640	R45986 AW966652		ab:EST378726 MAGE resequences, MAGI Homo	3.2	3.8
_	408806		Hs.289005 I	Homo sapiens cDNA: FLJ21532 fis, clone C	3.2	2.4 3.2
5	446015		Hs.13531	Hypothicucal protest i co i co i v	3.2 3.2	2.2
	425495	AA358454	Hs.78026		3.2	2.9
	403092 452971	A1873878		L313	3.2	4.5
	454100	AI693231	Hs.126043	Childring Office 21 Open reduing we no 4.	3.2 3.2	2.7 2.8
10	448440	AA173467		DS INCOCASI (SOL-COOLUME INVOCA - CA	3.2 3.2	2.7
	421200 440827	AA284811 Al733110		ESTs ESTs	3.2	2.1
	429809	AL162010		Homo sapiens mRNA; cDNA DKFZp761D09121 (3.2	4.3
	420156	AW449258		ESTs	3.2	19.0 2.0
15	457535	AA609685		membrane component, chromosome 11, surfa	3.2 3.1	8.7
	419956	AL137939 AA332697	Hs.40096 Hs.42721	ESTs ESTs	3.1	2.7
	423930 417868	AI078534	Hs.122592	ESTs	3.1	12.6
	423346	AI267677	Hs.127416	synaptojanin 1	3.1	12.0
20	441921	A1733376	Hs.164478	hypothetical protein FLJ21939 similar to	3.1 3.1	4.3 5.3
	429470	AI878901	Hs.203862 Hs.279860	guanine nucleotide binding protein (G pr tumor protein, translationally-controlle	3.1	7.1
	408217 427322	AI433201 AK002017	Hs.176227	hypothetical protein FLJ11155	3.1	6.3
	449078	AK001256	Hs.22975	KIAA1576 protein	3.1	30.1
25	429608	U49250	Hs.210862	T-box, brain, 1	3.1 3.1	2.2 3.0
	442308	AA989402	Hs.111 Hs.71346	fibroblast growth factor 9 (glia-activat neurofilament 3 (150kD medium)	3.1	10.9
	411666	AF106564 AA416931	Hs.11346 Hs.126065	ESTs	3.1	7.5
	427865 430708	U78308	Hs.278485	olfactory receptor, family 1, subfamily	3.1	3.4
30	451829	AW964081	Hs.247377	ESTs	3.0	6.2 2.4
	405911			COT.	3.0 3.0	6.2
	418808	AI821836	Hs.10359 Hs.22869	ESTs ESTs, Moderately similar to KIAA1395 pro	3.0	5.1
	452893 423952	H18017 AW877787	Hs.136102	KIAA0853 protein	3.0	2.1
35	412000	AW576555	Hs.15780	ATP-binding cassette, sub-family A (ABC1	3.0	2.1
	405793				3.0 3.0	2.7 14.3
	410711	AB002316	Hs.65746	KIAA0318 protein	3.0	2.1
	427071	AA397958	Hs.192719 Hs.33187	ESTs KIAA0748 gene product	3.0	14.5
40	453534 413903	NM_014796 AA496493	Hs.23136	ESTs	3.0	2.2
70	426866	U02330	Hs.172816	neuregulin 1	3.0	11.3
	434945	AB033065	Hs.4280	KIAA1239 protein	3.0 2.9	3.5 4.9
	412639	AW961284	Hs.296235	ESTs MAAGEM amtain	29	33.1
45	453590	AF150278 AL133721	Hs.33578 Hs.224680	KIAA0820 protein ESTs	2.9	2.3
40	414502 434367	AB020700	Hs.3830	KIAA0893 protein	2.9	23.1
	425121	AI797511	Hs.154679	synaptotagmin I	2.9	8.1
	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1	2.9 2.9	20.8 3.2
60	401213	********	11- 50040	hypothetical protein FLJ20331	2.9	3.4
50	401028 415191	AW673312 AA190381	Hs.50848 Hs.120810		2.9	3.0
	449275	AW450848	Hs.205457	neriaxin	2.9	5.6
	419863	AW952691	Hs.93485	Homo sapiens mRNA; cDNA DKFZp761D191 (fr	2.9 2.9	35.0 2.0
F.E	411421	BE272110	Hs.21177	ESTs HSPC125 protein	2.9	11.4
55	430865	Al073424 AW952089	Hs.5232 Hs.5636	RAB6A, member RAS oncogene family	29	2.2
	437486 442357		Hs.135706	S ESTs	2.9	6.0
	408274	R17315		gb:yg12g11.r1 Soares infant brain 1NIB H	2.9 2.8	2.2 5.0
6 0	444185		Hs.66020	ESTs	2.8	5.1
60	420173		Hs.22999	ESTs 5 Stargardt disease 3 (autosomal dominant)	2.8	7.0
	428358 447252		Hs.101915 Hs.12449		2.8	4.4
	440260		Hs.7130	copine IV	2.8	10.6
	417084	H08370	Hs.33067		2.8 2.8	8.4 2.8
65	438257			4 ESTs ESTs	2.8	6.2
	441934 447885		Hs.7344 Hs.30317		2.8	3.5
	423552		Hs.12978	3 sodium channel, voltage-gated, type II.	2.8	3.4
	450940		Hs.14320		2.8	14.4 21.7
70	410011		Hs.57856		2.8 2.8	5.1
	445887		Hs.14559 Hs.78026		2.8	2.4
	425494 43820				2.8	11.9
	43619		Hs.12795	ii hypothetical protein FLJ14503	2.8	6.0
75	43482	6 AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	2.8	2.4
	41546		Hs.12698		2.8 2.8	3.4 4.5
	41807 43214				2.8	9.5
	43037		Hs.24011	12 KIAA0276 protein	2.8	7.0
80	43735		Hs.33166	66 Homo sapiens mRNA; cONA DKFZp76202215 (f	2.7	2.5
	41583	8 R44336	Hs.7093		2.7 2.7	3.6 2.5
	43867			68 ESTs gb:EST365749 MAGE resequences, MAGC Homo		3.1
	41955	8 AW95367	-			

	446318	AI949389	Hs.18067	ESTs	2.7	4.1
	445183	AB007877	Hs.12385	KIAA0417 gene product	2.7	5.3
	457012	R41480	Hs.127630	ESTs	2.7	19.0
_	431988	AC002302	Hs.77202	protein kinase C, beta 1	2.7	7.2
5	430223	NM_002514	Hs.235935	nephroblastoma overexpressed gena	2.7	2.8
	447932	AA837474	Hs.20021	vesicle-associated membrane protein 1 (s	2.7	3.8
	450214	BE439763 AA648049	Hs.227571 Hs.121518	regulator of G-protein signalling 4 ESTs	2.7 2.7	6.9 5.0
	434731 428839	A1767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	2.7	5.2
10	407709	AA456135	Hs.23023	ESTs	2.7	2.5
	422420	U03398	Hs.1524	turnor necrosis factor (ligand) superfami	2.7	3.3
	443305	AI050693	Hs.133318	ESTs	2.7	5.9
	435648	H24347	Hs.27524	ESTs	2.7	15.0
16	418407	AL044818	Hs.84928	nuclear transcription factor Y, beta	2.7	2.7
15	436771	AW975687	Hs.292979	ESTs	2.7	6.0
	428689 440503	NM_014351 NM_006539	Hs.189810 Hs.7235	sutfortranferase family 4A, member 1 calcium channel, voltage-dependent, gamm	2.7 2.7	4.8 4.4
	441006	AW605267	Hs.7627	CGI-60 protein	27	3.1
	410330	AW023630	Hs.46786	ESTs	2.6	29.5
20	434398	AA121098	Hs.3838	serum-inducible kinase	2.6	2.6
_	438831	BE263273	Hs.6439	synapsin II	26	7.8
	419066	Z98492	Hs.6975	PRO1073 protein	2.6	3.4
	412643	AW971239	Hs.293982	ESTs	2.6	2.2
25	430456	AA314998	Hs.241503	hypothetical protein	2.6	17.9
25	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	2.6 2.6	2.9 2.0
	401421 419530	X98330	Hs.90821	ryanodine receptor 2 (cardiac)	2.6	4.2
	441817	AW969706	Hs.293332	ESTs	2.6	3.8
	439203	AA448930	Hs.8453	KIAA1587 protein	2.6	4.2
30	426054	U12431	Hs.166109	ELAV (embryonic lethal, abnormal vision,	2.6	5.1
	444583	AW994403	Hs.100861	hypothetical protein FLJ14600	2.6	3.7
	417919	AI928203	Hs.86379	ESTs	2.6	3.0
	434293	NM_004445	Hs.3796	EphB6	2.6	3.2
25	431716	D89053	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	2.6	6.4
35	443037	AW500305	Hs.299166 Hs.265848	syntaxin 7 myomegalin	2.6 2.6	2.2 7.1
	440736 404648	D56919	ns.200040	пуспедам	2.6	3.0
	429995	AA463571		gb:zx72e09.r1 Soares_total_fetus_Nb2HF8_	2.6	3.5
	436508	AW604381	Hs.121121	ESTs, Weakly similar to \$00755 pleckstri	2.6	3.9
40	441190	H09073	Hs.25046	ESTs	2.6	3.1
	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	2.6	2.9
	442731	AI868167	Hs.131044	ESTs	2.6	4.1
	416836	D54745	Hs.80247	cholecystokinin	2.6	14.9
45	449071	NM_005872	Hs.22960	breast carcinoma amplified sequence 2	2.5	2.4
43	436321	AA709133	Hs.180144	ESTs ESTs	2.5 2.5	2.8 3.6
	439693 443212	A1741816 AW269515	Hs.125897 Hs.102500	hypothetical protein FLJ20481	2.5	2.8
	423981	AL122104	Hs.136664	Homo sapiens mRNA; cDNA DKFZp434A1627 (f	2.5	3.8
	407868	NM_000950	Hs.40637	profine-rich Gla (G-carboxyglutamic acid	2.5	3.1
50	443992	AW022228	Hs.322922	ESTs	2.5	27.9
	444124	R43097	Hs.6818	ESTs	2.5	5.3
	411379	AI816344	Hs.12554	ESTs, Weakly similar to NPL4_HUMAN NUCLE	2.5	38.0
	440474	AI207936	Hs.7195	gamma-aminobutyric acid (GABA) A recepto	2.5 2.5	3.8 2.2
55	446277 410111	AI284218 AI620206	Hs.159204 Hs.189647	ESTs ESTs	2.5	3.5
33	445162	AB011131	Hs.12376	piccolo (presynaptic cylomatrix protein)	2.5	4.8
	410718	AI920783	Hs.191435	ESTs	2.5	4.5
	417201	T60432	Hs.269084	ESTs, Moderately similar to AF097994 1 L	2.5	2.9
	420274	AW968000	Hs.143389	ESTs, Weakly similar to T14318 ubiquitin	2.5	2.8
60	433496	AF064254	Hs.49765	VLCS-H1 protein	2.5	4.7
	437331	AL353933	Hs.21710	hypothetical protein OKFZp761G0313	2.5	3.3
	437368	AJ471969	Hs.182606	ESTs	2.5 2.5	3.0 3.6
	441985 410025	8E047625 BE220489	Hs.169815 Hs.113592	ESTs ESTs, Moderately similar to IS4374 gene	2.5	9.2
65	414680	AA743331	Hs.272572	hemoglobin, alpha 2	2.5	3.6
05	429956	Al374651	Hs.22542	ESTs	2.5	23.9
	429028	AA443439	Hs.48797	ESTs	2.5	2.8
	438109	AI076621	Hs.71367	ESTs, Moderately similar to ALU7_HUMAN A	2.5	3.1
70	439780	AL109688		gb:Homo sapiens mRNA full length insert	2.5	2.3
70	440888	N45600	Hs.326880	ESTs	2.5	3.9
	445246	AJ217713	Hs.147586	ESTs KIAAA379 acetain	2.5	2.6
	440152	AB002376	Hs.7006 Hs.278898	KIAA0378 protein tumor necrosis factor alpha-inducible ce	2.4 2.4	23.6 2.1
	432740 415122	AF061034 D60708	Hs.270090 Hs.22245	ESTs	2.4	3.9
75	432298	AL118812	Hs.274293		24	9.8
	437948	AA772920	Hs.303527	ESTs	2.4	9.8
	421360	AA297012	Hs.103839	erythrocyte membrane protein band 4.1-li	2.4	2.8
	427115	AW972853	Hs.112237	EŠTs	2.4	2.2
QΛ	452074	BE299035	Hs.27747	G protein-coupled receptor 37 (endotheli	2.4	10.0
80	436639	D14838	Hs.111	fibroblast growth factor 9 (glia-activat	24	3.5 3.1
	434520 411529	AA205273 AA430348	Hs.177011 Hs.317596	hypothetical protein Homo sapiens cDNA FLJ12927 fis, clone NT	2.4 2.4	3.0
	442272	AA988302	Hs.129172		2.4	21
						-

	100007	A145747700	Hs.301423	calcium binding protein 1 (calbrain)	2.4	2.7
	422927 444647			Human clone 23589 mRNA sequence	2.4	2.8
	415827		Hs.23079	ESTs	2.4	15.0
_	451397			ESTs, Weakly similar to Z202_HUMAN ZINC	24	3.9
5	445200	AA084460		somatostatin	2.4 2.4	3.7 2.4
	451062	AL110125 Y19062		Homo sapiens mRNA; cDNA DKFZp564C1416 (f staufen (Drosophila, RNA-binding protein	2.4	4.3
	420328 432122	AA526514		gb:ni60f02.s1 NCI_CGAP_Ov2 Homo sapiens	2.4	4.3
	444125	A1124882	Hs.118121	ESTs -	24	3.5
10	430538	AB032435	Hs.242821	differentiation-associated Na-dependent	2.4	10.8
	457519	X69438	Hs.3052	early growth response 4	2.4 2.4	2.4 2.1
	409371	R51736	Hs.12381	ESTs ESTs	2.4	3.2
	456303 440105	AA224872 AA694010	Hs.115088 Hs.6932	Homo sapiens clone 23809 mRNA sequence	2.4	23.4
15	400979	700000	113.0006		2.4	4.1
	435296	R49685	Hs.24980	ESTs	2.4	6.5
	408950	AA707814	Hs.14945	long fatty acyl-CoA synthetase 2 gene	2.4 2.4	18.5 2.2
	452032	BE244005	Hs.27610	retinoic acid- and interferon-inducible cytochrome P450 retinoid metabolizing pr	24	2.7
20	432098 408974	AF252297 AW015458	Hs.91546 Hs.297017	ESTs	2.4	2.5
20	412177	223091	Hs.73734	glycoprotein V (platelet)	2.4	2.8
	413153	N94205		gb:za27a08.r1 Soares fetal liver spleen	2.4	2.5
	417583	AA668782	Hs.191284	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.4 2.3	2.6 3.0
25	452034	F12234	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G) ESTs	2.3	6.3
25	424940 431706	AA985308 AI816086	Hs.194327 Hs.296341	adenytyl cyclase-associated protein 2	2.3	4.1
	419125	AA642452	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro	23	2.9
	423641	AL137256	Hs.130489	ATPase, aminophospholipid transporter-li	2.3	8.7
••	436407	T88803	Hs.271507	ESTs, Weakly similar to TIM_HUMAN PROBAB	2.3	3.2 5.2
30	448681	AL109781	Hs.21754	Homo sapiens mRNA full length insert cDN	2.3 2.3	5.2 54.7
	415669	NM_005025 Al694972	Hs.78589 Hs.66180	serine (or cysteine) proteinase inhibito nucleosome assembly protein 1-like 2	2.3	9.1
	410765 422386	AF105374	Hs.115830	heparan sulfate (glucosamine) 3-O-sulfot	2.3	5.0
	414828	AA156651	110.110000	gb:zl05h05.r1 Soares_pregnant_uterus_NbH	23	2.4
35	445556	AI910241	Hs.12887	actin-related protein 3-beta	2.3	8.5
	426968	U07616	Hs.173034	amphiphysin (Stiff-Mann syndrome with br	2.3 2.3	26.3 2.5
	444562	AA186715	Hs.336429 Hs.128382	RIKEN cDNA 9130422N19 gene Homo sapiens mRNA; cDNA DKFZp761I1224 (f	2.3	7.6
	423420 439450	A1571364 R51613	Hs. 125304	ESTs	23	26.3
40	427127	AW802282	Hs.22265	pyruvate dehydrogenase phosphatase	23	2.2
	447179	AW015633	Hs.157299	ESTs	2.3	3.8
	414711	AI310440	Hs.288735	Homo sapiens cDNA FLJ13522 fis, clone PL	2.3 2.3	2.3 3.8
	433449	AW772282	11- 20002	gb:hn71b05.x1 NCI_CGAP_Kid11 Homo sapien	2.3 2.3	2.5
45	414320	U13616 M16505	Hs.75893 Hs.79876	ankyrin 3, node of Ranvier (ankyrin G) steroid sulfatase (microsomal), arylsulf	2.3	7.8
70	416778 425130	AA448208	Hs.99163	ESTs	2.3	4.1
	456664	AW963354	Hs.334409	metallothionein 1G	2.3	2.5
	438283	AI458931	Hs.37282	ESTs	2.3	4.2
50	417455	AW007066	Hs.18949	ESTs, Weakly similar to CA2B_HUMAN COLLA	2.3 2.3	3.0 3.7
50	412100 448981	AW892731	Hs.195387	gb:CM0-NN0005-100300-279-c02 NN0005 Homo ESTs	2.3	3.2
	416101	AI968719 R24854	Hs.268806	ESTs	2.3	6.5
	439731	AI953135	Hs.45140	hypothetical protein FLJ14084	2.3	17.8
	415734	NM_014747		KIAA0237 gene product	2.3	40.1
55	424596	AB020639	Hs.151017		2.3 2.3	2.9 2.4
	420230	AL034344	Hs.284186 Hs.20935	hypothetical protein DKFZp761D221	2.3	5.7
	451559 404835	AL119980	115.20333	hypothetical protests or a spro-sec-	2.3	21
	456765	AI497900	Hs.33067	ESTs	2.3	4.1
60	455517	AW984068		gb:RC0-HN0006-160300-011-e06 HN0006 Hamo	23 22	2.4 18.5
	408206	AF041853	Hs.43670	kinesin family member 3A	2.2	3.9
	411770	NM_014278	Hs.71992 Hs.2540	heat shock protein (hsp110 family) cholinergic receptor, nicotinic, alpha p	2.2	2.6
	430105 458694	X70297 F12832	Hs.13298	ESTs	2.2	4.9
65	415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	2.2	4.4
	439642	W81441	Hs.153967		2.2	2.4
	450138	AW152104	Hs.200879	ESTS	2.2 2.2	4.9 3.7
	454222		Hs.7589	ESTs, Weakly similar to A46010 X-linked	2.2	2.7
70	405326 431342		Hs.21659	ESTs	2.2	5.2
,,	453101		Hs.94943	ESTs	2.2	3.3
	408897		Hs.28370		2.2	2.8
	451398		Hs.14447		2.2 2.2	4.6 10.4
75	438208		Hs.65379 B Hs.16616		2.2	6.1
13	408449 414130		Hs.71592		2.2	3.1
	445016		Hs.12246	reetin	2.2	3.9
	424375	AF070547	Hs.14631	2 Homo sapiens clone 24820 mRNA sequence	2.2	2.3
00	424645				2.2 2.2	· 11.7
80	409729		Hs.10628 Hs.13170		2.2	19.9
	432809 422890		Hs.75893		2.2	10.4
	428532		Hs.18478		2.2	6.5

	413074	AI871368	Hs.8417	hypothetical protein DKFZp761M0423	2.2	3.4
	414442	AA156238	Hs.32501	ESTs	2.2	3.2
	452768	AW069459	Hs.61539	ESTs	2.2	2.0
•	450440	AB024334	Hs.25001	tyrosine 3-monoxygenase/typtophan 5-mo	2.2	3.2
5	426281	AK000987	Hs.169111	oxidation resistance 1	2.2 2.2	2.3 2.3
	428411 413787	AW291464 AJ352558	Hs.10338 Hs.75544	ESTs tyrosine 3-monooxygenase/tryptophan 5-mo	2.2	31
	451734	NM_006176	Hs.26944	neurogranin (protein kinase C substrate,	2.2	8.5
	439108	AW163034	Hs.6467	synaptogyrin 3	2.2	7.9
10	405385				2.2	2.4
	447285	Al371849	Hs.200696	ATPase, Class VI, type 11C	2.2 2.2	2.2
	452667 422234	T87219 AF119818	Hs.13219 Hs.113287	ESTs discs, large (Drosophila) homolog-associ	2.2	3.1 8.3
	410339	AP115810 AI916499	Hs.298258	ESTs	2.1	3.2
15	413231	D87461	Hs.75244	BCL2-like 2	2.1	4.5
	447104	R19085	Hs.210706	Homo sapiens cDNA FLJ 13182 ffs, clone NT	2.1	2.2
	451952	AL120173	Hs.301663	ESTs	2.1	36.5
	415841	Z45637	Hs.7093 Hs.213490	ESTs ESTs, Wealthy similar to N33_HUMAN N33 PR	2.1 2.1	2.4 2.2
20	441086 450407	AI928489 NM_000810	Hs.24969	gamma-aminobutyric acid (GABA) A recepto	2.1	6.6
	427627	R87582	Hs.179915	guanine nucleotide binding protein (G pr	21	5.3
	449712	R56545	Hs.6100	ESTs	21	4.5
	409660	AW452065	Hs.258905	ESTs	21	2.1
25	430434	AL049548	Hs.241420	Homo saptens mRNA for KIAA1756 protein,	2.1 2.1	5.4 3.0
23	434138 448610	AA625804 NM_006157	Hs.21602	gb:zu86h01.s1 Soares_testis_NHT Homo sap nel (chicken)-like 1	2.1	4.8
	418948	AJ217097	110.2.002	gb:qd43h07.x1 Soares_fetal_heart_NbHH19W	21	2.9
	414876	AW950925	Hs.924	crystallin, mu	21	3.4
20	440426	AI159800	Hs.7181	Homo sapiens cDNA FLJ13663 fis, clone PL	2.1	3.7
30	451249	AA016227	Hs.27280	ESTs	2.1 2.1	4.1
	451475 448743	T19093 AB032962	Hs.26450 Hs.21896	KIAA0725 protein KIAA1136 protein	2.1	2.1 29.7
	430814	U89336	Hs.247993	NGS protein	2.1	2.7
	426990	AL044315	Hs.173094	Homo sapiens mRNA for KIAA1750 protein,	21	2.3
35	426642	AW068223	Hs.171581	ubiquitin C-terminal hydrotase UCH37	2.1	4.5
	427335	AA448542	Hs.251677	G antigen 78	21	2.2
	459089	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp56401763 (f Bruno (Drosophila) -like 4, RNA binding	2.1 2.1	2.3 5.9
	435832 446383	AA425688 T05816	Hs.41641 Hs.92511	ESTs	21	2.9
40	412768	AW996044	Hs.26239	Human DNA sequence from clone RP11-438B2	2.1	2.1
	453976	BE463830	Hs.163714	ESTs	2.1	4.2
	415111	R39039	Hs.328455	EST	2.1	3.3
	452238	F01811	Hs.187931	ESTS	2.1 2.1	4.9 9.8
45	445279 448799	R41900 Al937094	Hs.22245 Hs.179080	ESTs ESTs	2.1	3.1
43	418338	NM_002522	Hs.84154	neuronal pentraxin I	2.1	8.3
	445725	AK000956	Hs.13209	hypothetical protein FLJ10094	2.1	5.4
	443537	D13305	Hs.203	cholecystokinin B receptor	2.1	4.1
50	454066	X00356	Hs.37058	calcitonin/calcitonin-related polypeptid	2.1 2.1	6.4
30	429954 415292	AI918130 H29016	Hs.21374 Hs.200576	ESTs ESTs	2.1	7.2 3.9
	423563	R34734	Hs.75209	protein kinase (cAMP-dependent, catalyti	2.1	3.1
	424906	AI566086	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3'	2.1	4.7
	459309	AA040620	Hs.5672	hypothetical protein AF140225	2.1	2.2
55	439340	AB032436	Hs.6535	brain-specific Na-dependent inorganic ph	2.1 2.1	4,7 5.4
	402598 435406	BE314624 F26698	Hs.3128 Hs.4884	polymerase (RNA) II (DNA directed) polyp calcium/calmodulin-dependent protein kin	2.1	6.6
	448792	R42550	Hs.12826	ESTs	2.1	4.1
	449500	AW956345	Hs.12926	ESTs	2.1	2.4
60	441134	W29092	Hs.7678	cellular retinoic acid-binding protein 1	21	5.8
	433361	AW469373	Hs.300141	ribosomal protein L39	2.1	2.7 5.0
	452946	X95425 AF039023	Hs.31092 Hs.167496	EphA5 RAN binding protein 6	2.1 2.0	2.2
	426167 453666	AW015681	Hs.135229	ESTs, Wealthy similar to A2BP_HUMAN ATAXI	2.0	3.1
65	424632	AB014523	Hs.151406		2.0	3.5
	448589	AF017090	Hs.21554	KIAA1107 protein	2.0	4.1
	430416	AC005531	Hs.57806	Homo sapiens PAC clone RP4-701016 from 7	2.0	2.3
	445627	AW818475	Hs.7363 Hs.181165	ESTs eukaryotic translation elongation factor	2.0 2.0	2.1 2.5
70	417092 453653	H97508 AW505554	Hs.144559		2.0	4.7
, ,	435850	AF250847	Hs.283514		2.0	3.7
	435086	AW975243	Hs.122596	ESTs	2.0	2.1
	423191	D61506	Hs.8417	hypothetical protein DKFZp761M0423	2.0	2.1
75	411562	AL050201	Hs.70769 Hs.266483	hypothetical protein DKFZp586E1923 dynein light chain-A	2.0 2.0	2.8 2.5
, 5	431645 429834	AF078849 AI929645	Hs.200483		2.0	2.5 3.6
	439607	8E540565	Hs.159460		2.0	17.5
	408033	AW138045	Hs.242256	ESTs	2.0	4.0
90	430317	A8020645	Hs.239189		2.0	2.7
80	419631	AW188117	Hs.303154		2.0 2.0	2.6 2.3
	432660 454048	AI288430 H05626	Hs.64004 Hs.6921	ESTs ESTs	2.0	23 15.9
	426917	AA913814	Hs.172854		2.0	3.1

```
spectrin, alpha, non-erythrocytic 1 (alp
                                                        Hs.77196
               423246
                                 AL119114
                                                                                                                                                                 2.0
                                                         Hs.317584
                                                                             ESTs
                                 AI267700
               415989
                                                                                                                                                                                     5.1
15.9
                                                                             ESTs, Highly similar to SORL_HUMAN SORTI
                                                                                                                                                                 2.0
                                 AA290938
                                                         Hs.190561
               420276
                                                                                                                                                                 2.0
                                 AI742434
                                                         Hs.169911
                                                                             ESTs
                424983
                                                                                                                                                                                      2.7
                                                                              Homo sapiens cDNA FLJ13155 fis, clone NT
                                                                                                                                                                 2.0
                446296
                                  AA985662
                                                         Hs 63131
                                  AI241555
                                                         Hs.60171
                450006
                TABLE 27B:
                                                Unique Eos probeset identifier number
                                                Gene cluster number
10
                CAT number:
                                                Genbank accession numbers
                Accession:
                                  CAT Number
                                                          R17315 Z43964 AA053547
                                   104999_1
                 408274
                                                          BE180342 BE180347 AW901900 BE180222 BE180218 BE180226 BE180413 BE180416 AW901899 BE180228 AW901897 BE180224 AW901898 BE180223 BE180219 BE180343 BE180343 BE180245 BE180221 BE180341 AW901894 BE180217 BE180227 AW901891 BE180345
                                   1277224_1
15
                 412100
                                    1277883_1
                 412112
                                                           AW893614 AW893615 H85799 H83501 BE180220
                                                          N94205 BE067565 BE067556
F13044 T77009 BE145525 BE145493
                                    1350849_1
                 413153
20
                 413510
                                    1374377_1
                                                           AA156651 AA156622 R14472
                  414828
                                    149563_1
                                                           AA130031 MA130022 N14412
A1217097 AW886090 W38035 W38792 AA232835 AW936043
AW953679 AW953680 AA244436 H82527 AA361046 AA244483 H82526
AA285362 AW752386 AW847155 AA285373 AW879575 AW879558
                                    180808_1
                 418948
419558
                                    185904_1
                                    200649_1
                  421249
                                                           AW966652 AW966653 AA294989 AA385977
25
                  421640
                                    204833_1
311738_1
                                                            AA463571 AI277645 AL118763
                  429995
                                                            AA469153 AI718503 AA469225
                                    314437_1
                  430212
                                                            AA526514 AW973343 AA554293
                                     341756_1
                   432122
                                                            AW772282 AA592974
                   433449
                                     366532 1
                                                            AA625804 AW418787 AW074833 Al675642 Al393368
 30
                                     380572 1
                   434138
                                                            AL390174 AW898817
AL109688 R23665 R26578
                                     43756_1
                   437483
                   439780
                                     47673_1
                                                             AI904296 BE007223 R30687
                                     919733.1
                   452502
                                                            AW984068 AW984072 AW984077
                   455517
                                     1321782 1
                                                             AW968614 AA243209 AA281411
  35
                                     184986_1
                   456407
                   TABLE 27C:
                                                   unique number corresponding to an cos proceset
Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
Indicates DNA strand from which exons were predicted.
                    Pkey:
                    Ref:
  40
                    Strand:
                                                    Indicates nucleotide positions of predicted exons.
                     Nt_position:
                                                                                  Nt_position
160842-161028
                                       Ref
   45
                     400979
                                       8072554
                                                              Plus
                                                                                   98243-98380,98489-98619
                     401213
                                       9858408
                                                              Phis
                                                                                   142291-142461
                                       7452889
                                                              Minus
                     401421
                                                                                   174720-175016,175104-175406,175508-175813
                                       8954241
                     403092
                                                                                   115334-116020
                                       9796894
                                                              Minus
                      404648
                                                                                   61087-61590
    50
                      404793
                                        7232206
                                                               Minus
                                                                                    85462-85684,88139-88287,90338-91018,94827-94990
10633-10709,30805-30893,38078-38253,55112-55327,57718-57818,66696-66841
                                                               Plus
                      404835
                                        6970743
                                        4375975
                                                               Plus
                      405326
                                                                                    48332-48454
                                                               Plus
                                        6552772
                      405385
                                                                                    89197-89453
                      405793
                                        1405887
6758795
                                                               Minus
                                                                                     101008-101643
    55
                                                               Plus
                      405911
                                        8247789
                                                                                     135548-136177
                      405977
                     TABLE 28A: About 139 genes up-regulated in glioma compared to normal adult tissues.

Table 28A lists about 139 genes up-regulated in glioma compared to normal adult tissues. In order to identify new genes that are associated with glioma, a non-redundant set of 6614 genes that have been previously identified were removed from the starting collection of 59680 probesets on the Affymetrix/Eos-Hu03 GeneChip® array. Genes associated with genes that have been previously identified were removed from the starting collection of 59680 probesets on the Affymetrix/Eos-Hu03 GeneChip® array. Genes associated with genes that have been previously identified were removed from the remaining 53005 probesets such that the ratio of "average" glioma to "average" normal adult tissues was greater than or equal to 2.5, and the "average" glioma value was greater than or equal to 50 units (this selects for the most abundant of the up-regulated genes). The "average" glioma level was set to the 94th percentile value amongst variou glioblastoma, astrocytoma, and ofigodendroglioma specimens; the "average" normal adult tissue level was set to the 85th percentile value amongst various glioblastoma, astrocytoma, and ofigodendroglioma specimens; the "average" normal adult tissue level was set to the 85th percentile value amongst various non-malignant brain tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst various non-malignant itssues was subtracted from both the numerator and the denominator before the ratio was evaluated. Predicted protein domains are noted.

Previous formation of the protein domains are noted.
     60
     65
                                                      Unique Eos probeset identifier number
                       Pkey:
                                                       Exemplar Accession number, Genbank accession number
                       ExAcon:
                                                       Unigene number
                       UnigenelD:
      70
                                                      Unigene gene title
Predicted Protein Domains
                       Unigene Title:
                       Prof. Doms:
                                                       glioma vs normal adult tissues
                       R1:
                                                                                                                                                                         Protein Domains
                                                                 UniGene ID
                                                                                      Unigene Title
                                                                                                                                                                                                                                                            4.0
                                                                                      N-ethylmaleimide-sensitive factor a
       75
                                                                  Hs.12600
                        443902
                                          W28470
                                                                                                                                                                                                                                                             4.0
                                                                  Hs.173134
                                                                                       ESTs
                        441476
                                          R44566
                                                                                                                                                                                                                                                             3.8
3.7
                                                                                      KIAA1811 protein
                                                                  Hs.182081
                        446048
                                           AL272364
                                                                                       gb:H.sapiens PTX3 gene promotor reg
                        407061
                                           X97748
                                                                                                                                                                                                                                                             3.6
3.6
                                                                                                                                                                          fn3;TM;
                                                                                       KIAA0273 gene product
Homo sepiens mRNA full length inser
                                           NM_014759
                                                                  Hs.334688
                        414323
                                                                                                                                                                          lactamase_B,Rhomboid,TPR
       80
                                           AA448828
                                                                  Hs.30596
                        439769
                                                                                                                                                                                                                                                             3.6
                                                                                                                                                                          nkinase:TM:SS
                                                                                       similar to calcium/calmodulin depen
                                                                  Hs 199068
                                           AL023754
                         429319
                                                                                                                                                                                                                                                             3.5
                                                                                       angiotensin receptor-like 1
                                                                  Hs.9305
                         443412
                                           W84893
                                                                                        angiotensin receptor-like 1
                                                                  Hs.9305
                                           T47802
                         425533
```

	408610			ESTs	ion_trans,K_tetra,Kv2chan	3.4 3.4
	450678			Homo sapiens mRNA full length inser orotein tyrosine phosphatase, recep	Y_phosphatase_ART;TM;SS	3.4
	419171 445875			Homo sapiens clone 24453 mRNA seque	- Theophomochan (1940)	3.4
5	412581			ESTs, Moderately similar to alterna		3.3
	424911			ESTs	COM TOIC	3.3 3.3
	452753 436648			SEC14 (S. cerevisiae)-like 2 ESTs	CRAL_TRIO pkinase,pkinase_C,PMP22_C	3.2
	452130		Hs.28088	SGC32445 protein	T82_DP1_HVA22;TM;SS	3.2
10	448848	AF131851	Hs.22241	hypothetical protein		3.2
	426470	AA528794		ESTs	ank, DAGKa, DAGKc, DAG_PE-bi	3.2 3.2
	419344 439783	U94905 Al125760	Hs.277445 Hs.24835	diacylglycerol kinase, zeta (104kD) hypothetical protein FLJ14594	ig.LRR.LRRNT,LRRCT;TM;S	3.2
	411358	R47479	Hs.94761	KIAA1691 protein	TM;SS	3.2
15	409433	AA074382		ADAMTS14		3.2
	456940	H46986	Hs.31861	ESTs	Course	3.1 3.1
	423744 432227	D26158 U28389	Hs.1701 Hs.274122	ELAV (embryonic lethal, abnormal vi erythrocyte membrane protein band 4	mm,Gene66; VHP;TM;	31
	449181	X96783	Hs.23179	synaptotagmin V	C2:TM:SS	3.1
20	422274	NM_015564	Hs.114169	KIAA0416 protein	LRR, LRRNT, LRRCT; TM; SS	3.1
	424607	NM_016848	Hs.151123	neuronal Shc	PID,SH2;	3.1 3.1
	416898 438162	BE219510 NM_014618	Hs.234074 Hs.6090	Homo sapiens mRNA; cDNA DKFZp761G02 deleted in bladder cancer chromosom	EGF,Rhabd_glycop;TM;SS= TM;SS	3.1
	439892	AL043463	Hs.6755	RaP2 interacting protein 8	RUN;SS	3.1
25	445330	R52656	Hs.21691	EST8	7tm_1	3.0
	451766	NM_001406		ephrin-B3	Ephrin;TM;SS	3.0 3.0
	444457	· AI204146 R14439	Hs.92556 Hs.209194	ESTs ESTs	Fork_head	3.0
	458247 424616	U72671	Hs.151250	intercellular adhesion molecule 5,	ig,ICAM_N;TM;SS	3.0
30	408971	R38990	Hs.13485	ESTs	<u>-</u>	3.0
	423940	NM_012429	Hs.277728	SEC14 (S. cerevisiae)-like 2	CRAL_TRIO;TM;	3.0
	458124	AW005548	Hs.124590	ESTs		3.0 3.0
	410491 444808	AA465131 H20019	Hs.64001 Hs.286084	Homo sapiens clone 25218 mRNA seque ESTs	ank,ras,PH,ArfGap,HCO3_co	3.0
35	437696	Z83844	Hs.5790	hypothetical protein dJ37E16.5	Hydrolase;TM;	2.9
	424016	AW163729	Hs.6140	hypothetical protein MGC15730	ig:SS	2.9
	421580	AL031186	Hs.289106	Human DNA sequence from clone CTA-9	Collagen;TM;SS	2.9 2.9
	418055	R18516	Hs.351299	ESTs, Wealty similar to 138022 hypo	<u>n.n.</u>	2.9
40	444819 420524	Al697836 AB010575	Hs.148433 Hs.98547	ESTs amiloride-sensitive cation channel	ASC:TM:	2.9
70	416237	H30684	Hs.159863	ESTs		2.9
	432270	AK001008	Hs.274233	Homo sapiens cDNA FLJ10146 ffs, clo		2.9
	405569			NM_031481*:Homo sapiens solute carr	mito_carr,TM;SS	2.9 2.9
45	428950	BE311879	Hs.194673	phosphoprotein enriched in astrocyt gamma-aminobutyric acid (GABA) B re	DED;TM; 7tm_3,sushi,ANF_receptor;	29
43	426128 447758	NM_001471 H17302	Hs.167017 Hs.93967	ESTs, Weakly similar to NBHUC8 deco	LRR LRRNT, LRRCT; TM; SS	2.9
	445331	H04489	Hs.12520	Homo sapiens clone 23568, 23621, 23	PC_rep	2.9
	431010	BE251246	Hs.248214	complexin 1	TM;	2.9 2.9
50	433065	N62902	Hs.343660	Homo sapiens PAC clone RP4-651K2 fr	;SS EB1,CH;TM;	2.9
30	426845 454360	AB025186 L78207	Hs.172740 Hs.54470	microtubule-associated protein, RP/ ATP-binding cassette, sub-family C	ABC_tran_ABC_membrane,PRK	2.9
	438859	AI559626	Hs.93522	Homo sapiens mRNA for KIAA1647 prot	bZIP,K-box,7tm_2,EGF,cadh	2.9
	410515	F12086	Hs.4257	ESTs	PID,SH2,PID,SH2	2.8 2.8
55	434022	R18374	Hs.117956	ESTs	hormone_rec,zf-C4 Carta_C4,RPH3A_effector;T	2.6 2.8
55	428960 426290	AF052224 AB007918	Hs.194684 Hs.169182	bassoon (presynaptic cytomatrix pro KIAA0449 protein	WD40;TM;	2.8
	417287	AI831678	Hs.285714		C2;TM;	2.8
	422575	AK000546	Hs.118552	hypothetical protein FLJ20539	PTR2;TM;SS	2.6
40	417941	A1056049	Hs.96297	ESTs	Band_41,ERM	2.8 2.8
60	452707 424873	AI093823 AB018294	Hs.45070 Hs.153610	ESTs KIAA0751 gene product	C2,PDZ;TM;	2.8
	408209	NM_004454		ets variant gene 5 (ets-related mol	Ets;TM;	2.8
	415935	H09663	Hs.106490		PID	2.8
	437999	AW905038	Hs.90242	ESTs	ion_trans	2.8 2.8
65	428248	AJ126772	Hs.40479	ESTs ESTs, Moderately similar to ALU1_HU	Getsotin,VHP,p450	2.8
	414001 406634	AI610347 AA386235	Hs.103812 Hs.74576	GDP dissociation inhibitor 1	GDI;TM;	2.8
	453439	AI572438	Hs.32976	guanine nucleotide binding protein	G-gamma:TM;	2.8
	433320	D60647	Hs.250879		m .	2.8
70	420888	AB006713	Hs.100058		Dihydroorotase;TM;	2.7 2.7
	440001	AI740721	Hs.128292		WH2TM	2.7
	417622 438626		Hs.82318 Hs.26370	WAS protein family, member 3 ESTs	ver and a real	2.7
	404439	72.50005	110.2001	ENSP00000067222*:Mitochondrial 28S	OUF;SS	2.7
75	448375			adaptor-related protein complex 3,	Adaptin_N;TM;	2.7 2.7
	420989		Hs.323833	syntaphilin cAMP-regulated guanine nucleotide e	TM; cNMP_binding,DEP,RasGEF,R	2.7
	419651 414562		Hs.91971 Hs.112195		trim trimillier have h	2.7
_	410865		Hs.66727	ESTs, Wealty similar to T31613 hypo	IRK	2.7
80	421146		Hs.97993	ESTs, Moderately similar to SERP1 (2.7
	419087		Hs.24835	hypothetical protein FLJ14594	ig_LRR_LRRNT,LRRCT;TM;S ptinase,Peptidase_M1;TM	2.7 2.7
	421499 425014		Hs.236131 Hs.171939		PID,PDZ	2.7
	423014	Al251449	Fig. 17 1903			

	448655	AL035289	Hs.21708	hypothetical protein from clone 248	TM;	SS	2.7 2.7
	424410	W79027	Hs.271762	ESTs			2.7
	447117	AI362798	Hs.40183	ESTs	m3	SPRY;TM;	2.7
5	447478	BE618843	Hs.28144 Hs.21164	fibronectin type 3 and SPRY domain- ESTs		Q1 711 (1 m),	2.7
)	437645 433698	R20728 H24201	Hs.247423	adducin 2 (beta)	Ald	olase_II;TM;	2.7
	419701	AA248999	Hs.7913	ESTs		en et en etan anna DA	2.7 2.7
	410510	AW294625	Hs.64064	potassium voltage-gated channel, su		MP_binding,ion_trans,PA	2.7
• •	452869	AB014534	Hs.30898	KIAA0634 protein	fn3 ;SS		2.7
10	428045	T15465	Hs.182231 Hs.155182	thyrotropin-releasing hormone KIAA1036 protein	TM		2.7
	425218 425558	NM_014909 AF040723	Hs.158300	huntingtin-associated protein 1 (ne	TM		2.6
	440789	AB007857	Hs.7416	KIAA0397 gene product		C,RUN;TM;	2.6 2.6
	418423	NM_014732	Hs.301658	KIAA0513 gene product	TN	tin_c	2.6
15	450400	Al694722	Hs.279744	ESTs sprouty (Drosophila) homolog 4		IZ,SH3;TM;SS	2.6
	413566	AW604451 BE390832	Hs.285814 Hs.134729	FXYD domain-containing ion transpor		PIG1_PLM_MAT8;TM;SS	2.6
	443759 425069	AA687465	Hs.298184	potassium voltage-gated channel, sh	ato	lo_ket_red	2.6 2.6
	429291	AI933057	Hs.349189	mannosyl (alpha-1,3-)-glycoprotein			2.6
20	424798	AW016523	Hs.182850	ESTs	TA	A:SS	2.6
	447455	H38335	Hs.6750	Homo sapiens mRNA for FLJ00058 prot		N,E2_C,DNA_mis_repair.	2.6
	417212	AW952823 BE382679	Hs.351547 Hs.285753			athmin;TM;SS	2.6
	432265 417005	C21115	Hs.26612	ESTs, Moderately similar to S23650			2.6 2.6
25	421091	W22821	Hs.351612	ribosomal protein L26	TI		2.6
	445472	AB006631	Hs.12784	Homo sapiens mRNA for KIAA0293 gene		omeobox,CUT;TM; igar_tr;TM;SS	26
	431967	AJ243653	Hs.373498			arb_anhydrase;TM;SS	2.6
	439151	AW135066	Hs.283110 Hs.140950			UF176;SS	. 26
30	424134 430213	AF070637 AW993446	Hs.235445			RAM;TM;	2.6 2.6
50	445954	AA148926	Hs.27836	hypothetical protein FLJ22362		:3;TM;	2.6
	445084	H38914	Hs.250848	hypothetical protein FLJ14761		M;SS ı3,ig,pkinase;TM;	2.6
	445236	NM_006293		TYRO3 protein tyrosine kinase		H,RhoGAP	2.6
35	433706	AW947250 AB011094	Hs.283645 Hs.129892			H,bZIP,IQ,Sec7;TM;	2.5
33	423606 438915	AA280174	Hs.285681				2.5 2.5
	448923	AL034562	Hs.22584	prodynorphin	C)piods_neuropep;SS	2.5
	408115	AB033107	Hs.42796				2.5
40	446772	AW294404	Hs.14451		1	M;SS	2.5
40	427989	H85525 BE259178	Hs.40479 Hs.41641		ſ	rm;TM;	2.5
	435833 423797	BE259364	Hs.13289			neme_1,FA_desaturase;TM	2.5 2.5
	448277	BE622827	Hs.99486		,	nito_carr;TM;SS	2.5 2.5
	417298	AW665639	Hs.37958			KH-domain;TM;	2.5
45	415577	AF257770	Hs.20930			g;TM;SS	2.5
	420742		Hs.99902 Hs.17271			pkinase,LRRCT,ig,LRR,LRRN	2.5
	419109	BE169157	FIS. 17271			·	
	TABLE	28C:					
50	Pkey:		ique number	corresponding to an Eos probeset e. The 7 digit numbers in this column are Gents	ont Identifier	GI\ numbers "Dunham, et al." re	efers to the publication entitled "The DNA
	Ref:	Se	equence source	e. The 7 digit numbers in this cultural are Genomian chromosome 22° Dunham, et al. (1999) Nat	ure 402:489-4	95.	•
	Strand:	se to	dicates DNA s	trand from which exons were predicted.			
	Nt_pos	ition: In	dicates nucleo	tide positions of predicted exons.			
55	_						
	Pkey	Ref	Strand	Nt_position 99719-99873			
	405569 404439		Plus Plus	55316-55585			
60	TABLE	29A: ABOUT 3	62 GENES UF	REGULATED IN GLIOMA COMPARED TO NO	ON-MALIGNA	NT ADULT BRAIN TISSUE	Table 28A except that the ratio of "average" glioma
• •	Table :	29A fists about 3	62 genes up-	regulated in glioma compared to non-margnant a	June eat to the	o Ooth nementile value amongst t	Table 28A, except that the ratio of "average" glioma various glioma specimens, the "average" normal value was greater than or equal to 50 units.
	to ave	rage" normal br	ain was greate	er than or equal to 3.0, the laverage guidha level percentile value amongst various non-malignant	a was ser to u I adult brain s	pecimens, the "average" glioma va	value was greater than or equal to 50 units.
	adult ti	ssue level was s led protein dom:	ince and on 195	BeiDeune Agine grinningst Agricus restrictional com-			
65	Pkey:		Inique Fos ord	sbeset identifier number			
05	ExAcc	n: Ē	xemplar Acce	ssion number, Genbank accession number			
	Unige		Inigene numb				
			Inigene gene				
70	Protes R1:	n Domains: F	Predicted Prote	malignant adult brain tissue			
70	KI.	•	MOITE VS HOIP	in Large 19 and			R1
	Pkey	ExAcca	Unigen			Protein Domains pkinase,LRR,TM;SS	11.2
	41447		Hs.762	28 amplified in osteosarcoma gb:Human omega light chain protein		TM;	10.9
75	40724		0 Hs.493			TM;	7.0
13	40897 4175		u ns.433 Hs.822	26 glycoprotein (transmembrane) nmb		PKD:TM;SS	6.9
	4140			812 ESTs, Moderately similar to ALU1_HU		Getsolin,VHP,p450	6.3 6.2
	4288	47 AI954833		81 ESTs			5.4
00	4070			gb:H.sapiens PTX3 gene promotor reg			5.4
80	4400 4088						5.3
	4068 4068		Hs.156			- -	5.2
	4076					crystall;TM;	5.1
					260		

		100000	U- 110004	NIA 000142Nama anciesa NAONIII. biarin		5.1
	435013 424916	H91923 AW867440	Hs.110024 Hs.23096	NM_020142:Homo sapiens NADH:ubiquin ESTs	am.	5.1
	409659	AW970843	Hs.55682	eukaryotic translation initiation f	:SS	5.1
	432576	AW157424	Hs.165954	ESTs, Wealthy similar to 138022 hypo	m	5.1
5	406621	X57809	Hs.181125	immunoglobulin tambda locus	ig,HSP70,Ppx-GppA;TM;SS	5.1 5.1
	430418	R98852	Hs.36029	heart and neural crest derivatives	HLH TM:SS	5.0
	441633	AW958544 W76631	Hs.112242 Hs.211819	normal mucosa of esophagus specific matrix metalloproteinase 238	ig,Peptidase_M10;TM;SS=	5.0
	429707 438915	W/6631 AA280174	Hs.285681	Williams-Beuren syndrome chromosome	- Bit chance	5.0
10	441321	H17182	Hs.7771	B-cell associated protein	Band_7;TM;	5.0
10	406848	AI264844	Hs.275865	ribosomal protein \$18	Ribosomal_S13;	4.9
	423505	AF064090	Hs.129708	turnor necrosis factor (ligand) supe	TNF;TM;SS	4.8 4.8
	433848	AF095719	Hs.93764	carboxypeptidase A4	Zn_carbOpept,Propep_M14;T	4.8
15	431882	NM_001426	Hs.271977 Hs.101660	engrailed homolog 1 ESTs, Wealdy similar to T14171 atax	homeobax;TM; LIM	4.8
13	446295 409170	Al355029 W91994	Hs.16145	ESTS. Weakly suitable to 114171 alex	m	4.8
	421155	H87879	Hs.102267	lysyl oxidase	Lysyl_oxidase,Aldose_epim	4.7
	409202	AA236881	Hs.51043	hexosaminidase B (beta polypeptide)	Glyco_hydro_20,Glyco_hydr	4.7
••	412115	AK001763	Hs.73239	hypothetical protein FLJ10901	;\$\$	4.7 4.7
20	450463	AW952018	Hs.201398	G protein coupled receptor interact	C1q,Collagen;TM;SS zf-C2H2,bZIP	4.7
	445960	AI268399	Hs.140489	ESTs, Weathy similar to LIN1_HUMAN	Ribosomal_S4,S4,tRNA_int_	4.6
	406807 409190	AA057605 AU076536	Hs.180920 Hs.50984	ribosomal protein S9 sarcoma amplified sequence	transmembrane4;TM;SS	4.6
	401699	AUUTUSS	15.50504	Target Exon	TM;	4.6
25	408901	AK001330	Hs.48855	hypothetical protein FLJ10468	TM;	4.6
	441669	R78195	Hs.29692	Homo sapiens cDNA FLJ11436 fis, clo		4.6
	406868	AA505445	Hs.300697	immunoglobulin heavy constant gamma	ig;TM;	4.6 4.6
	406699	L06505	Hs.182979	ribusomal protein L12	Ribosomal_L11;TM; ;SS	4.6
30	406663	U24683	Hs.2186	immunoglobulin heavy constant mu eukaryotic translation etongation f	COX8,SHMT,MIF,GST_C,EF1G_	4.6
30	427714 407260	AF119850 L09095	rs.2100	gb:Homo sapiens mRNA fragment.	00/0/0/0/0/0/0/0/0/0/0/0/0/0/0/0/0/0/0/0	4.5
	406803	H42321	Hs.163593	ribosomal protein L18a	Ribosomal_L18ae;TM;	4.5
	430397	AI924533	Hs.105607	bicarbonate transporter related pro	HCO3_cotransp;TM;	4.5
	414044	BE614194	Hs.75721	profilin 1	profilin;TM;	4.5 4.5
35	424238	AA337401	Hs.137635	ESTs	TM;SS Armadillo_seg,HEAT;TM;S	4.4
•	421532	AW138207	Hs.146170 Hs.102866	hypothetical protein FLJ22959 transketolase-like 1	transketolase,transket_py	4.4
	421241 436398	X91817 H87136	Hs.5174	ribosomal protein S17	Ribosomal_S17e,PotyA_pol;	4.4
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and	pkinase,ICE_p10,ICE_p20;T	4.4
40	446921	AB012113	Hs.16530	small inducible cytokine subfamily	IL8;SS	4.3
	433271	BE621697	Hs.14317	nucleolar protein family A, member	;	4.3 4.3
	406964	M21305		FGENES predicted novel secreted pro	ADC1-The	4.3
	432191	AA043193	Hs.273186	hypothetical protein, clone Teletho	ABC1;TM; Glucosamine_iso;TM;	4.3
45	420890 413053	AA434058 AW963263	Hs.100071 Hs.65377	6-phosphogluconolactonase ESTs, Moderately similar to KIAA139	TM;	4.3
73	406687	M31126	Hs.352054	matrix metalloproteinase 11 (strome	hemopexin,Peptidase_M10;T	4.2
	425157	NM_006227		phospholipid transfer protein	LBP_BPI_CETP,LBP_BPI_CETP	4.2
	426386	AA748850	Hs.125830	bladder cancer overexpressed protei		4.2 4.2
50	446490	AK000706	Hs.15125	hypothetical protein FLJ20699	TM; cpn60_TCP1	4.2
50	431750	AA514986	Hs.283705	ESTs ESTs	cystatin,Coprogen_oxidas,	4.2
	428327 417342	AW206236 W40277	Hs.28773 Hs.81994	glycophorin C (Gerbich blood group)	TM;	4.1
	433688	AA628467	Hs.112572		••••	4.1
	433170	AB037816	Hs.8982	KIAA1395	TM;	4,1
55	423084	AU076474	Hs.123178		rm The sec	4.1 4.1
	407926	AW956382	Hs.59771	ESTs	TYA;SS	4.1
	445636	AW105401	Hs.350068		filament.GTP_EFTU.EFG_C,G	4.1
	418689 450690	AI360883 AA296696	Hs.375584 Hs.333418		ATP1G1_PLM_MAT8;TM;SS	4.1
60	419092	J05581	Hs.89603	mucin 1, transmembrane	SEA;TM;SS	4.0
•	447813	AI394345	Hs.238513	A	ubiquitin;TM;SS	4.0
	436419	AJ948626	Hs.171356	ESTs	AT_hook,ATHILA	4.0 4.0
	458147	AW752597		gb:IL3-CT0214-161299-045-806 CT0214	PMM POZ LIM objecto	4.0
65	443402		Hs.356316		PDZ,LIM,pkinase EF_TS,UBA;	4.0
03	433435	BE545277 AW235215	Hs.340959 Hs.16145	Ts translation elongation factor, m ESTs	mu E1 _10,000	4.0
	413595 412607		Hs.74115	immunoglobulin superfamily, member	ig;TM;SS	4.0
	419913			ESTs	EPH_lbd,fn3.pkinase,	4.0
	415209		Hs.172004	l tilin		4.0
70	439310		Hs.102793		casein_kappa,pkinase,ig,n	3.9 3.9
	421777		Hs.108196		TM; Collagen,fibrinogen_C;TM≔	3.9 3.9
	409485		Hs.252130	5 ficolin (collagen/fibrinogen domain Target Exon	p450;TM;SS	3.9
	402241 432716		Hs.205180		LRR.UPAR_LY6:TM;	3.9
75	418140		Hs.83551	microfibrillar-associated protein 2	TM;SS	3.9
	434214		Hs.15586	hypothetical protein PRO2268	;SS	3.9
	406855	AA902829		gb:ok72e06.s1 NCI_CGAP_GC4 Homo sap	hamanaria Bastidana MAGAT	3.9 3.9
	421567		Hs.19826		hemopexin,Peptidase_M10;T	3.9
80	403364		He 21/40	Target Exon 6 ESTs	SH2,Y_phosphatase tubufin	3.8
00	412339 423007				TIMP	3.8
	427600				PA28_alpha,PA28_beta;	3.8
	405201			Target Exon	mito_carr,SH2,SH3,Alpha_a	3.8

	436906	H95990	Hs.181244	major histocompatibility complex, c	ig,MHC_I;TM;SS	3.8 3.8
	407319	AI743332		ESTs, Moderately similar to ALU7_HU	rm,Lipoprotein_2	3.8
	400290	H18836		hypothetical protein FLJ20041	Cys_knot HEAT_PBS;TM;	3.8
5	430240	BE303038		Homo sapiens, clone IMAGE:2905978, hypothetical protein, estradiol-ind	LRR LRRNT;TM;SS	3.8
3	442487 408135	AF191019 AA317248		methyltransferase-like 1	Methyltransf_4;TM;	3.8
	419942	U25138		potassium large conductance calcium	CaKB;TM;SS	3.8 3.8
	410584	AB011112		KIAA0540 protein	LIM:SS	3.8
• •	440676	NM_004987		LIM and senescent cell antigen-like	Ribosomal_L13e;SS	3.7
10	406874	AW161706		ribosomal protein L13 egf-like module containing, mucin-l	7tm_2,EGF,GPS,S_locus_gly	3.7
	429249	X81479 C19035	Hs.2375 Hs.164259	ESTs	FKBP,TPR	3.7
	430799 453099	H62087	Hs.31659	thyroid hormone receptor-associated	WD40;TM;	3.7
	421794	X86096	Hs.108371	E2F transcription factor 4, p107/p1	E2F_TDP,KOW,Ribosomal_L14	3.7 3.7
15	444795	AI193356	Hs.160316	ESTs	Tropornyosin,ACOX CUB,MAM,F5_F8_type_C	3.7
	443834	AI741510	Hs.173548	ESTs beta-carotene 15,15'-dioxygenase	RPE65;SS	3.7
	429731	AK001592 L38969	Hs.212172 Hs.169875	thrombospondin 3	TSPN,tsp_3,EGF,toxin;TM	3.7
	426433 426395	BE151985	Hs.355669	hypothetical protein FLJ23316	pkinase	3.7
20	406704	M21665	Hs.929	myosin, heavy polypeptide 7, cardia	myosin_head,lQ,Myosin_tal	3.7 3.7
	447860	AF193807	Hs.131835	Rhesus blood group, B glycoprotein	Ammonium_transp,FecCD;TM= mito_carr,homeobox;TM;S	3.7
	430281	AI878842	Hs.237924	CGI-69 protein Homo sapiens mRNA; cDNA DKFZp566P23	1140_001,1011000001,11110	3.7
	448360	AL117560 Al420227	Hs.306352 Hs.366053	Trp-p8 transient receptor potential		3.7
25	446057 432078	BE314877	Hs.24553	hypothetical protein FLJ12541 simil	TM;SS	3.7 3.7
23	406854	AA613705	Hs.252259	ribosomal protein S3	KH-domain,Ribosomal_S3_C;	3.7
	422532	AL008726	Hs.118126	protective protein for beta-galacto	serine_carbpept,GalP_UDP_ Ribosomal_L29;	3.6
	428171	AA489323	Hs.182825	ribosomal protein L35	robosona_czs,	3.6
20	442285	W28729	Hs.356072 Hs.4786	uncharacterized hypothalamus protei Homo sapiens cDNA: FLJ22849 fis, cf	cadherin	3.6
30	411281 457657	BE392792 AW411509	Hs.352567	hypothetical protein PRO2121	UQ_con;TM;	3.6
	414624	BE389320	Hs.23628	3 beta-hydroxy-delta 5-C27-steroid		3.6 3.6
	451564	AU076698	Hs.132760	hypothetical protein MGC15729	sugar_tr,Condensation;TM=	3.6
	445411	AL137255	Hs.12646	hypothetical protein FLJ22693	hormane_rec,zf-CCCH;TM; TM;SS	3.6
35	400785		11- 224240	C11000861:gi[9938016 ref NP_064687. hypothetical protein MGC13045	TM;	3.6
	413343	BE392026 NM_005534	Hs.334346 Hs.177559	interferon gamma receptor 2 (interf	fn3;TM;SS	3.6
	427380 427818	AW511222	Hs.193765	ESTs		3.6
	449957	D31365	Hs.24220	hypothetical protein	TM;	3.6 3.6
40	451529	Al917901	Hs.208641	ESTs	actin Nol1_Nop2_Sun;TM;	3.6
	446528	AU076640	Hs.15243	nucleotar protein 1 (120kD)	Totex-1;TM;	3.6
	431659	AA031875	Hs.266940 Hs.10362	t-complex-associated-testis-express Homo sapiens cDNA: FLJ20944 fis, cl	zI-C3HC4,SPRY	3.6
	433350 412896	BE563152 AW804157	Hs.375570		ig,MHC_II_beta;TM;SS	3.6
45	441748	R14439	Hs.209194			3.6 3.5
,,,	406853	AA614553	Hs.252259		KH-domain,Ribosomal_S3_C;	3.5 3.5
	457464	AW972234	Hs.126680	ESTs		3.5
	429619	AL120751	Hs.211568 Hs.126782		sushi,HYR;SS	3.5
50	423309 438682		Hs.375594			3.5
50	453022		Hs.118489	ESTs	Amino_oxidase	· 3.5 3.5
	434042		Hs.8254	Homo sapiens, Similar to tumor diff	TM;SS	3.5
	424867		Hs.153591		(M,55	3.5
55	417298		Hs.37958	ESTs C5000355:gij4503225kefjNP_000765.1		3.5
23	403943 429497		Hs.204121		fn3;TM;	3.5
	426613		Hs.171280		adh_short;TM;SS	3.5 3.5
	428343		Hs.12705		WD40;SS death:TM:	3.5 3.5
60	456376		Hs.89862		geau, im,	3.5
60	400348		Hs.35258	B Target Target Exon	;SS	3.5
	404854 427930		Hs.37212			3.5
	453143		Hs.35628		serpin;SS	3.5 3.5
	406806			6 ribosomal protein, large, P0	TM;	3.5
65	406793			guarine nucleotide binding protein	WD40;TM;	3.5
	41452		Hs.45184 Hs.93871		Glyco_hydro_47;TM;SS	3.5
	41995		ns.930/1	NM_006778:Homo sapiens ring finger	zf-C3HC4,zf-B_box;TM;SS	3.4
	40424 42461		21 Hs.15113	9 E74-tike factor 4 (ets domain trans	Ets;SS	3.4
70	43283			9 ESTs, Weakly similar to 138022 hypo	7.4	3.4 3.4
	41394				TM; death,DED;SS	3.4
	41855				CUE;TM;	3.4
	40893		Hs.33468	Target Exon	HMG_box;SS	3.4
75	40324 41633		t Hs.7922		Glyco_hydro_35;TM;SS	3.4
, ,	40486			NM_025204*:Homo sapiens hypothetica	:	3.4 3.4
	44138	4 AA447849			7tm_3	3.4 3.4
	43028				RNA_pol_L,RNA_pol_L,RasGA	3.4
80	43366		9 Hs.1942 Hs.7623		S10_plectin;TM;	3.4
60	45605 42231			48 cytokine receptor-like factor 1	fn3;TM;	3.4
	40890			79 ESTs, Weakly similar to T26022 hypo	de aite at the constitution	3.4 3.4
	4280		Hs.1820		death,pkinase;TM;	3.4
					271	

	424213	BE390125	Hs.143187	hypothetical protein	DEAD,helicase_C;TM;	3.4
	416432	BE391767	Hs.79322	glutaminyl-IRNA synthetase		3.4
	400233			Eas Control	Ribosomal_S9;	3.4
•	403252			Target Exon	TM;SS	3.4
5	409433	AA074382	Hs.135255	ADAMTS14	.	3.4
	426053	U68105	Hs.172182	poly(A)-binding protein, cytoplasmi	mm,PABP;TM;	3.4
	448222	A1548587	Hs.20725	Mov10 (Moloney leukamia virus 10, m	TM;	3.4
	432982	AA531058	Hs.182248	truncated calcium binding protein	OPR.ZZ;TM;	3.4
10	453914	NM_000507	Hs.574	fructose-1,6-bisphosphatase 1	FBPase;TM;	3.4
10	444626	AA320893	Hs.117062	hypothetical protein FLJ14497	pyr_redox;TM;SS	3.4
	427751	AF000152	Hs.355816	conserved gene amplified in osteosa	NIF;TM:	3.4
	416971	R34657	Hs.80658	uncoupling protein 2 (mitochondrial	mito_carr,TM;	3.4
	428046	AW812795	Hs.337534	ESTs, Moderately similar to 138022	ank	3.4
1.5	456575	AW063659	Hs.191649	EST ₈	Myosin_tail	3.4
15	407366	AF026942	Hs.17518	gb:Homo sapiens cig33 mRNA, partial	IBR	3.4
	414738	L24038	Hs.77183	v-raf murine sarcoma 3611 viral onc	pkinase,DAG_PE-bind,RBD;T	3.4
	456356	M74715	Hs.89560	iduronidase, alpha-L-	Glyco_hydro_39;SS	3.3
	429668	AA626142	Hs.179991	ESTs, Wealthy similar to S28942 prot	_	3.3
20	404913			NM_024408*:Homo sapiens Notch (Dros	EGF,ank.notch.metalthio,E	3.3
20	426059	BE292842	Hs.166120	interferon regulatory factor 7	IRF;SS	3.3
	451619	AA018854	Hs.353196	glutathione peroxidase 3 (plasma)	PH;SS	3.3
	410225	AW608964	Hs.12030	ESTs		3.3
	402534			Target Exon	;	3.3
0.0	433750	H15448	Hs.31330	Homo sapiens clone HQ0319	GLFV_dehydrog,GLFV_dehydr	3.3
25	421712	AK000140	Hs.107139	hypothetical protein	TM;SS	3.3
	433333	AI016521	Hs.71816	v-ald murine thymorna viral oncogene	pkinase,PH,pkinase_C	3.3
	424915	R42755	Hs.23096	ESTs	rm	3.3
	408494	AA554714	Hs.187578	Homo sapiens cDNA FLJ11639 fis, clo		3.3
	445084	H38914	Hs.250848	hypothetical protein FLI14761	TM;SS	3.3
30	446478	AI950021	Hs.370306	ESTs .	TM;	3.3
	425274	BE281191	Hs.155462	minichromosome maintenance deficien	MCM;TM;	3.3
	456655	Al376736	Hs.111779	secreted protein, acidic, cysteine-	kazat;SS	3.3
	438912	AF085843		gb:Homo sapiens full length insert		3.3
	428396	U70539	Hs.184161	exostoses (multiple) 1	Exostosin;TM;SS	3.3
35	437546	AW074836	Hs.173984	T-box 1	T-box,WD40;TM;	3.3
	410693	BE044206		gb:ho40c08.x1 Soares_NFL_T_GBC_S1 H	C1g, Collagen, cystati	3.3
	414961	U27266	Hs.927	myosin-binding protein H	fn3,ig;TM;	3.3
	422766	AA334108	Hs.159572	heparan sulfate (glucosamine) 3-O-s	-	3.3
	426120	AA325243	Hs.166887	copine I	C2,mm;TM;	3.3
40	452383	T70900	Hs.27189	ESTs	zi-C2H2,PRK	3.3
	456799	AC004923	Hs.135187	unc93 (C.elegans) homolog 8	TM;	3.3
	409227	AA806165	Hs.130323	Homo sapiens, clone IMAGE:3960432,	NA;NA	3.3
	432659	AA281633	Hs.278586	KIAA1108 protein	TBC;TM;	3.3
	448997	AA130390	Hs.25549	hypothetical protein FLJ20898	TMLSS	3.3
45	446990	AI354717	Hs.223908	ESTs	transmembrane4	3.3
	437259	AI377755	Hs.120695	ESTs	MHC_II_alpha,ig	3.3
	423461	AB020527	Hs.128827	solute carrier family 17 (sodium ph	sugar_tr;TM;	3.3
	421563	NM_006433	Hs.105806	granutysin	;SS	3.3
	453804	AA300204	Hs.35276	KIAA0852 protein	TM;	3.3
50	428810	AF068236	Hs.193788	nitric oxide synthase 2A (inducible	NAD_binding,flavodoxin,FA	3.3
	453933	A1452933	Hs.65377	ESTs	EF_TS,UBA,transmembr	3.3
	449267	AI638640	Hs.220624	ESTs		3.3
	418165	R45959	Hs.6637	ESTs	mito_carr	3.3
	446673	NM_016361	Hs.15871	LPAP for tysophosphatidic acid phos	acid_phosphat;TM;SS	3.3
55	402475	<u>-</u> 0		ubiquitin specific protease 18	:	3.2
-	404233			Target Exon	нт	3.2
	406655	M21533	Hs.277477	major histocompatibility complex, c	ig.MHC_I;TM;SS	3.2
	414556	AW975063	Hs.343443	ribosomal protein L36	Ribosomal L36e:	3.2
	450191	AW137243	Hs.248074	EST ₈	homeobox;TM;	3.2
60	435906	AI686379	Hs.110796	SAR1 protein	art,ras;TM;	3.2
•	412540	C18341	Hs.73999	thyroid hormone receptor interactor	SH3,FCH;SS	3.2
	422562	AI962060	Hs.118397		Zn_carbOpept.F5_F8_type_C	3.2
	431051	AA491143	Hs.283374		TM;	3.2
	407984	AW134708	Hs.243569	ESTs	· ····,	3.2
65	441494	AW452344	Hs.129977	EST ₆		3.2
05	423114	AU076497	Hs.1514	cholinergic receptor, nicotinic, al	Neur_chan_LBD,Neur_chan_m	3.2
	419833	AA251131	Hs.220697	ESTs	WHEP-TRS,IRNA-synt_1b,non	3.2
	419036	180967	Hs.372603	gb:yd23/12.s1 Soares fetal liver sp	141/Et -11/9'8/10-2\inf	3.2
	431222	X56777	Hs.273790	zona pellucida glycoprotein 3A (spe	zona_peltucida;TM;SS	3.2
70	453094	AA74092B	Hs.27356	ESTs	Zuria_periocola i incoo	3.2
70	426989	AI815206	Hs.367644	ESTs	BAG, ubiquitin	3.2
	445033	AV652402	Hs.72901	cyclin-dependent kinase inhibitor 2		3.2
	446272	BE268912	Hs.14601	hematopoietic cell-specific Lyn sub	ank; SH3,HS1_rep;TM;	3.2
	438930	AW843633	Hs.343261	hypothetical protein AL110115		3.2
75			Hs.6101	hypothetical protein MGC3178	HLH thinsed:TU:	3.2 3.2
, ,	438183	BE263252			thiored;TM;	
	421310	AW630087	Hs.103315	trinucleotide repeat containing 1	PHD	3.2
	409293	R02673	Hs.110156	ESTs ribosomal protein S10	C10 electionThir	3.2
	407115	AA084921	Hs.76230		S10_plectin;TM;	3.2
80	401174			Target Exon Eos Control	transmembrane4,EF_TS,UBA	3.2
ou	400217	AIDIEIDO	He 57475	sex comb on midleg homolog 1	ræ;SS	3.2
	408676	AI815189	Hs.57475	transmembrane, prostate androgen in	TAACC	3.2
	418245	AA088767	Hs.83883	Target Exon	TM;SS	3.2
	403694			1 to Act rows.	UDPGT	3.2

	414265	BE410411	Hs.75864	endoplasmic reticulum glycoprotein	505 711.00	3.2
	451118	Al862096	Hs.60640	ESTs	EGF,vwc,TIL;SS	3.2 3.2
	422624	BE616678	Hs.76152 Hs.14478	KDEL (Lys-Asp-Glu-Leu) endoplasmic Homo sapiens mRNA; cDNA DKFZp762H18	ER_lumen_recept	3.2
5	437388 429150	AL359586 AF120103	Hs.197366	smoothened (Drosophila) homolog	COX8,SHMT,MIF,GST_C,EF1G_	3.2
•	430379	AF134149	Hs.240395	potassium channet, subfamily K, mem	ion_trans;TM;SS	3.2
	434956	BE266566	Hs.4288	hypothetical protein DKFZp434K046	Cullin;TM;	3.2
	422166	W72424	Hs.112405	S100 calcium-binding protein A9 (ca	efhand,S_100;TM;	3.2
10	452493	AI904031	Hs.106826	KIAA1696 protein	PHD,Myc-LZ,DC1,AT_hook;TM	3.2 3.2
10	413100	BE065208	Un 40000	gb:RC1-8T0314-310300-015-b09 BT0314 hypothetical protein SP329	F-box;TM;	3.2
	420764 421680	BE250676 AL031186	Hs.19928 Hs.289106	Human DNA sequence from clone CTA-9	Collagen; TMtSS	3.2
	406738	AA587983	15.203100	gb:ni30b09.s1 NCI_CGAP_AA1 Homo sap	TIM, Ribosomal_S5; TM; SS=	3.1
	434288	AW189075	Hs.116265	fibrillin3	EGF,granulin,TB,EB,TIL;TM	3.1
15	438264	T86773	Hs.6133	calpain 5	Cafpain_III,Peptidase_C2,	3.1
	436819	AA731746	Hs.120232	ESTs	m	3.1
	459298	R86701		gb:ym86d09.r1 Soares adult brain N2	TM;	3.1 3.1
	452127	BE562126	Hs.28081	eukaryotic translation initiation f	mm,7tm_1,SNF;TM;	3.1
20	422305 414393	AI928242 AA146855	Hs.293438	ESTs, Highly similar to AF198488 1 gb:zo41h10,r1 Stratagene endothelia		3.1
20	423369	BE219099	Hs.279513	ESTs		3.1
	429457	BE243065	Hs.202955	hypothetical protein FLJ20507	Cys-protease-3C;TM;	3.1
	409124	AW292809	Hs.50727	N-acetylghucosaminidase, alpha- (Sa	TM;SS	3.1
	429615	AF258627	Hs.211562	ATP-binding cassette, sub-family A	ABC_tran;TM;SS	3.1
25	445519	AI635202	Hs.170132	hypothetical protein FLJ22494	TM;	3.1 3.1
	410007	AW950887	Hs.57813	zinc ribbon domain containing, 1	TFIIS;TM; globin;TM;	3.1
	407228	M25079	Hs.155376 Hs.70823	hemoglobin, beta KIAA1077 protein	Sulfatase;TM;	3.1
	411573 406654	AB029000 M90686	Hs.73885	HLA-G histocompatibility antigen, c	ig,MHC_I;TM;SS	3.1
30	435072	AW592176	Hs.116932	ESTs	zf-RanBP,MDM2	3.1
-	456642	AW451623	Hs.109752	putative c-Myc-responsive	;SS	3.1
	445457	AF168793	Hs.12743	camitine O-octanoytransferase	Carn_acyttransf;TM;	3.1
	448389	AW188950	Hs.345838	ESTs	20G-Fell_Oxy,mm,SH3,ras	3.1
25	458248	BE407379	Hs.108082	ESTs, Weakly similar to T31636 hypo	C1q,Collagen;TM;SS	3.1 3.1
35	451310	AW250651	Hs.26213	Human DNA sequence from clone RP3-4 for protein disulfide isomerase-rel	TM; thiored;SS	3.1
	414688 428797	A1750246 AA496205	Hs.76901 Hs.193700	Homo sapiens mRNA; cDNA DKFZp586103	LIM,Ran_BP1,GRIP,TPR.pro_	3.1
	425067	BE223071	Hs.169142	ESTs		3.1
	410639	BE269047	Hs.65234	hypothetical protein FLJ20596	DEAD,helicase_C,PRK,AIP3;	3.1
40	413011	AW068115	Hs.821	biglycan	LRR,LRRNT;SS	3.1
	421502	AF111856	Hs.105039	solute carrier family 34 (sodium ph	Ribosomal_L20,Na_Pi_cotra	3.1
	447164	AF026941	Hs.17518	vipirin; similar to inflammatory r	MoaA_NifB_PqqE:TM;	3.1 3.1
	414907	X90725	Hs.77597	polo (Drosophia)-like kinase	Ribosomal_L37ae,pkinase,P	3.1
45	418613	AA744529	Hs.86575	mitogen-activated protein kinase ki gb:to16h12.x1 NCI_CGAP_Ut2 Homo sap	pkinase,CNH;TM;	3.1
43	406734 410188	Al565616 Al096739	Hs.107260	hypothetical protein OKFZp586H0623	Ricin_B_lectin,Glycos_tra	3.1
	437959	AI472068	Hs.375604	KIAA1856 protein	elF5_elF2B,W2;TM;	3.1
	406764	AA429825	Hs.343443		Ribosomal_L36e;	3.1
	406637	U14966	Hs.180946	ribosomal protein L5	Ribosomal_L18p;	3.1
50	451080	H41082	Hs.271783		is an ion also TARPO	3.1 3.1
	414875	H42679	Hs.77522	major histocompatibility complex, c	ig,MHC_II_alpha:TM;SS DENN,dDENN,uDENN;TM;SS=	3.1
	416365 400261	U15131	Hs.79265	suppression of tumorigenicity 5 Eos Control	ig,MHC_II_beta;TM;SS	3.1
	412270	AC005262	Hs.73797	guanine nucleotide binding protein	G-alpha, arf; TM;	3.1
55	456843	BE301883	Hs.152707	glioblastoma amplified sequence	:	3.1
	443071	AL080021	Hs.8986	complement component 1, q subcompon	C1q,Collagen;SS	3.1
	426196	BE272095	Hs.167791		efhand;SS	3.1
	424010	AL080188	Hs.137556		cadherin;TM;SS	3.1 3.1
60	439975	AW328081	Hs.6817	inosine triphosphatase (nucleoside Homo sapiens cDNA FLJ14192 fis, clo	Ham1p_like;TM;	3.1
UU	450761 418322	R75930 AA284166	Hs.174838 Hs.84113	cyclin-dependent kinase inhibitor 3	Y_phosphatase,DSPc;TM;S	3.1
	432396	AW295956	Hs.11900	hypothetical protein FLJ14972	Xlink,zf-CCCH,G-patch,non	3.1
	407904	W44735	Hs.107260		• • • •	3.1
	452500	AW373011	Hs.54558	hypothetical protein FLJ22222		3.1
65	432171	AI202503	Hs.343661		WD40	3.1
	416768	AA363733	Hs.1032	regenerating islet-derived 1 alpha	lectin_c;TM;SS	3.1 3.0
	442492	AA528489	Hs.234518		Ribosomal_L14; TM;SS	3.0
	421210	U80016	Hs.102598	mucosal vascular addressin cell adh gb:AF150286 Human mRNA from cd34 st	RA,Band_7,MBOAT	3.0
70	439429 447463	AF150286 AW378685	Hs.18625	Mitochondrial Acyl-CoA Thioesterase	Acyl-CoA_hydro;TM;	3.0
, ,	448352	AA337951	Hs.20991	SET domain, bifurcated 1	AhoC-TSA,SET,MBD;TM;SS=	3.0
	428291	AA534009	Hs.183487		·	3.0
	445669	AI570830	Hs.174870) ESTs		3.0
75	452862	AW378065	Hs.8687	ADAMTS2 (a disintegrin-like and me	Pep_M12B_propep.tsp_1,Rep	3.0
75	430069	Al219293	Hs.293660		SPRY,zf-B_box,zf-C3HC4;TM	3.0 3.0
	451028	AA021258	Hs.123073 Hs.286	3 ESTs ribosomal protein L4	Ribosomal_L4;TM;	3.0
	446021 434652	BE389213 AF148713	Hs.200 Hs.125830		WD40,DUF6;	3.0
	425829		Hs.134126		crystall;TM;	3.0
80	424909		Hs.15375		Rhodanese;SS	3.0
	423579	NM_004121	Hs.1675	gamma-glutamyttransferase-like acti	G_glu_transpept;TM;SS	3.0
	444652		Hs.11538		WD40;TM;	3.0
	441283	AA927670	Hs.13170	4 ESTs	CUB,MAM,F5_F8_type_C	3.0

						30
•	437415	AL137400	Hs.306456	pre-mRNA processing factor 18	Band_41,hormone2,Prp18;TM	3.0
	444542	AI161293	Hs.280380	arninopeptidase	NAD_binding,flavodoxin,FA	3.0
	442426	A1373062	Hs.332938	hypothetical protein MGC5370	zf-RanBP,MDM2	30
_	447910	AL137679	Hs.20000	Homo saplens mRNA; cDNA DKFZp434D24	Exonuclease;SS	3.0 3.0
5	426858	NM_004182	Hs.172791	ubiquitously-expressed transcript	DUF232;SS	3.0
	445417	AK001058	Hs.12680	a disintegrin-like and metalloprote	tsp_1,Reprolysin,Pep_M12B	3.0
	430482	AF131810	Hs.241545	hypothetical protein	TM;SS	3.0
	427661	AA410292	Hs.104761	ESTs	wni	3.0
	451876	T63141		gb:yb99a12.s1 Stratagene lung (9372	SH3	3.0
10	453862	AL137493	Hs.35945	Homo sepiens mRNA; cDNA DKFZp434B12	ig:TM;	3.0
	452965	Al904779	Hs.247525	Human DNA sequence from clone RP11-	C2,PHD,RPH3A_effector,zf-	3.0
	441455	AJ271671	Hs.7854	zincfron regulated transporter-lik	Zip;TM;SS	3.0
	452600	AJ910842	Hs.103381	ESTs	Exo_endo_phos TGFb_propeptide,TGF-beta,	3.0
1 =	450775	AA902384	Hs.73853	bone morphogenetic protein 2	GSH_synthase;TM;	3.0
15	417634	W27202	Hs.82327	glutathione synthetase	GSH_Synthese, i.m.	3.0
	415152	W22644	Hs.278712	Homo sapiens cDNA FLJ11074 fis, clo		3.0
	410093	AW589558	Hs.299883	ESTs, Weakly similar to KIAA0970 pr	•	3.0
	412404	AW075995	Hs.86228	TRIAD3 protein	pkinase,RIO1;TM;	3.0
20	443466	BE243123	Hs.321045	(KK-related kinase epsilon; inducib	paios, 100 1, 1 m,	
20		_				
	TABLE 29			مراسية المرازات		
	Pkey:			set identifier number		
	CAT numb		e cluster numb			
25	Accession	; Gen	bank accessio	n numbers		
25	_	04711				
	Pkey	CAT Number	Accession	AW848490 AW849062 AW752597 AW752699		
	458147	1030220_1	4.4000000			
	406855	0_0	AA902829	NM_001020 BC007977 M60854 BM050628 BG82	9809 RE385504 RG744451 81826914 BE440007	BI260656 BE395117 BE389334
30	400233	11259_1	00000000	DHOA460 DIGGD218 D110A376 RC716213 RG71A	IOR RF 197513 AV722219 AW328077 BM424171	BIRSBSD1 WAAGOOOG BYGOS 1838
30			DE202043	0C204022 DIREPOLE DIREPTSA RER21019 RG706	995 RF7919R5 RF9674R4 FH193635 BG761859 B	M46653/ BG/4/165 BG82/400 Al 133300
			D14044E44	01227202 0C400212 DC472722 RC727720 RISS	1880 RC831707 RC324692 RM470427 BUB3889	BG831605 BG/54114 BG420530
			DESABORA	DC294212 DC932271 BC828032 BC481641 RF2	15675 RFR99041 BE271558 BI193807 BI159866	BC413189 BC331119 BH34450 BH11510
			DC760226	DOTESSON RESTANCE REMARKS REALISST RM020598 RGR	31082 BG829943 BG829501 BF306557 BE56251	11 RW020142 RW011210 D1122224
35			014007641	2146A224 DAZE4OG1 DEG72249 REEE3224 REA32	537 RF388168 RM009051 RH92794 BG831002 E	3G830459 BG764737 BG761808
55			DC40170E	DOLOASIA DIMERSES DISSISON RORSIRST ROR	31684 RG829852 RG765030 BG760419 BG76028	99 8C/43/95 RC480300 RC413051
			DC049771	DED76642 DMD42223 RH61140 RG831302 RG8	30033 RGR29626 BM050064 BI193014 BI161360	RP875153 RP 1003 DP 100300
			DISCOSER	DAGG 1002 DIAKERSAL BINDIGETS BITETSEN BITTA	.178 RG481969 RG474870 HF974048 BF9/1122	RF (41402 RF 232503 DPD25675
			0.0031460	OC 400006 BM413638 BC043539 BC831013 RG	829471 RG686284 RG337575 BG336551 BF2060	3// BIX28301 BI100340 BG102023
40			05403073	DM460643 DM03991 DC9330M3 BC831333 RHS	4545 RU16096R RG755930 BG706018 BE743865	MM402142 BC031221 DC/14230
			00000161	PERMANEN PRINCESON PRINCESON PRINCESON PROPERTY.	7091 RGS46643 RF984863 RH60206 BIZZ640Z B	1/2/6336 AVV3/8/30 BC333430 BF3/2434
			DEDDOOD	DISCORDE DISCORDE L D.C. 200764 R.C. 200860 R.C.75	8360 RF568278 RI818782 BI457127 BG831491 B	(G/59884 AI830010 BF300301 BE301230
			DI4C1472	DI 16772 DC027162 DC025088 RG335419 RG10	QANA A1979NKR RE9NK354 KE4UX564 KMU45UUU	BC273011 BC505134 DC222101
			DEDATACA	ncccons+ p/030061 B/3/0306 B/3/60397 AIQ	22228 RF 301975 AW516455 HG48U919 HG48U0	(0 AVV 1300 17 DC33020 1 DE300 137
45			05305747	0C201127 DI102061 DC820757 RC476379 RF3	31536 RF394727 RF257695 BE9U5344 AI4335//	RF934410 BE000225 BE402557
			DCA24766	- n=nA4A77 p=030000 DE000163 DE007908 RE3	95767 AIR71751 KF 744523 BU192663 BU831669	AUUUUZZO BET40000 BEZTZOTO MAURUUTU
			DIALCTON	1 DC202276 DE202022 AW170187 RE720061 RF	3954 IN RE744577 RE392297 BE391448 BE3907	80 RE300051 RE500411 BE200310
			DEMO1567	r pegggg 22 Deggg226 RE726889 RE910504 RE3	90753 RF390131 AA650542 BE744156 BEJY412	2 RF (4550) RE323503 DE325245
			DE004330	: pc370333 pc000036 pc004660 RE393704 RF6	20999 RF515162 RF378753 BE272370 BE90745	8 RE015901 BE335404 DE301000
50			BE907353	BE910491 BE909796 BE905331 AW248173 AIG	83576 BE908826 BE620180 BF037570 BE90831	2 BE015015 BE2303// BE/400/5
			BE394133	3 BE391478 BE910068 BE907185 BE742109 AAS	95746 BE561195 BE908825 BE906472 BE90650	9 BE300017 BE310442 BE314037
			BI261969	BE741707 BE392216 BM042793 BF570283 BI26	2119 BE395707 BE378298 AW327827 BE394427	2 BF 303176 BE203240 A1700312
			BG83029	0 BF569308 BF569156 BI194587 BE390831 BG7	45096 Alb81675 BE395614 AA136372 BE279692	MAGGE AA242240 DE388601 AW404280
			AA305904	F33366 BE394852 F29153 F33618 A1133637 A	(300009 F 34063 F 29455 AU 09909 F AF905005 AF	X00030 XX343243 02300031 XXX404200
55				3 F29022 BF089981 F31013 F24305		
	438912	4071_1		3 R70623 R70523	•	•
	410693	1054267_1		5 AW797320 BE161676 AW797356 AW797352		
	413100	1490226_1		4 BE065168 BE065313 BE065208		
60	406738	0_0	AA58798		1 00000036	
60	459298	90831_2	AL15/65	5 BF802216 R86701 BF802224 R84600 BF35615 2 B1092731 A1765546 AA393801 A1129669 A1393	538 AW519008 AI432598 AW295856 AI650941 A	1470541 AL550388 AA146856 AI074762
	414393	15833_3	AL532974	5 Y 7303063 BIUE3003 5 BIO35131 M1402340 WW32300 I WITS2002 W232	00 M11313000 70-02230 M1120000 1 11000 1 1 1 1	
				7 AA393867 BI052082	•	
	406734	0_0	A1565616	i a1190141 7 x03066 nm_002120 m26040 aw469119 aw46	0127 A1200772 AW518149 A1144456 AW628070	A1629032 A1358810 A1880433 A1440472
<i>(</i>	400261	23110_1	RCOODUS	A1865365 AW014799 A1767973 AW518041 AA9	NO 30R AW/7ERENE	
65	****	450504 4		6 Y/430000 V V63E8E2	73330 ATT 00000	
	439429			6 AV739062 AA835857 \1821021 BF370092 BF370127 BF370060 T62998	1	
	451876	2328579_1	1001417	4821021 Br310032 Br310121 Bi 510000 102530	•	·
	TABLE	200-				
70	Pkey:		nique cumber	corresponding to an Eos probeset		
70	Ref:	č	anuence saum	e. The 7 digit numbers in this column are Genbar	ik identifier (GI) numbers. "Dunham, el al." refers	to the publication entitled "The DNA
	rvei.		edocure again	man chromosome 22" Dunham, et al. (1999) Natur	e 402:489-495.	
	Strand:			trand from which exons were predicted.	• •	
	Nt_posi			slide positions of predicted exons.		
75	· · Chro			end browning at the colored area.		
	Pkey	Ref	Strand	Nt_position		
	401699		Minus	33285-34084		
	402241		Minus	125073-125206,130996-131125		
	403364		Plus	120351-120465		
80	405201		Plus	36934-37314		
	400785	8131682	Plus	43113-43967		
	403943	7711864	Plus	100742-100904,101322-101503		
	404854	7143420	Plus	14260-14537		

PCT/US02/29560 WO 03/025138

5	404243 403246 404864 403252 404913 402534 402475 404233	5672609 7637831 5263010 7677983 7341740 9801061 7547191 8218045	Ptus Minus Ptus Ptus Ptus Ptus Minus Minus	74695-75123 143547-143654,143741-143900 94495-94661,95055-95195,97396-97506,9760 102214-102692 97717-97976 58989-59457 65363-65725 84791-85123 132847-133917
10	401174 403694	9438414 7107765	Plus	142925-143080,165505-166186,167486-16763

TABLE 30A: ABOUT 282 GENES UP-REGULATED IN GLIOMA COMPARED TO NON-MALIGNANT ADULT BRAIN TISSUES THAT ARE LIKELY TO ENCODE EXTRACELLULAR

TABLE 30A: ABOUT 282 GENES UP-REGULATED IN GLOWAR COMPANED TO NOT CELL-SURFACE PROTEINS

OR CELL-SURFACE PROTEINS

Table 30A lists about 282 genes up-regulated in glioma compared to non-malignant adult brain tissues that are likely to encode extracellular or cell-surface proteins. These were selected as for Table 28A, except that the ratio of "average" glioma to "average" normal adult issues was greater than or equal to 4.0, the "average" glioma level was set to the 99th selected as for Table 28A, except that the ratio of "average" glioma round adult brain tissue level was set to the 75th percentile value amongst various glioma specimens, the "average" glioma value was greater than or equal to 50 units (this selects for the most abundant of the up-regulated genes), and the predicted protein contained a structural them of equal to 50 units (this selects for the most abundant of the up-regulated genes), and the predicted protein contained a structural domain that is indicative of extracellular localization (e.g. ig. fn3, efg., 7tm domains, signal sequences, transmembrane domains). Predicted protein domains are noted.

Pkey:

Unique Eos proteset Identifier number

Execusic

Livingen number 15

20

Unigene number Unigene gene title UnigenelD: Unigene Title:

Protein Domains: Predicted Protein Domains glioma vs. non-malignant adult brain tissues likely to encode extracellular or cell-surface proteins 25 R1:

				U-lean Tile	Protein Domains	R1
	Pkey	, 400000.	UniGene ID	Unigene Title immunoglobutin heavy constant gamma	ig;TM;	37.6
	406868	AA505445	Hs.300697	gb:Human omega light chain protein	TM:	22.7
	407241	M34516		amplified in osteosarcoma	pkinase,LRR;TM;SS	22.7
30	414477	U41635	Hs.76228	glycoprotein (transmembrane) nmb	PKD:TM:SS	15.4
	417512	X76534		ribosomal protein L18a	Ribosomal_L18ae;TM;	14.2
	406803	H42321	Hs.163593		ig,Peptidase_M10;TM;SS=	12.8
	429707	W76631	Hs.211819	matrix metalloproteinase 238	SEA:TM;SS	12.8
	419092	J05581	Hs.89603	mucin 1, transmembrane	pkinase, DAG_PE-bind, RBD;T	12.4
35	414738	L24038	Hs.77183	v-raf murine sarcoma 3611 viral onc	7tm_3,none	11.6
•	441384	AA447849	Hs.288660	Homo sapiens cDNA: FLJ22182 fis, cl	ig,HSP70,Ppx-GppA;TM;SS	11.0
	406621	X57809	Hs.181125	immunoglobulin lambda locus	none	11.0
	410584	AB011112	Hs.64742	KIAA0540 protein	pkinase,none	10.7
	426395	BE151985	Hs.355669	hypothetical protein FLJ23316	ig:TMtSS	10.7
40	425184	8E278288	Hs.155048	Lutheran blood group (Auberger b an	ion_trans;TM;SS	10.3
	430379	AF134149	Hs.240395	potassium channel, subfamily K, mem	TM;	9.9
	408972	AL050100	Hs.49378	DKFZP586D0919 protein	11.8:55	9.9
	446921	AB012113	Hs.16530	small inducible cytokine subfamily	Pep_M12B_propep,tsp_1,Rep	9.7
	452862	AW378065	Hs.8687	ADAMTS2 (a disintegrin-like and me	connexin:TM;SS	8.5
45	418101	AL047476	Hs.296310	gap junction protein, alpha 4, 37kD		8.4
7.5	400290	H18836	Hs.31608	hypothetical protein FLJ20041	Cys_knot	8.1
	401699			Target Exon	TM;	8.1
	423309	BE006775	Hs.126782	sushi-repeat protein	sushi,HYR;SS	7.9
	427600	AW630918	Hs.179774	proteasome (prosome, macropain) act	PA28_alpha,PA28_beta;	7.8
50	436906	H95990	Hs.181244	major histocompatibility complex, c	ig,MHC_I;TM;SS	7.7
30	425335	BE394327	Hs.296267	follistatin-like 1	efnand,kazal,arf,ras,7tm_	7.7
-	413011	AW068115	Hs.821	biglycan	LRR,LRRNT;SS	7.7
	446295	Al355029	Hs.101660	ESTs. Weakly similar to T14171 atax	UM	7.6
	436398	H87136	Hs.5174	ribosomal protein \$17	Ribosomal_S17e,PolyA_pol;	7.0 7.4
55		H91923	Hs.110024	NM 020142:Homo sapiens NADH:ubiquin	none	
22	435013	AI623488	Hs.333488	Homo sagiens, clone IMAGE:3603998,	TM;SS	7.4
	431809	X80695	Hs.151134	oxidase (cytochrome c) assembly 1-4	60KD_IMP;TM;	7.3
	424508 438560	AA481690	Hs.300697		ig .	7.3
		X82494	Hs.198862		EGF, ANATO, TIL, spidertoxin	7.3
60	429297	AW952018	Hs.201398		C1q,Collagen;TM;SS	7.2
OO	450463	W40277	Hs.81994	glycophorin C (Gerbich blood group)	TM;	7.2
	417342		Hs.76901	for protein disulfide isomerase-rel	thiored;SS	7.2
	414688	A1750246	Hs.75721	profilin 1	profilin;TM;	7.1
	414044		NS./3/21	NM_025204*:Horno sapiens hypothetica		7.1
	404864		Hs.28081	eukaryotic translation initiation f	rrm,7tm_1,SNF;TM;	7.0
65	452127		Hs.73239	hypothetical protein FLJ10901	:SS	7.0
	412115				none	6.9
	409826			DKFZP564C1940 protein	kil_recept_a;TM;	6.9
	434343		Hs.3804	eukaryotic translation elongation f	COX8,SHMT,MIF,GST_C,EF1G_	6.9
70	427714		Hs.2186		MHC_tl_alpha.ig,none	6.9
70	437259		Hs.12069		7tm 1;TM;	6.8
	429212		4 Hs.19825		Neur_chan_LBD,Neur_chan_m	6.8
	448988		Hs.22785		TNF:TM:SS	6.8
	423505		Hs.12970		TM:	6.7
	413053				Ribosomal_L13,LACT,arf,ra	6.7
75	430542		Hs.11912		arf.ras:TM:	6.6
	43590		Hs.11079	6 SAR1 protein	bZiP;TM;	6.4
	42930	7 AU076592	Hs.19895		none	6.4
	43738	8 AL359586			taminin_EGF,taminin_G,Tro	6.3
_•-	41571				filament bZIP Apolipoprot	6.3
80	40673				20G-Fell_Oxy;TM;SS	6.3
- •	41129			growth suppressor 1		6.3
	44132		Hs.7771	B-cell associated protein	Band_7;TM;	6.3
	44463		Hs.1149	fibulin 5	EGF,TIL;SS	

	413731	BE243845	Hs.75511	connective tissue growth factor		Cys_knot,tsp_1,vwc,IGFBP;	6.2
	422901	R81935	Hs.374568	ribosomal protein L44		sushi,none	6.2
	430397	AI924533	Hs.105607	bicarbonate transporter related pro		HCO3_cotransp;TM;	6.1
5	429630	M85289	Hs.211573	heparan sulfate proteoglycan 2 (per		EGF,ig,laminin_B,laminin_ CARA CommbionorTARCC	6.1
J	434867 431449	AF159442 M55994	Hs.103382 Hs.256278	phosphotipid scramblase 3 turnor necrosis factor receptor supe		SAPA,Scramblase;TM;SS TNFR_c6;TM;SS	6.1 6.1
	440676	NM_004987	Hs.112378	LIM and senescent cell antigen-like		LIM;SS	6.0
	424658	NM_002406	Hs.151513	mannosyl (alpha-1,3-)-glycoprotein		GNT-I,Glycos_transf_2;TM=	5.9
	439310	AF086120	Hs.102793	ESTs		casein_kappa,pkinase,ig,n	5.9
10	410169	AJ373741	Hs.59384	hypothetical protein MGC3047		ig;TM;	5.8
	423007	AA320134	Hs.196029	Homo sapiens mRNA for KIAA1657 prot		TIMP,none	5.8
	414265	BE410411	Hs.75864	endoplasmic reticulum glycoprotein		none	5.8
	427715	BE245274	Hs.180428	KIAA1181 protein		TM; TNFR_c6,death,Lipoprotein	5.8 5.8
15	409220 450690	BE243323 AA296696	Hs.51233 Hs.333418	turnor necrosis factor receptor supe FXYD domain-containing ion transpor		ATP1G1_PLM_MAT8;TMtSS	5.8
13	433848	AF095719	Hs.93764	carboxypeptidase A4		Zn_carbOpept,Propep_M14;T	5.7
	446404	AA019961	Hs.26216	LOC50627		none	5.7
	441641	AI650417	Hs.247068	ESTs, Moderately similar to ALU8_HU		Pterin_4a,fibrinogen_C,Co	5.7
•	418875	W19971	Hs.233459	ESTs		Xlink,none	5.7
20	424748	AA346257	Hs.134933	ESTs		none	5.7
	439737	AI751438	Hs.41271	Homo sapiens collagen, type VIII, a		C1q,Collagen,none	5.7 5.6
	448950 406654	AF288687 M90686	Hs.9275 Hs.73885	CGI-152 protein HLA-G histocompatibility antigen, c		E1-E2_ATPase,Hydrolase;TM ig,MHC_I;TM;SS	5.6
	423084	AU076474	Hs.123178	translocase of inner mitochondrial		mn	5.6
25	402241	7,00,04,4	12.1250	Target Exon		p450;TM;SS	5.6
	425157	NM_006227	Hs.283007	phospholipid transfer protein		LBP_BPI_CETP,LBP_BPI_CETP	5.6
	428343	AL043021	Hs.12705	ESTs		WD40;SS	5.6
	447990	BE048821	Hs.20144	small inducible cytokine subfamily	•	IL8;SS	5.6
20	412607	Z33642	Hs.74115	immunoglobulin superfamily, member		ig;TM;SS	· 5.5
30	447625	AW505364	Hs.19074 Hs.42331	LATS (large tumor suppressor, Droso		pkinase,pkinase_C,UBA,Pol Ephrin;TM;SS	5.5 5.5
	408056 445960	AA312329 AI268399	Hs.140489	ephrin-A4 ESTs, Weakly similar to LIN1_HUMAN		zf-C2H2,bZiP,none	5.5
	406874	AW161706	Hs. 180842	ribosomal protein L13		Ribosomal_L13e;SS	5.4
	418558	AW082266	Hs.86131	Fas (TNFRSF6)-associated via death		death,DED;SS	5.4
35	414638	W03516	Hs.76698	stress-associated endoplasmic retic		TM;SS	5.4
	409190	AU076536	Hs.50984	sarcoma amplified sequence		transmembrane4;TM;SS	5.4
	429150	AF120103	Hs.197366	smoothened (Orosophila) homolog		COX8,SHMT,MIF,GST_C,EF1G_	5.3
	453099	H62087	Hs.31659	thyroid hormone receptor-associated		WD40;TM;	5.3 5.3
40	414443	AU077268	Hs.76144 Hs.131704	platelet-derived growth factor rece ESTs		ig.pkinase;TM; CUB,MAM,F5_F8_type_C,none	5.3
40	441283 414249	AA927670 A1797994	Hs.279929	gp25L2 protein		Sulfotransfer,EMP24_GP25L	5.3
	451154	AA015879	Hs.33536	ESTs		TIMP,none	5.2
	406655	M21533	Hs.277477	major histocompatibility complex, c		ig,MHC_I;TM;SS	5.2
	406656	M16714	Hs.89643	major histocompatibility complex, c		transketolase,transket_py	5.2
45	449224	AW995911	Hs.299883	hypothetical protein FLJ23399		fn3;TM;	5.2
	422562	A1962060	Hs.118397	AE-binding protein 1		Zn_carbOpept,F5_F8_type_C	5.2
	436127	W94824	Hs.11565	RIKEN cDNA 2010100012 gene		TM;SS	5.2 5.2
	428327 427080	AW206236 AW068287	Hs.28773 Hs.301175	ESTs ras-related C3 botulinum toxin subs		cystatin,Coprogen_oxidas, ras;TM;	5.2 5.2
50	414624	BE389320	Hs.23628	3 beta-hydroxy-delta 5-C27-steroid		none	5.2
50	430281	AI878842	Hs.237924	CGI-69 protein		mito_cerr,homeobox;TM;S	5.2
	426433	L38969	Hs.169875	thrombospondin 3		TSPN,tsp_3,EGF,toxin;TM	5.1
	432716	A1762964	Hs.205180	ESTs		LRR.UPAR_LY6;TM;	5.1
E	451564	AU076698	Hs.132760	hypothetical protein MGC15729		sugar_tr,Condensation;TM=	5.1
55	409340	BE174629	Hs.321130	hypothetical protein MGC2771		aa_permeases,pyridoxal_de TM:SS	5.1 5.1
	432680 404913	T47364	Hs.278613	interferon, alpha-inducible protein NM_024408*:Homo sapiens Notch (Dros		EGF, ank, notch, metalthio, E	5.1
	409485	S80990	Hs.252136	ficolin (collagen/fibrinogen domain		Collagen,fibrinogen_C;TM=	5.1
	432078	BE314877	Hs.24553	hypothetical protein FLJ12541 simil		TM:SS	5.1
60	406687	M31126	Hs.352054	matrix metalloproteinase 11 (strome		hemopexin,Peptidase_M10;T	5.1
	423712	W46802	Hs.81988	disabled (Drosophila) homolog 2 (mi		PID,MACPF,ldl_recept_a,ts	5.0
	441595	AW206035	Hs.356457	ESTs		sugar_tr,none	5.0
	450435	AI695975	Hs.201805	ESTs		EGF,taminin_B,taminin_EGF	5.0 5.0
65	443177 433435	BE268461 BE545277	Hs.202 Hs.340959	benzodiazapine receptor (peripheral Ts translation elongation factor, m		TspO_MBR;TM;SS EF_TS,UBA;	5.0
UJ	426386	AA748850	Hs.125830	bladder cancer overexpressed protei		none	5.0
	419913	AW270040	Hs.34455	ESTs		EPH_tbd,fn3,pkinase,	5.0
	446696	AF279265	Hs.298476			Sulfate_transp,STAS,xan_u	5.0
	448997	AA130390	Hs.25549	hypothetical protein FLJ20898		TM;SS	5.0
70	413891	BE271020	Hs.355753			none	5.0
	453143	AA382234	Hs.356289			serpin;SS	5.0
	448249	AW855331	Hs.337124			carb_anhydrase,UCH-1,UCH-	5.0
	412819 426059	T25829 BE292842	Hs.24048 Hs.166120	FK506 binding protein precursor interferon regulatory factor 7		FKBP;TM;SS IRF;SS	5.0 5.0
75	432295	BE091049	Hs.343665			Ribosomat_S8,RNase_PH,KH-	5.0
	412540	C18341	Hs.73999	thyroid hormone receptor interactor		SH3, FCH; SS	5.0
	414465	AW270645	Hs.76194	ribosomal protein S5		Ribosomal_S7;	5.0
	456655	AI376736	Hs.111779			kazal;SS	5.0
00	421794	X86096	Hs.108371			E2F_TDP,KOW,Ribosomal_L14	4.9
80	444824	AA843575	Hs.12056	asialoglycoprotein receptor 1		lectin c, Tropomyosin; TM	4.9 4.9
	438278 418140	BE409248 BE613836	Hs.57988 Hs.83551	hypothetical protein FLJ22357 simil microfibrillar-associated protein 2		TFIIS,RNA_POL_M_15KD,UPF0 TM:SS	4.9 4.9
	429457	BE243065	Hs.202955			Cys-protease-3C;TM;	4.9
	-50-01			• • • • • • • • • • • • • • • • • • • •	051		
					376		

449475 Al348027 Hs.108557 hypothetical protein PP1057 transmembrane4; IM;SS MCM:TM; Richard PR113008 Hs.15462 minichromosome maintenance deficien ribosomal protein S20 rone minichromosome maintenance deficien ribosomal protein S20 rone Ribosomal_S10; TM; none 145209 F00183 Hs.172004 titin rone 147380 NM_005534 Hs.177559 Hs.198265 rone 147380 NM_2016534 Hs.177559 Hs.198265 rone 145021 R54409 Hs.301693 Hs.27596 Hs.11900 hr.32396 AW295956 Hs.11900 hr.32396 AW295956 Hs.1900 hr.324597 D31365 Hs.24220 hr.324570 Hs.24570 rone roscrosis factor (TNF superfam hypothetical protein rome consist factor (TNF superfam hypothetical protein FL114972 rone roscrosis factor (TNF superfam hypothetical protein rome consist factor (TNF superfam hypothetical protein from clone 247 rone roscrosis factor (TNF superfam hypothetical protein from clone 247 rone roscrosis factor (TNF superfam hypothetical protein from clone 247 rone roscrosis factor (TNF superfam hypothetical protein from clone 247 rone roscrosis factor (TNF superfam hypothetical protein from clone 247 rone roscrosis factor (TNF superfam hypothetical protein from clone 247 rone roscrosis factor (TNF superfam hypothetical protein from clone 247 rone roscrosis factor (TNF superfam hypothetical protein from clone 247 rone roscrosis factor (TNF superfam hypothetical protein from clone 247 rone roscrosis factor (TNF superfam hypothetical protein from clone 247 rone roscrosis factor (TNF superfam hypothetical protein from clone 247 rone roscrosis factor (TNF superfam hypothetical protein from clone 247 rone roscrosis factor (TNF superfam hypothetical protein from clone 247 rone roscrosis factor (TNF superfam hypothetical protein from clone 247 rone roscrosis factor (TNF superfam hypothetical protein from clone 247 rone roscrosis factor (TNF superfam hypothetical protein from clone 247 rone roscrosis factor (TNF superfam hypothetical protein for rone close 247 rone roscrosis factor (TNF superfam hypothetical protein for rone close 247 rone roscrosis factor (TNF superfam hypothetic	4.9 4.9 4.9 4.9 4.9 4.9 4.9
442110 AF113008 Hs.8102 nibosomal protein S20 histormal protein from clone 247 histormal protein fr	4.9 4.9 4.9 4.9 4.9
5 415209 F00183 Hs.172004 bitin hypothetical protein from clone 247 421567 A1721017 Hs. 198265 427380 NM_005534 Hs.177559 Hs.177559 Interferon garman receptor 2 (interferon garman recept	4.9 4.9 4.9 4.9
421567 A1792201 Hs. 198265 427380 NM_005534 Hs. 177559 431303 AW241605 Hs. 177559 432396 AW295956 Hs. 177559 43603 R54409 Hs. 301693 hrs. 241570 Hs. 241570 449957 D31365 Hs. 24220 hypothetical protein FLJ14972 Nink, ZI-CCCH, G-patich, non none 430498 X02910 Hs. 241570 hrs. 241570 hypothetical protein FLJ14972 Nink, ZI-CCCH, G-patich, non none 430498 X02910 Hs. 241570 hrs. 241570 hypothetical protein FLJ14972 Nink, ZI-CCCH, G-patich, non none 449957 D31365 Hs. 24220 hypothetical protein FLJ14972 Nink, ZI-CCCH, G-patich, non none 449957 Hs. 91956 hrs. 24250 hypothetical protein FLJ14972 Nink, ZI-CCCH, G-patich, non none 449957 D31365 Hs. 24250 hypothetical protein FLJ14972 Nink, ZI-CCCH, G-patich, non none 449957 D31365 Hs. 24250 hypothetical protein FLJ14972 Nink, ZI-CCCH, G-patich, non none 449957 D31365 Hs. 24250 hypothetical protein FLJ14972 Nink, ZI-CCCH, G-patich, non none 449957 D31365 Hs. 24250 hypothetical protein FLJ14972 Nink, ZI-CCCH, G-patich, non none 449957 D31365 Hs. 24250 hypothetical protein FLJ14972 Nink, ZI-CCCH, G-patich, non none 449957 D31365 Hs. 24210 hypothetical protein FLJ14972 Nink, ZI-CCCH, G-patich, non none 449957 D31365 Hs. 2421570 hypothetical protein FLJ14972 Nink, ZI-CCCH, G-patich, non none 449957 D31365 Hs. 2421570 hypothetical protein FLJ14972 Nink, ZI-CCCH, G-patich, non none 449957 D31365 Hs. 2421570 hypothetical protein FLJ14972 Nink, ZI-CCCH, G-patich, non none 449957 D31365 Hs. 2421570 hypothetical protein FLJ14972 Nink, ZI-CCCH, G-patich, non none 449957 D31365 Hs. 2421570 hypothetical protein FLJ14972 Nink, ZI-CCCH, G-patich, non none 449957 D31365 Hs. 2421570 hypothetical protein FLJ14972 Nink, ZI-CCCH, G-patich, non none 449957 D31365 Hs. 2421570 hypothetical protein FLJ14972 Nink, ZI-CCCH, G-patich, non none 449957 D31365 Hs. 2421570 hypothetical protein FLJ14972 Nink, ZI-CCCH, G-patich, non none 449957 D31365 Hs. 2421570 hypothetical protein FLJ14972 Nink, ZI-CCCH, G-patich, non none 449957 D31365 Hs. 2421570 hypothetical protein FLJ14972 Nink, ZI-CCCH, G-patich, n	4.9 4.9 4.9
427380 Mk 005534 ks.177559 interferon garma receptor 2 (interf	4.9
A31303	
10 415021 R54409 Hs.301693 Hmor agriers, clone IMAGE:3638994, tumor necrosis factor (TNF superfam hypothetical protein FL114972 Xink,zf-CCCH,G-patich,non none 430498 X02910 Hs.241570 tumor necrosis factor (TNF superfam hypothetical protein FL114972 Xink,zf-CCCH,G-patich,non none TNF:TM;SS tumor necrosis factor (TNF superfam hypothetical protein FL114972 Xink,zf-CCCH,G-patich,non none TNF:TM;SS tumor necrosis factor (TNF superfam hypothetical protein FL114972 Xink,zf-CCCH,G-patich,non none TNF:TM;SS tumor necrosis factor (TNF superfam hypothetical protein FL114972 Xink,zf-CCCH,G-patich,non none TNF:TM;SS tumor necrosis factor (TNF superfam hypothetical protein FL114972 Xink,zf-CCCH,G-patich,non none TNF:TM;SS tumor necrosis factor (TNF superfam hypothetical protein FL114972 Xink,zf-CCCH,G-patich,non none TNF:TM;SS tumor necrosis factor (TNF superfam hypothetical protein FL114972 Xink,zf-CCCH,G-patich,non none TNF:TM;SS tumor necrosis factor (TNF superfam hypothetical protein FL114972 Xink,zf-CCCH,G-patich,non none TNF:TM;SS tumor necrosis factor (TNF superfam hypothetical protein FL114972 Xink,zf-CCCH,G-patich,non none TNF:TM;SS tumor necrosis factor (TNF superfam hypothetical protein FL114972 Xink,zf-CCCH,G-patich,non none TNF:TM;SS tumor necrosis factor (TNF superfam hypothetical protein FL114972 Xink,zf-CCCH,G-patich,non none TNF:TM;SS tumor necrosis factor (TNF superfam hypothetical protein FL114972 Xink,zf-CCCH,G-patich,non none TNF:TM;SS tumor necrosis factor (TNF superfam hypothetical protein fL114972 Xink,zf-CCCH,G-patich,non none TNF:TM;SS tumor necrosis factor (TNF superfam hypothetical protein fL114972 XInk,zf-CCCH,G-patich,non none TNF:TM;SS tumor necrosis factor (TNF superfam hypothetical protein fL114972 XInk,zf-CCCH,G-patich,non none TNF:TM;SS tumor necrosis factor (TNF superfam hypothetical protein fL114972 XInk,zf-CCCH,G-patich,non none TNF:TM;SS tumor necrosis factor (TNF superfam hypothetical protein fL114972 XIII xf-patich,non none TNF:TM;SS tumor necrosis factor (TNF superfam hypothetical pr	4.9
10 415021 R54409 Hs.301693 Homo sapiens, clone IMAGE:3538994, mone 439494 Ms.241570 tumor necrosis factor (TNF superfam hypothetical protein PL6 protein ras homolog gene family, member C Ribosomal_L20,Na_Pi_cotra	4.8
430498 X02910 Hs.241570 tumor necross factor (1NF superam hypothetical protein hypothetical protein hypothetical protein GMPdecase;TM;SS 427508 L25081 Hs.179735 ras homolog gene family, member C ras, none Ribosomal_L20,Na_Pi_cotra	4.8
449507 D31305 Hs.19568 Hs.19568 Pl.6 protein as homolog gene family, member C ras, none Ribosomal_L20,Na_Pi_cotra	4.8
15003 BE20279 Rs. 179735 ras horndog gene family, member C ras, none Ribosomal_L20,Na_Pi_cotra	4.8
15 421502 AF111856 Hs. 105039 solute carrier family 34 (sodium ph	4.8
15 12:00	4.8
	4.7 4.7
411281 BE392792 Hs.4786 Homo sepiens CDNA: FLJZZ849 fs, cl cannetin	4.7
414045 NM_002951 Hs.75722 ribophorin II gpdh.gpdh_C.piii_assembly	4.7
431630 T10043 FIS.211001 SHORE RESERVE OF COMMON OF COMMON PARTIES OF COMMON OF COMMON PARTIES OF COMMON OF COMMON PARTIES OF COMMON PARTI	4.7
2U 412090 ANOU4131 15.313370 India transmembraned TM:SS	4.7
451508 Y15187 Hs 26880 endothelin converting enzyme-fike 1 Peptidase_M13;TM;	4.7
A20097 AVANCER 23 He 119206 insulin-like growth factor binding zf-C2H2,ig,none	4.7 4.7
444542 A1161293 Hs.280380 aminopeptidase MAD Tital (1977)	4.7
2.) 429833 MM_U12U19 115.200027 disayigiyee.co o ayasaa a	4.7
4303/0 AA003304 FIS.03002 FIG. 100 FIS.03002 MHC III sinha in none	4.7
438308 130003 113.11133 1130 1130 1130 1130 11	4.7
A201486 AE(136365 Hs 98303 caveolin 3 Caveolin;TM;	4.6
3.0 435123 AW205274 Hs.154695 phosphomannomutase 2 PMM;SS	4.6 4.6
439512 AA418287 Hs.58093 Homo sapiens, Clone IMAGE: 3103399, Earlinia: Edition (Control of the Image)	4.6
418424 113022 IIS.03001 total to the collection of the CAUCA SPRY none	4.6
433350 6E363132 Fis.10322 Final March 1	4.6
43/259 AAZ81033 ISSZ 76300 NUTATION (The and matellineants to 1 Rengilysin Pen M128	4.6
437408 At 359598 Hs 36606 Homo sapiens mRNA; cDNA DKFZp547808 none	4.6
427349 AA360154 Hs. 177415 Finkel-Biskis-Reitly murine sarcoma ubiquitin; i Wc	4.6 4.6
418918 X07871 Hs.89476 CD2 antigen (p50), sheep red blood (g:1M;55)	4.6
421310 AW630087 Hs.103315 trinucleotide repeat containing 1 PHD 421310 AW630087 Hs.103315 trinucleotide repeat containing 1 PH	4.6
42/369 NM_001303 FIS.2230 Processor Representation Amountain transp FecCO.TM=	4.6
44/800 AF 193007 (13.13103) (13.13103) (13.13103) (13.13103) (13.13103) (13.13103)	4,6
418916 BE392781 Hs.89474 ADP-moosylation raction o 425720 AA362394 Hs.293984 hypothetical protein MGC13102 TM-SS CHORINACS	4.6
A199A2 1125138 Hs 93841 potassium large conductance calcium CaKB;TM;SS	4.6
45 403105 Target Exon ISK_Channet; I M;SS	4.6 4.6
418067 Al127958 Hs.83393 cystatin E/M CTP_CTC_TM	4.5
42/863 AF 103/12 FIS.101602 MEZ 07/00/4 404/00 045 DOS CT03/4 PLIM 0009	4.5
458147 AW/32337 guille 10 10 10 10 10 10 10 10 10 10 10 10 10	4.5
50 427136 At 117415 Hs 173716 a disintegrin and metalloproteinase	4.5
458766 AW183618 Hs.55610 solute carrier family 30 (zinc tran Cation_efflux; TM; SS	4.5 4.5
445033 AV652402 Hs.72901 cyclin-dependent kinase inhibitor 2 and	4.5 4.5
441201 BE001247 F35.144004 E013	4.5
439/20 Al333202 HS.STAT TANKS SEPTEMBER OF THE BOY OF CHICATEM	4.5
55 410184 AW503667 Hs.59545 ring finger protein 15 431760 NM_005317 Hs.268531 granzyme M (lymphocyte met-ase 1) typsin:TM:SS	4.5
446990 A1354717 Hs.223908 ESTs transmemorane4	4.5
407366 AF026942 Hs. 17518 gb:Homo sapiens cig33 mRNA, partial ISK	4.5 4.5
426156 BE244537 Hs. 167382 natriuretic peptide receptor A/guan ANF_receptor,guanylate_cy 60 43044 A1975738 Hs. 16857 cysteine-rich annipoentic inducer. Cys_knot_tsp_1,vwc.IGFBP;	4.5
00 442941 A0070720 13.5007 System of the SS	4.5
	4.4
431116 A1002030 13.00000 E013 11.000124 IIO mo:TM:	4.4
457657 AW411509 Hs.352567 hypothetical protein PRO2121 UQ_con;TM;	
457167 AW411509 Hs.352567 hypothetical protein PRO2121 UQ_con;TM; 437016 AU076916 Hs.5398 guarine monphosphate synthetase PHD,SET,zf-CXXC,EGF,ank,r 429497 AR028953 Hs.204121 KIA41030 protein fi3;TM;	4.4
457657 AW411509 Hs.352567 hypothetical protein PRO2121 UQ_ con;TM; 437016 AU076916 Hs.5398 guarine monphosphate synthetase PHD,SET,zt-CXXC,EGF,ank,r 429497 AB028953 Hs.204121 KIAA1030 protein 65 A44990 S69115 Hs.10306 natural killer cell group 7 sequenc PMP22_Claudin;TM;SS	4.4
457657 AW411509 Hs.352567 hypothetical protein PRO2121 UQ. con;TM; 437016 AU076916 Hs.5398 guarine monphosphate synthetase Hs.204121 KIAA1030 protein Hs.204121 KIAA1030 protein Hs.204121 Hs.10306 hs.204121 KIAA1030 protein Hs.204121 KIAA	4.4 4.4
1.502/030 1.50	4.4
457657 AW411509 Hs.352567 hypothetical protein PRO2121 UQ_con;TM; 437016 AU076916 Hs.5398 guanine monphosphate synthetase flat flat flat flat flat flat flat flat	4.4 4.4 4.4
August A	4.4 4.4 4.4 4.4 4.4
457657 AW411509 Hs.352567 hypothetical protein PRO2121 UQ_con;TM; 437016 AU076916 Hs.5398 Hs.5264121 guanine monphosphate synthetase KIAA1030 protein Hs.10306 A54095 AF039237 Hs.288600 Hs.73797 A06729 AA069711 4067129 AA069711 404610 TO 422311 AF073515 Hs.114948 Hs.10306 receptor-file factor 1 42391 AF073515 Hs.114948 Hs.198253 major histocompatibility complex, c	4.4 4.4 4.4 4.4 4.4 4.4
457657 AW411509 Hs. 352567 hypothetical protein PRO2121 hypothetical protein PRO2121 UQ. con;TM; PHD,SET,zf-CXXC,EGF,ank,r 429497 AB028953 Hs. 204121 Actual killer cell group 7 sequenc hypothetical protein MGC3123 Hs. 203600 Hs. 288600 Hs. 288600 AF039237 Hs. 288600 Hs. 2886	4,4 4,4 4,4 4,4 4,4 4,4 4,4
457657 AW411509 Hs. 352567 hypothetical protein PRO2121 bypothetical protein PRO2122 bypothetical prote	4.4 4.4 4.4 4.4 4.4 4.4 4.4
1.00 1.00	4.4 4.4 4.4 4.4 4.4 4.4 4.4
1.00 1.00	4.4 4.4 4.4 4.4 4.4 4.4 4.4 4.4
457657 AW411509 Hs. 352567 hypothetical protein PRO2121 hypothetical protein MGC3123 hypothetical prote	4.4 4.4 4.4 4.4 4.4 4.4 4.4 4.4 4.4 4.4
1.00 1.00	4.4 4.4 4.4 4.4 4.4 4.4 4.4 4.4 4.4 4.4
457657 AW411509 Hs. 352567 hypothetical protein PRO2121 yuanine monphosphate synthetase 429497 AB028953 Hs. 204121 A4090 S69115 Hs. 10306 hs. 204121 dutated binding protein MGC3123 yuanine mucleotide binding protein MGC3123 yuanine nucleotide binding protein bypothetical protein MGC3123 yuanine nucleotide binding protein dutated killer cell group 7 sequenc hypothetical protein MGC3123 yuanine nucleotide binding protein bypothetical protein MGC3123 yuanine nucleotide binding protein dutated killer cell group 7 sequenc hypothetical protein MGC3123 yuanine nucleotide binding protein bypothetical protein MGC3123 yuanine nucleotide binding protein bypothetinal bypothetical protein MGC3123 yuanine nucleotide binding protein bypothetinal bypothetinal bypothetinal bypothetinal bypothetinal bypothetinal bypothetinal bypothetinal protein MGC3123 yuanine nucleotide binding protein bypothetinal bypoth	4.4 4.4 4.4 4.4 4.4 4.4 4.4 4.4 4.4 4.4
457657 AW411509 Hs. 352567 hypothetical protein PRO2121 yuanine monphosphate synthetase 429497 AB028953 Hs. 204121 A4090 S69115 Hs. 10306 A54005 AF039237 Hs. 288600 Hs. 73797 A06729 AA069711 406672 AA069711 A406973 AA069711 Hs. 114948 Hs. 198253 Hs. 198253 A43834 A1741510 Hs. 177415 Finkel-Biskis-Reilly murine sarcoma NM_006778:Homo sapiens ring finger 440643 A4071146 Hs. 343354 Hs. 198253 A43930 AF035292 Hs. 6654 A40257 AF14264 Hs. 216381 Hsm sapichs cone HH409 unknown mR	4.4 4.4 4.4 4.4 4.4 4.4 4.4 4.4 4.4 4.4
457657 AW411509 Hs.352567 hypothetical protein PRO2121 yuanine monphosphate synthetase 429497 AB028953 Hs.204121 KIAA1030 protein KIAA1030 protein 420407 AC005262 Hs.73797 yuanine mucleotide binding protein ybzm52b11.s1 Stratagene fibroblast Homo sapiens cDNA FLU11027 fis, clo cytokine receptor-like factor 1 major histocompatibility complex, c 43834 A1741510 Hs.173548 Hs.39573 A4071146 Hs.343354 Hs.395730 AF035292 Hs.6654 Hs.07352 Hs.6654 Hs.07352 Hs.6654 Hs.07552	4.4 4.4 4.4 4.4 4.4 4.4 4.4 4.4 4.4 4.4
457657 AW411509 Hs. 352567 hypothetical protein PRO2121 hypothetical protein PRO2121 dyagnine morphosphate synthetase KIAA1030 protein KIAA1030 protein S69115 Hs. 10306 hs. 204121 dyagnine morphosphate synthetase KIAA1030 protein KIAA1030 protein KIAA1030 protein Hs. 204121 dyagnine mucleotide binding protein MGC3123 guarnine nucleotide binding protein guarnine nucleotide binding protein dyagnine from the protein MGC3123 guarnine nucleotide binding protein dyagnine from the protein	4.4 4.4 4.4 4.4 4.4 4.4 4.4 4.4 4.4 4.4

	433541	AW081538	Hs.220324	hypothetical protein FLJ13052	NAD_kinase;TM;	4.3
	400575			NM_022145:Homo sapiens neuropeptide	7tm_1;TM;SS	4.3
	427661	AA410292	Hs.104761	ESTs	wnt.none	4.3 4.3
5	452056	AW955065	Hs.101150	Homo sapiens, clone IMAGE:4054156,	TM; RNA_pol_L,RNA_pol_L,RasGA	4.3
,	433669 422624	AL047879 BE616678	Hs.194251 Hs.76152	ESTs, Wealthy similar to ALU2_HUMAN KDEL (Lys-Asp-Gtu-Leu) endoptasmic	ER_tumen_recept_none	4.3
	421680	AL031186	Hs.289106	Human DNA sequence from done CTA-9	Collagen; TM; SS	4.3
	422766	AA334108	Hs.159572	heparan sulfate (glucosamine) 3-0-s	none	4.3
	437596	AA761490	Hs.351250	ESTs, Moderately similar to \$65657	pkinase,WD40	4.3
10	419285	D31887	Hs.89868	KIAA0062 protein	Zip;TM;SS	4.3
	453082	H18835	Hs.31608	hypothetical protein FLJ20041	ion_trans;TM;SS	4.2
	410693	BE044206		gb:ho40c08.x1 Soares_NFL_T_GBC_S1 H	C1q,Collagen,cystati	4.2 4.2
	413100 432497	BE065208 AA551104		gb:RC1-BT0314-310300-015-b09 BT0314 ESTs, Moderately similar to ALUC_HU	none	4.2
15	423041	BE170842	Hs.123059	chloride channel Kb	CBS,voltage_CLC;TM;SS	4.2
	449799	Al143466	Hs.125060	ESTs	none	4.2
	438472	AW974907	Hs.86228	TRIAD3 protein	none	4.2
	432179	X75208	Hs.2913	EphB3	EPH_lbd,fn3.pkinase,SAM;T	4.2
20	424488	AK000413	Hs.149227	hypothetical protein FLJ20406	Xlink,zl-CCCH,G-patch;TM=	4.2
20	406809	AF000574	Hs.22405	teukocyte immunogłobulin-lika recep	ig.Gemini_mov;TM;SS	4.2 4.2
	407586	Z37544 M25079	Hs.37121	phospholipase C, beta 3 (phosphatid hemoglobin, beta	C2,PI-PLC-Y,PI-PLC-X;TM globin;TM;	4.2
	407228 450900	H61005	Hs.155376 Hs.37902	ESTs	none	4.2
	410188	AL096739	Hs.107260	hypothetical protein DKFZp586H0623	Ricin_B_lectin,Glycos_tra	4.2
25	458248	BE407379	Hs.108082	ESTs, Weakly similar to T31636 hypo	C1q,Cottagen;TM;SS	4.2
	403138			NM_006056:Homo sapiens G protein-co	7tm_1,KECT;TM;SS	4.2
	432074	AA525248	Hs.149723	ESTs	Y_phosphatase,none	4.2
	438682	AA354489	Hs.375594	EBPS0-PDZ interactor of 64 kD	none TM;SS	4.2 · 4.2
30	401908 451287	AK002158	Hs.26194	C17000154:gi 12003980 gb AAG43830.1 likely homolog of mouse immunity-as	TM;	4.2
50	407904	W44735	Hs.107260	Homo sapiens cDNA: FLJ21278 fis, cl	none	4.1
,	403694			Target Exon	UDPGT-	4.1
	423461	AB020527	Hs.128827	solute carrier family 17 (sodium ph	sugar_tr;TM;	4.1
25	425603	U52219	Hs.158329	G protein-coupled receptor 50	7tm_1;TM;SS	4.1
35	421485	AA243499	Hs.104800	hypothetical protein FLJ10134	TM;SS transmembrane4;TM;SS	4,1 4,1
	414509 423313	AW161311 NM_014269	Hs.76294 Hs.126838	CD63 antigen (melanoma 1 antigen) a disintegrin and metalloproteinase	disintegrin, Reprotysin, Pe	4.1
	432171	AJ202503	Hs.343661	ESTs, Weakly similar to ALUB_HUMAN	WD40	4.1
	434652	AF148713	Hs.125830	bladder cancer overexpressed protei	WD40,DUF6;	4,1
40	429592	AB029041	Hs.209646	KIAA1118 protein	Troponin,Exo_endo_phos,IQ	4.1
	432982	AA531058	Hs.182248	truncated calcium binding protein	OPR,ZZ;TM;	4.1
	424867	AJ024860	Hs.153591	Not56 (D. melanogaster)-like protei	TM;SS Zip;TM;SS	4.1 4.1
	441455 400785	AJ271671	Hs.7854	zinc/iron regulated transporter-lik C11000861:gij9938016/ref NP_064687.	TM;SS	4.1
45	447232	AW499834	Hs.327	interlaukin 10 receptor, alpha	TM;SS	4.1
	450785	AA852713	Hs.108885	Homo sapiens, alpha-1 (VI) collagen	vwa,Collagen;TM;SS	4.1
	424027	AW337575	Hs.201591	ESTs	7tm_2,HRM,none	4.1
	435857	AF253468	Hs.3736	delta-like 4 homolog (Drosophila)	EGF,DSL,EB;TM;SS	4.1
50	437118	AB037857	Hs.300591 Hs.69954	CD9 partner 1	none laminin_B,laminin_EGF,lam	4.1 4.1
50	411410 413902	R20693 AU076743	Hs.75613	taminin, gamma 3 CD36 antigen (collagen type I recep	E2F_TDP,CD36;SS	4.1
	428938	AC002425	Hs.194660	ceroid-lipofuscinosis, neuronal 3,	CLN3;TM;SS	4.1
	453094	AA740928	Hs.27356	ESTs	none	4.1
	440811	BE384713	Hs.74655	ESTs, Weakly similar to T34482 hypo	hormone_rec,zf-C4,none	4.0
55	407287	A1678812	Hs.345139	gb:tu59d08.x1 NCI_CGAP_Gas4 Homo sa	ras,cadherin	4.0
	428028	U52112	Hs.182018	interleukin-1 receptor-associated k	death,pkinase;TM;	4.0 4.0
	428469 423114	BE549205 AU076497	Hs.184488 Hs.1614	flotillin 2 cholinergic receptor, nicotinic, al	none Neur_chan_LBD,Neur_chan_m	4.0
	426858	NM_004182		ubiquitously-expressed transcript	DUF232:SS	4.0
60	444626	AA320893	Hs.117062		pyr_redox;TM;SS	4.0
	TABLE 3		Cb	and International Community		
	Pkey: CAT num		ive Eos proces le cluster numb	set identifier number		
65	Accessio		bank accessio			
	Pkey	CAT Number				
	458147	1030220_1		AW848490 AW849062 AW752597 AW752699		
70	406729 410693	0_0 1054267_1	AA069711	AW797320 BE161676 AW797356 AW797352		
70	413100	1490226_1		BE065168 BE065313 BE065208		
	432497	852_71		R94134 AA551104 AA777322 AI033094 BE247143		
		-	-			
76	TABLE 3					
75	Pkey:	Unid	que number co	rresponding to an Eos probeset The 7 digit numbers in this column are Genbank Ide	olifor ICI) oumbon "Punham at at " and	pre in the nubication entitled "The DNA
	Ret:			rne 7 digit numbers in dies conumit are Genbardt ide in chromosome 22° Dunham, et al. (1999) <u>Nature</u> 402		and the homestern disease. The pre-
	Strand:			and from which exons were predicted.		
~~	Nt_positi			de positions of predicted exons.		
80				N. 10 - 10 - 10 - 10 - 10 - 10 - 10 - 10		
	Pkey	Ref 3176654	Strand	Nt_position 33285-34084		
	401699 404864	5263010	Minus Plus	94495-94661,95055-95195,97398-97506,9760		
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	402241	r690131 N	Vinus 13	25073-125206,130996-131125		
				7717-97976		
	10100		-	1260-14537 4577-145744		
-		,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,		45287-145744 9583-89725,90402-90555,91428-91673		
5		000000	_	4695-75123		
				5821-56037		
				31603-132095		
				64684-165066,167757-168651		
10			Minue 1	26888-127024		
10			Plus 1	42925-143080,165505-166186,167486-16763		
				3113-43967		
	400703	0131002				
					AAAA ACAAAAT ADAN T DOANN TISSUE	
15	TABLE 31A	: ABOUT 189 G	ENES DOWN-F	REGULATED IN GLIOMA COMPARED TO NON- dated in glioma compared to non-malignant adult	MALIGNANT ADULT BROATT 11350L	able 30A, except that the numerator was set to
••	Table 31A	ists about 189 ge	enes down-regu	dated in glioma compared to non-malignant adult alignant brain specimens, the denominator was s	nt to the 90th percentile value amondst val	ious ofiornas, the numerator was greater than
	the 90th per	centile amongst	various non-m	alignant brain specimens, the denominator was a	on in brain tumor vs. normal brain).	
	or equal to	50 units, and the	tabo was grea	ISL (USI) OL GÓRSI IO 573 fro. 575-1000 com a canada	yrat dicari conserve and	
••	Pkey:	Unique	e Eos probeset	identifier number number, Genbank accession number		
20	ExAccn:			number, General accessor nones		
	UnigenelD:	<b>.</b> ~	ne number			
	Unigene Tr		ne gene title sted Protein Do	maine		
	Protein Do	mains: Fleuk	l thine tneament	orain tissue vs. glioma		
25	R1:	IIII	augnant acont	Adm added to grand		D4
23	Char.	ExAcon	UniGene ID	Unigene Title	Protein Domains	R1 14.5
	Pkey	AA417813	Hs.44208	hypothetical protein FLJ23153	F420_oxidored;TM;SS	
	412524 432874	W94322	Hs.279651	melanoma inhibitory activity	SH3;TM;SS	8.3 - 8.2
	452669	AA216363	Hs.262958	hypothetical protein DKFZp434B044	SCP,LCCL;TM;SS	- 8.2 8.2
30	426300	U15979	Hs.169228	delta-like homolog (Drosophila)	EGF,taminin_EGF;TM;SS	7.3
50	447990	BE048821	Hs.20144	small inducible cytokine subfamily	ILB;SS	7.1
	439477	W69813	Hs.58042	ESTs, Moderately similar to GFR3_HU	GDNF,TPR	6.1
	411602	L01406	Hs.767	growth hormone releasing hormone re	7tm_2,HRM;TM;SS	6.0
	417067	AJ001417	Hs.81086	solute carrier family 22 (extraneur	sugar_tr;TM;SS adh_zinc;TM;	5.9
35	426488	X03350	Hs.4	alcohol dehydrogenase 18 (class I),	SH3,PH;TM;	5.3
	447656	NM_003726	Hs.19126	src kinase-associated phosphoprotei	abhydrolase, Hydrolase, TM=	5.2
	436950	L05779	Hs.113	epoxide hydrolase 2, cytoplasmic	Estiforoscop. If a constant	4.9
	406837	R70292	Hs.156110	immunoglobulin kappa constant		4.8
40	410387	A1277367	Hs.47094	ESTs secreted frizzled-related protein 5	Fz,NTR;TM;SS	4.7
40	432855	AF017988	Hs.279565	ESTs		4.6
	441499	AW298235	Hs.101689	KIAA1324 protein	TM;SS	4.5
	421481	AW391972	Hs.104696	membrane metallo-endopeptidase (neu	Peptidase_M13;TM;SS	4.5
	420255	NM_007289	Hs.1298 Hs.182265	keratin 19	filament,bZIP;SS	4.4
45	407230 412445	AA157857 X51362	Hs.73893	dopamine receptor D2	7tm_1;TM;SS	4.3
40	412445	AA133935	Hs.173704	ESTs, Moderately similar to A53959		4.2 4.2
	415165	AW887604	Hs.78065	complement component 7	tdl_recept_a,sushi,tsp_1,	4.2 4.2
	420103	AA382259	Hs.95197	aldehyde dehydrogenase 1 family, me	aldedh;TM;	4.1
	426723	AW003069	Hs.183860	ESTs	GNT4;TM;SS	4.0
50	409081	AJ010277	Hs.50403	T-box 19	T-box;TM; Na_sutph_symp;TM;	4.0
	407142	AA412535		gb:zt99b10.s1 Soares_testis_NHT Hom	LRRNT, LRR, LRR, LRRNT	4.0
	414449	AA557660	Hs.76152	decorin	Somatomedin_B,Endonucleas	3.9
	444784	D12485	Hs.11951	ectonucleotide pyrophosphatase/phos	tsp_1;SS	3.8
	420321	D78761	Hs.96657	hyothetical protein Target Exon	TM;	3.8
55	401700	NO 10101	H= 00046	deoxyribonuclease I-like 3	Exo_endo_phos;TM;SS	3.8
	418807	NM_004944		· · · · · · · · · · · · · · · · · · ·	TCTP;TM;	3.7
	406746 449077	AA580395 AW262836	Hs.279860 Hs.252844			3.7
		F30631	Hs.200237		isoamytase_N	3.7
60	415718 402449	1.30031	10.200201	Target Exon	pkinase,LRR,LRRCT;TM;SS	3.6 3.6
UU	457489	AI693815	Hs.127179	cryptic gene	TM;SS	3.6
	406743		Hs.279860	tumor protein, translationally-cont	TCTP;TM;	3.6
	416950		Hs.80552	dermatopontin		3.6
	451554		Hs.193237	r ESTs	Euk_porin,Enterotoxin_A.P	3.5
65	440708		Hs.7381	voltage-dependent anion channel 3	WD40,none	3.5
	426095	AI278023	Hs.89986	ESTs	TCTP;TM;	3.5
	406742		Hs.27986		VHS,ENTH,UIM;SS	3.4
	429343			) Homo sapiens, Similar to epsin 3, c ab:Homo sapiens tull length insert	***************************************	3.4
70	439457			<b>4</b>	hormone_rec.zf-C4	3.4
70				daudin 1	PMP22_Claudin;TM;SS	3.4
	44065				UDPGP;SS	3.4
	41504: 41796:			nuclear receptor subfamily 4, group	hormone_rec,zf-C4,none	3.3
	44523			•	14-3-3,none	3.3
75	44323			calpain 1, (mu/l) large subunit	efhand, Peptidase_C2, Calpa	3.3
,,	42048				7tm_1,CIDE-N;TM;SS	3.3 3.3
	41368			9 ESTs	TM;SS	3.3
	42892			7 cadherin 1, type 1, E-cadherin (epi	cadherin,Cadherin_C_term,	3.3
	40973			insulin induced gene 1	-4 COUR CET-TIA-	3.2
80	44204	6 AA97457	5 Hs.2873	35 ESTs	zt-C2H2,SET;TM;	3.2
	41312	7 BE06652		gb:RC3-BT0333-300300-017-a12 BT0333	MAM;TM;	3.2
	42935				LRR none	3.2
	42798	0 AA41B30	5 Hs.3032	05 EST		
					270	

				A	AIP3:TM:SS	3.2
	424498	AB033043	Hs.149377 Hs.4980	hypothetical protein DKFZp761L0424 LIM domain binding 2	LIM_bind;TM;	3.2
	435684 402632	NM_001290	113.11300	Target Exon	ig:TM;SS	3.1
_	431130	NM_006103	Hs.2719	HE4; epididymis-specific, whey-acid	wap;TM;SS	3.1
5	410636	AA088177	Hs.172870	ESTs	TM;SS	3.1
	452658	N88604	Hs.30212	thyroid receptor interacting protei	PCI;TM;	3.1 3.1
	453180	N46243	Hs.110373	ESTs, Highly similar to T42626 secr	taminin_G,LRRCT,none TM:SS	3.1
	430319 438424	AI480214 AI912498	Hs.356075 Hs.25895	ninjurin 2 hypothetical protein FLJ14996	C2:TM:	3.1
10	456063	NM_006744	Hs.76461	retinol-binding protein 4, Intersti	lipocalin, TGF-beta, TGFb_p	3.1
10	429798	AL117578	Hs.222909	DKFZP434C128 protein	TM;	3.1
	417677	NM_016055	Hs.82389	CGI-118 protein		3.1
	443792	A1763073	Hs.204873	ESTs	70 tu	3.1 3.1
16	445861	BE293423	Hs.11809	single Ig IL-1R-related molecule	TIR; TM; LRR,none	3.1
15	407815	AW373860	Hs.183860	hypothetical protein FLJ20277	ion_trans,K_tetra;TM;SS	3.1
	456689 446492	NM_002251 AW205115	Hs.117780 Hs.161287	potassium voltage-gated channel, de ESTs	SPRY,zi-B_box,PAAD_D	3.1
	427706	AW971225	Hs.293800	ESTs, Weakly similar to ALU1_HUMAN	G. 111 D. G.	3.0
	458008	AA809314	Hs.123295	ESTs	SCAN,zf-C2H2,none	3.0
20	449708	A1694598	Hs.202126	ESTs		3.0
	410132	NM_003480	Hs.300946	Microfibril-associated glycoprotein	TM;SS	3.0 3.0
	423778	Y09267	Hs.132821	flavin containing monooxygenase 2	FMO-like,pyr_redox;TM;S PEPCX;TM;	3.0
	425280	U31519	Hs.1872 Hs.223747	phosphoenolpyruvate carboxykinase 1 ESTs	zi-C2H2,none	3.0
25	453177 416781	AW389509 AF072928	Hs.79877	myotubularin related protein 6		3.0
23	447582	BE293520	Hs.18910	prostate cancer overexpressed gene	sugar_tr;TM;SS	3.0
	417365	050683	Hs.82028	transforming growth factor, beta re	pkinase,WD40;TM;	3.0
	452540	AW161048	Hs.150549	ESTs, Weakly similar to T33997 hypo		2.9
20	430233	AW367902	Hs.236443	Homo sapiens mRNA: cDNA DKFZp564N10	PH,Ets,CH,spectrin,Ca_cha	· 2.9 2.9
30	418127	BE2439B2	Hs. <b>83532</b>	membrane cofactor protein (CD46, tr	sushi;TM;SS	2.9
	404445 423323	AI951628	Hs.127007	Target Exon potassium channel, subfamily K, mem	ion_trans;TMtSS	2.9
	452093	AA447453	Hs.27860	Homo sapiens mRNA; cDNA DKFZp586M07	7tm_1,none	2.9
	427981	BE275986	Hs.181311	asparaginyl-tRNA synthetase	tRNA-synt_2,tRNA_anti,tRN	29
35	452242	R50956	Hs.159993	gycosyltransferase		2.9
	440232	AI766925	Hs.112554	ESTs		2.9 2.9
	444634	AW611988	Hs.197813	ESTs	CKS TM;	2.9
	445889	BE465186	Hs.266958	ESTs	1 M,	29
40	414483 453500	R25513 AI478427 .	Hs.10683 Hs.43125	ESTs esophageal cancer related gene 4 pr	TMtSS	2.9
70	419768	172104	Hs.93194	apolipoprotein A-I	Apolipoprotein;SS	2.9
	427804	AL049654	Hs.180871	protein kinase C, alpha binding pro	PDZ:SS	2.9
	423753	Y11312	Hs.132463	phosphoinositide-3-kinase, class 2,	C2,PI3_PI4_kinase,PI3Ka,P	2.9
	430699	AW969847	Hs.292718	ESTs, Weakly similar to RET2_HUMAN	tipocafin;SS	2.9 2.8
45	427842	AW936961		gb:RC1-DT0029-160200-013-a12 DT0029	efhand,mito_carr,none NAD_binding,FAD_binding_6	2.8
	432834	F06459	Hs.289113	cytochrome b5 reductase 1 (B5R.1)	MAD_matrid's Ap_mionid_o	2.8
	421435 402458	AW972072	Hs.372167	ESTs C1002064:gi 11993050 gb AAG42574.1	TM;SS	2.8
	410036	R57171	Hs.57975	calsequestrin 2 (cardiac muscle)	Calsequestrin;SS	2.8
50	412570	AA033517	Hs.74047	electron-transfer-flavoprotein, bet	ETF_beta;SS	2.8
	459439	AW402931	Hs.352411	gb:Ul-HF-8K0-abd-a-01-0-Ul.r1 NIH_M	•	2.8
	438622	L03151		gb:Homo sapiens cell-type T-cell im		2.8 2.8
	417023	AA192278	Hs.301596	ESTs, Moderately similar to S65657		2.8
55	453281	W46280	Hs.55940	ESTs, Weakly similar to A25704 syna Target Exon	trypsin,trefoil	2.8
23	403028 449029	N28989	Hs.22891	solute carrier family 7 (cationic a	aa_permeases;TM;SS	2.8
	425483	AF231022	Hs.158159		EGF,cadherin,laminin_G;TM	2.8
	406918	M88357		gb:Homo sapiens DNA-binding protein	zI-C2H2,KRAB,zI-BED;TM;	2.7
	435213	AA092510	Hs.5985	non-kinase Cdc42 effector protein S	TM;	2.7 2.7
60	443990	AW205085	Hs.39557	ESTs	Destident M13-TM	2.7
	451698	Y16187	Hs.26880	endothelin converting enzyme-like 1	Peptidase_M13;TM; Band_41;TM;	27
	431713	AK000388	Hs.267997 Hs.124159		SH3	2.7
	431469 400386	N49424 AF075290	115.124155	gap junction protein, alpha 3, 46kD	connexin;TM;SS	2.7
65	406684	X16354	Hs.50964	carcinoembryonic antigen-related ce	ig;TM;SS	2.7
-	449874		Hs.10083	Homo sapiens, clone IMAGE:4139786,	TM;	2.7
	403213			NM_019595:Homo sapiens intersectin	SH3,efhand,C2,PH,RhoGEF;T	2.7 2.7
	459665		Hs.47647	gb:MR0-HT0408-220300-001-h06 HT0408		2.7
70	421823		Hs.28625	ESTs	TCTP,none	2.7
70	422693 454906		Hs.279860 Hs.101077		TM;	2.7
	454900		Hs.12474		TM;	2.7
	450273		Hs.24743		rm,none	2.7
	434340		Hs.12868	5 ESTs, Weakly similar to T17226 hypo		2.7
75	436972		Hs.25640	claudin 3	PMP22_Claudin;TM;SS	2.7
	441379		Hs.33484		TM;	2.7 2.7
	421143		Hs.10217 Hs.11824		ig,LRR,LRRNT,LRRCT;TM;S Sec7,none	2.7
	422558 428900		HS.11824 HS.35232		SS SS	27
80	421153		Hs.10223			2.7
	427074		Hs.17858		efhand;TM;	2.6
	448133	AA723157	Hs.73769		Folate_rec,MIP;TM;SS	2.6
	419158	AF031475	Hs.89648	arginine vasopressin (neurophysin I	hormone5,hormone4;SS	26

## 45466 AM717289 is 2,103 of the company of the co							
Section   Sect		440406	AM/772209	He 21103	Homo sapiens mRNA; cDNA DKFZp564807		2.6
\$ 45975   \$61504   \$415121   \$25				1 141-		Galactosyl_T;TMt;SS	
Mail				Hs.12400			
## 18590   Maj. (2024)   Has.	_						
Miles   Mile	5			He 163990			
10					transforming growth factor, beta re		
453247   869198   Hs.11106   ET-1   ARCOCCAP   Hs.1106   ET-1   ARCOCCAP   Hs.1107   ET-1   ARCOCCAP   Hs.1107   Hs.1107   ET-1   ARCOCCAP   Hs.12011   Hs.1107   Hs.12011   H							
407744   A880CM29   H2-2017   H2-2	• •	453247				ABC tran PRK:TM;SS	
ASSIST   ASSIST   ASSIST   C144000CT-19/724573(b)  BA4925471,   Prefiction M27	10						
15   16   16   16   16   16   16   16							
15			NIGO I GOO	1.0.00			
March   Marc					glioma-associated oncogene homolog	25-02112,00	
A	15				collagen, type XIV, aipha i fundan		
46555 AVSS397 Hs. 29656   40133 ASS397 Hs. 179656   40133 ASS397 Hs. 179656   40133 ASS397 Hs. 13006   40133 ASS397 Hs. 13006   40134 ASS397 Hs. 13006   40135 ASS397 Hs. 13006   40136 ASS397 Hs. 13006   40136 ASS397 Ks. 14637 Hs. 13006   40237 Xs. 14637 Hs. 14637 Hs					solute carrier family 25 (mitochond	efhand,mito_carr,TM;SS=	
427223 a B286189 hts 174031 yorks/chrome contides about the 18274 https://doi.org/10.1001/j.com/chrome.contides about the 18274 https://doi.org/10.1001/j.com/chrome.contides about the 18274 https://doi.org/10.1001/j.com/chrome.contides about the 18274 https://doi.org/10.1001/j.com/chrome.contides about the 251 https://doi.org/10.1001/j.com/chrome.contides 251 http					ESTs, Wealdy similar to 138022 hypo	Auto EVER COYER 7m. 1	
42811 37877 FE. 2236 449103 ANDRESS F. 18-2149 449103 ANDRESS F. 18-2149 449103 ANDRESS F. 18-2149 44925 ANDRESS F. 18-2149 45925 ANDRESS F. 18-21					cytochrome c oxidase subunit VIb		
1993   ANJ3746   Hs 30136   Hs	20						
## 17/103   23905   Hs. 81218   hypothetical protein Moderal Prison					FXYD domain-containing ion transpor		
Value   Valu					hypothetical protein MGC3597		
49925 AJA/493 Hs. 13496 hs. 15704 AJS66 Hs. 15896 hs. 15704 AJS66 Hs. 15896					hypothetical protein PP1665	squash,GUPD,TM;	
430377 X53433 H1, 275 optimization of the composition of the compositi	25				Homo sapiens cDNA FLJZU/6/ hs, clo	GSHPx:SS	
Add					giutatrione peroxidase 2 (yasuum giotagendent kinase 5, regulato		
August					fatty acid binding protein 3, muscl		
## 246947 # A 146747 # Ls 191705 # Ls 1917			AA130040	(13.4300)	ENSP00000239776*:BA425A6.2 (similar		
40310	30		AF146747	Hs.232165	nolvovthemia rubra vera 1; cell sur	IM;SS	
## A3302 A064066 Hs. 200725 hs. 3032 hs. 3064066 hs. 200725 hs. 3032 hs. 306406 hs. 315095 hs. 30640 hs. 315095 hs. 316095 hs. 3	20		AW179023		gb:PM3-ST0036-170899-001-e08 S10036	Rand 41:	
183146   1802/75   1803/46   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/75   1805/							
Add   All					Homo saniens cDNA FLJ14883 fis, do	STT3;TM;SS	
AV079940	35				DKFZP566D213 protein		
A 21757   20087   A 1296279   A 184542   C3-127 protein   2.5	33				ESTs, Weakly similar to S32436 coll		
424657 A334719 424657 A32622 AW000458 Hs 258700 45702 AW000458 Hs 258700 47770 A8002417 Hs 19454 47770 A8002417 Hs 19454 47770 A8002417 Hs 19454 47770 A8002417 Hs 19454 4567023 A005868 Hs 56601 451846 T65840 Hs 11762 453876 AW0021748 Hs 110405 451846 T65849 Hs 11762 453876 AW0021748 Hs 110405 44488 AW09393 Hs 153927 44488 AW09393 Hs 153927 44488 AW09393 Hs 153927 44488 AW09393 Hs 153927 45249 AA73153 Hs 17864 Breed Hs 110405 45249 AA73153 Hs 17865 Home sopies cDNA: FLJ21333 fs, cl  TABLE 318: Ptey: CAT number: Cene duster number Genbank accession numbers  55  Pkey CAT Number Accession: Genbank accession numbers  60 427842 1164139_1 AW056374 BF33083 BF747375 BE066356 BE066292 BF330900 BF747142 BE066419 BF742510 BE066529 BE066298 BF742516 BF746603 439867 143127 151610_1 BC007796 BF330833 BF747375 BE066356 BE066292 BF330900 BF747142 BE066419 BF742510 BE066529 BE066298 BF742516 BF746603 427842 1164139_1 AW056347 AW35077 AA544719  65  TABLE 31C: Vinique number corresponding to an Eos probeset Squence of human chromosome 27 Dunham, et al. *refers to the publication entitled *The DNA sequence of human chromosome 27 Dunham, et al. *refers to the publication entitled *The DNA sequence of human chromosome 27 Dunham, et al. *profession* 100, 100, 100, 100, 100, 100, 100, 100,				Hs.296259		Arylesælæe,33	
437862   AVVDV9058   Hs. 268720   Avvision   Hs. 268		428475			CGI-127 protein		
## 427195 W277290 Hs.173912 eukaryotic translation initiation (	40				go:E5130901 Gail piagoda is ricino se		
### A	40						
ABB3568					frizzled (Drosophila) homolog 4	-• · · -	
451846 765840 Hs.11762 ESTS 432906 ESC5688 Hs.3123 lethel giant larvae (Drosophila) ho 452906 ESC5688 Hs. 3123 lethel giant larvae (Drosophila) ho 452907 AW02178 Hs.110406 ESTs, Weatly similar to 138022 hypo 414188 AW45035 Hs.7682 hypothetical protein FLI20312 TM; 2.5 452497 AA732153 Hs.27865 Homo sapiens cDNA: FLI21333 fs. cl  TABLE 31B: Pkey: CAT number: Gene duster number Accession: Genbank accession numbers  Fiey CAT Number Accession 439457 23338, 1 AF086274 W69434 W69517 439457 23338, 1 AF086274 W69434 W69517 439457 23338, 1 AF086274 W69434 W69517 439457 131510_1 BC007296 BF303053 BF747375 BE066356 BE066292 BF303090 BF747142 BE066419 BF742510 BE066529 BE066298 BF742516 BF746603  60 427842 1164139, 1 AW936960 AW936961 AA416706 R29415 438622 46171_1 L03151 L03155 L03161 427857 896375_1 AW963487 AA355077 AA344719  65 TABLE 31C: Pkey: Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 27 Dunham, et al. (1999) Nature 407-489-495.  NL position: Indicates DNA strand from which exons were predicted. NL position: Indicates DNA strand from which exons were predicted. NL position: Indicates DNA strand from which exons were predicted. NL position: Indicates DNA strand from which exons were predicted. NL position: Indicates DNA strand from which exons were predicted. NL position: Indicates DNA strand from which exons were predicted. NL position: Indicates DNA strand from which exons were predicted. NL position: Indicates DNA strand from which exons were predicted. NL position: Indicates DNA strand from which exons were predicted. NL position: Indicates DNA strand from which exons were predicted. NL position: Indicates DNA strand from which exons were predicted. NL position: Indicates DNA strand from which exons were predicted. NL position: Indicates DNA strand from which exons were predicted. NL position: Indicates DNA strand from which exons were predicted. NL position: Indicates DNA str					hypothetical protein MGC10986	pkinase,riorie	
433966 BE285489			T65840			WD40:TM:	
441488 AW450935 Hs. 7862 hypothetical protein FLJ20312 1M; 25 441689 F18939 Hs. 153827 ESTs 2.5  4362497 AA732153 Hs. 27865 Homo sapiens cDNA: FLJ21333 fis, cl  TABLE 31B: Puey: Unique Eos probeset identifier number Accession: Gene duster numbers  Accession: Gene duster number Accession: Gene duster number 439457 23338_1 AF086274 W56343 W69517 413127 151610_1 BG007296 BF330853 BF747375 BE066356 BE066292 BF330900 BF747142 BE066419 BF742510 BE066529 BE066298 BF742516 BF746603  60 427842 1164138_1 AW936960 AW936961 AA416706 R29415 428622 45171_1 CJ03151 L03155 L03151 CJ0315 L03155 L03151 427657 896375_1 AW963487 AA365077 AA344719  70 TABLE 31C: Piey: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402-489-495.  NL position: Indicates DNA strand from which exons were predicted. NL position: Indicates nucleotide positions of predicted exons.  Piey: Piey: Piey: Strand NL positions of predicted exons.  Piey: Piey: Piey: Strand NL positions of predicted exons.  170 Piey: Piey: Piey: Strand NL positions of predicted exons.  170 Piey: Piey: Piey: Strand NL positions of predicted exons.  170 Piey: Piey: Piey: Strand NL positions of predicted exons.  170 Piey: Piey: Piey: Strand NL positions of predicted exons.  170 Piey: Piey: Strand NL positions of predicted exons.  170 Piey: Piey: Strand NL positions of predicted exons.  170 Piey: Piey: Strand NL positions of predicted exons.  170 Piey: Piey: Piey: Strand NL position of predicted exons.  170 Piey: Piey: Piey: Piey: Strand NL position of predicted exons.  170 Piey: Pie	45				e COTA Washin similar to 138022 hvoo		
1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5   1.5					hypothetical protein FLJ20312	TM;	
TABLE 31B:					7 ESTs		
TABLE 31B: Pkey: Unique Eos probeset identifier number CAT number: Gene duster number Accession: Genbank accession numbers  Pkey CAT Number Accession 439457 23338.1 AF086274 W59434 W69517 43127 151610_1 BC007296 BF330833 BF747375 BE066356 BE066292 BF330900 BF747142 BE066419 BF742510 BE066298 BF742516 BF746603  BE066274 BF334312  60 427842 1164138_1 AW933696 AW936961 AA416706 R29415 438622 45171_1 L03151 L03155 L03161 424657 896375_1 AW963487 AA365077 AA344719  TABLE 31C: Pkey: Unique number corresponding to an Eos probeset Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402-489-495.  Strand: Indicates DNA strand from which exons were predicted. NL position: Indicates nucleotide positions of predicted exons.  Pkey Ref Strand NL position 10166-101419 10166-101419 10166-101419 10166-101419 10166-1014272 100777 Winus 114150-114272 1007777 Winus 114150-114272 1007777777 Winus 114150-114272 1007777777 Winus 114150-114272 1007777777 Winus 114150-114272 10077777777 Winus 114150-114272 1007777777 Winus 114150-114272 10077777777 Winus 114150-114272 100777777777777777777777777777777777					Homo sapiens cDNA: FLJ21333 fis, cl		2.0
Pkey:   Unique Eos probeset Identifier number	50						
CAT number: Gene cluster number Accession: Genbank accession numbers  Pkey CAT Number Accession 439457 2338_1			31B:	Inimus Ess scal	socat identifier number		
Accession:   Genbank accession numbers				Gene duster nu	mber		
Pkey							
439457   23338_1	55	7.333					
413127 151610_1 BG007296 BF330853 BF747375 BE066356 BE066292 BF-330900 BF747142 BE006419 GF74702 BE006419 GF747042 BE006				nber Accessio	N 24 WED 424 WED 517		DETACEON
BE066274 BF334312				AFU862	96 RE330853 BE747375 BE066356 BE066292	BF330900 BF747142 BE066419 BF742510	8E066529 BE066298 BF742516 BF746603
42/842 1164138_1 AW936960 AW936961 AA416706 R29415 438622 46171_1 L03151 L03155 L03161 424657 896375_1 AW963487 AA365077 AA344719  TABLE 31C:  Pkey: Unique number corresponding to an Eos probeset Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.  Strand: Indicates DNA strand from which exons were predicted. Nt_position: Indicates nucleotide positions of predicted exons.  Pkey Ref Strand Nt_position  Pkey Ref Strand Nt_position  401700 317654 Minus 35416-35534 402449 9796674 Pkus 99867-60039,62588-62828,63465-63623,6492  402632 9931268 Plus 101166-101419  402632 9931268 Plus 101166-101419  402638 9795762 Plus 1017679-171134 403028 7570577 Minus 114150-114272 403028 7570577 Minus 114150-114272		41312	7 151010_	RF0662	74 BF334312		
#38622 46171_1 L03151 L03155 L03161 #424657 896375_1 AW963487 AA365077 AA344719  TABLE 31C:  Pkey: Unique number corresponding to an Eos probeset Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.  Strand: Indicates DNA strand from which exons were predicted. Nt_position: Indicates nucleotide positions of predicted exons.  Pkey Ref Strand Nt_position  Pkey Ref Strand Nt_position  401700 317654 Minus 35416-35534 407449 9796674 Pkus 99867-60039,62588-62828,63465-63623,6492  402632 9931268 Plus 101166-101419  402632 9931268 Plus 101166-101419  402638 9795762 Plus 170479-171134 403028 7570577 Minus 114150-114272 403028 7570577 Minus 114150-114272	60	42784	2 1164138	_1 AW9369	60 AW936961 AA416706 R29415		
TABLE 31 C: Pkey:		43862	2 46171_1		L03155 L03161		
Pkey:		4246		1 AW963	187 AA365077 AA344719		
Pkey:		7401	F 240.				
Ref: Sequence source. The 7 digit numbers in this column are Gerhalik Identified (G) International Sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.  Strand: Indicates DNA strand from which exons were predicted.  Nt_position: Indicates nucleotide positions of predicted exons.  Pkey Ref Strand Nt_position 401700 3176654 Minus 35416-35534 402449 9796674 Plus 59867-60039,62588-62828,63465-63623,6492 402632 9931268 Plus 101166-101419 75 404445 7596866 Minus 31112-31423 4020458 9796782 Plus 170479-171134 403028 7570577 Minus 114150-114272 403028 7570577 Minus 114150-114272	65	I ABL		Lloinue numbe	corresponding to an Eos probeset		at a setum to the publication entitled "The DNA
Strand: Indicates DNA strand from which exons were predicted.  Nt_position: Indicates nucleotide positions of predicted exons.  Play Ref Strand Nt_position  Play Ref Strand Nt_position  401700 3176554 Minus 35416-35534  402449 9796674 Plus 59867-60039,62588-62828,63465-63623,6492  402632 9931268 Plus 101166-101419  402638 9796782 Plus 101166-101419  402458 9796782 Plus 170479-171134  403028 7570577 Minus 114150-114272  403028 7570577 Minus 114150-114272	05		•	C		bank Identifier (GI) numbers. "Dunnam, et	a. letels to the patriction of the
70    Pkey Ref Strand Nt_position   Nt_posit				enguence of h	uman chromosome ZZ Dunnam, et al. (1999) 🗓	<u>ature</u> 402:409-493.	
70  Pkey Ref Strand Ni position 35416-35534 401700 3176654 Minus 35416-35534 402449 9796674 Plus 59867-60039,62588-62828,63465-63623,6492 402632 9931268 Plus 101166-101419 75 404445 7596866 Minus 31112-31423 402458 9796782 Plus 170479-171134 403028 7570577 Minus 114150-114272 403028 7570577 Minus 114150-114272				Indicates DNA	strand from which exons were predicted.		
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401700 3176654 Minus 35416-35534 402449 9796674 Plus 59867-60039,62588-62828,63465-63623,6492 402632 9931268 Plus 101166-101419 75 404445 7596866 Minus 31112-31423 402458 9796782 Plus 170479-171134 403028 7670577 Minus 114150-114272 403028 7670577 Minus 114150-114272	/(		Def	Strand	Nt position		
402449 9796674 Plus 59867-60039,62588-62828,63465-63623,6492 402632 9931268 Plus 101166-101419 75 404445 7596866 Minus 31112-31423 403028 7570577 Minus 114150-114272 403028 7570577 Minus 114150-114272					35416-35534	0.000	
75 404445 7595866 Minus 31112-31423 402458 9796782 Phus 170479-171134 403028 7570577 Minus 114150-114272						3,6492	
402458 9795782 Plus 170479-171134 403028 7570577 Minus 114150-114272 403028 7570577 Minus 114150-114272		4026	32 993126				
403028 7670577 Manus 114150-114272	7:						
400020 101001					114150-114272		
4117/13 (03003) William 1000-0-1-1-1		403			162572-162739,164442-164540		
403153 9799871 Minus 42232-43389		403			42232-43389		
80 406337 9213455 Plus 90117-90337	8	0 406	337 92134	55 Plus			
400538 9797838 Plus 8752-9822		400	538 9797	838 Plus	0102-3044		

TABLE 32A: ABOUT 68 GENES UP-REGULATED IN GLIOMA COMPARED TO NORMAL ADULT TISSUES AND TO NON-MALIGNANT BRAIN TISSUES THAT ARE LIKELY TO ENCODE PROTEINS AMENABLE TO MODULATION BY SMALL MOLECULES, PEPTIDES, OR ANTIBODIES
Table 32A lists about 68 genes up-regulated in glioma compared to normal adult tissues and to non-matignant brain tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These were selected from the starting collection of 59680 probesets on the Affymetrix/Eos-Hu03 GeneChip® array as follows: the ratio of "average" gloma to "average" normal adult tissues was greater than or equal to 2.5, the ratio of "average" gloma to "average" gloma level was set to the 98th percentile value amongst various spoons specimens, the "average" normal adult tissue level was set to the 98th percentile value amongst various non-matignant tissues, the "average" gloma value was greater than or equal to 50 units, and the predicted protein contained a structural domain that is indicative of having an oncogenic function or of transducing an intracellular signal, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7m, phosphatase, or ion_transporter). Predicted protein domains are noted.

10 protein domains are noted.

Unique Eos probeset identifier number Exemplar Accession number, Genbank accession number Unigene number ExAcon:

UnigenelD: Unigene Title: Unigene gene title

15 Protein Domains: Predicted Protein Domains

glioma vs. normal adult tissues and non-malignant brain tissues that are likely to encode proteins

	Pkey	ExAcon	UniGene ID	Unigene Title	Protein Domains	R1
	424343	AW956360	Hs.4748	adenylate cyclase activating polype	7tm_2,HRM	8.8
20	418506	AA084248	Hs.85339	Unknown protein for MGC:29643 (form		7.8
	456723	Z43902	Hs.4748	adenylate cyclase activating polype	7tm_2,HRM	7.5 7.1
	430228	AW950939	Hs.6382	ESTs, Highly similar to T00391 hypo	ASC:TM:	6.3
	436480	AJ271643 AW955705	Hs.87469 Hs.62604	putative acid-sensing ion channel Homo sapiens, clone IMAGE:4299322,	TM;	6.0
25	407603 414825	XVV955705 X06370	Hs.77432	epidermal growth factor receptor (a	Furin-like.okinase.Recep_	6.0
23	423779	AW071837	Hs.57971	ESTs	TNFR_c6	5.5
	409638	AW450420	Hs.21335	ESTs	7tm_2,HRM	5.3
	442613	AI004002	Hs.130522	Kv channel-interacting protein 1	Neur_chan_LBD,Neur_c	5.2
••	436456	AW292677	Hs.248122	G protein-coupled receptor 24		· 5.1
30	424340	AA339036	Hs.7033	ESTs	lig_chan,ANF_receptor,non	5.0 4.7
	425115	R44664	Hs.123956	ESTs	7tm_1 CaMBD,SK_channel,CaMBD,SK	4.4
	446809	AW590171	Hs.101413 Hs.833	ESTs interferon-stimulated protein, 15 k	ubiquitin;SS	4.4
	413278 454360	BE563085 L78207	ns.533 Hs.54470	ATP-binding cassette, sub-family C	ABC_tran,ABC_membrane,PRK	4.2
35	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity I	ig:TM;SS	4.2
55	428141	D50402	Hs.182611	sotute carrier family 11 (proton-co	Nramp;TM;	4.1
	435472	AW972330	Hs.283022	triggering receptor expressed on my	ig:TM;SS	4.1
	435615	Y15065	Hs.4975	potassium voltage-gated channel, KQ	ion_trans,KCNQ1_channel;T	3.8
40	448204	AI475124	Hs.170561	ESTs	tig_chan,SBP_bac_3	3.7
40	433290	R20077	Hs.302185	Homo sapiens clone 23618 mRNA seque	tig_chan,S8P_bac_3,ANF_re	3.6 3.6
	408243	Y00787	Hs.624	interleukin 8	HLH,PAS,ILB;TM; 7tm_2,GPS,Ga1_Lectin,HRM,	3.5
	415849	R20529	Hs.6806	ESTs	fn3;TM;SS	3.4
	451099 445070	R52795 NM_000677	Hs.25954 Hs.258	interleukin 13 receptor, alpha 2 adenosine A3 receptor	7tm_1;TM;SS	3.4
45	428037	N47474	Hs.89230	potassium intermediate/small conduc	CaMBD,SK_channel	3.2
43	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	tdl_recept_a,PKD,MHC_I;TM	3.1
	447143	AW292408	Hs.152290	ESTs, Highly similar to JC2463 vaso		3.0
	418054	NM_002318	Hs.83354	lysyl oxidase-like 2	SRCR_Lysyl_oxidase;TM;S	3.0
60	424441	X14850	Hs.147097	H2A histone family, member X	histone,CBFD_NFYB_HMF;TM=	3.0
50	446057	A1420227	Hs.366053	Trp-p8 transient receptor potential	7 1	2.9 2.9
	438204	AI589645	Hs.128690	ESTs	7tm_1 GCV_H	2.9
	431674 424028	AA098901 AF055084	Hs.301642 Hs.153692	G-protein coupled receptor Homo sapiens cDNA FLJ14354 fis, cto	<b>90</b> ₹_⊓	2.9
	415209	F00183	Hs.172004	titin		2.8
55	438537	AK000511	Hs.6294	hypothetical protein DKFZp434L1435	tRNA-synt_1;TM;	2.8
	431053	S40369	Hs.249141	Glutamate receptor subunit	lig_chan_ANF_receptor;TM=	2.8
	408482	NM_000676	Hs.45743	adenosine A2b receptor	7tm_1;TM;SS	2.8
	414774	X02419	Hs.77274	plasminogen activator, urokinase	kringte,trypsin,plant_thi	2.8
<b>C</b> 0	426865	D63476	Hs.172813	PAK-interacting exchange factor bet	SH3,PH,RhoGEF,Terpene_syn	2.8 2.7
60	430897	U71092	Hs.248122	G protein-coupled receptor 24	7tm_1;TM; EGF,metatthio,integrin_B,	2.7
	438993	AA828995	Hs.54929	gb:od77b08.s1 NCI_CGAP_Ov2 Homo sap phosphorytase kinase, gamma 1 (musc	pkinase,Bac_DNA_binding;T	27
	409552 412817	AL119675 AL037159	Hs.74619	proteasome (prosome, macropain) 26S	PC_rep;TM;	2.7
	429150	AF120103	Hs.197366	smoothened (Drosophila) homolog	COX8,SHMT,MIF,GST_C,EF1G_	2.7
65	419508	AW997938	Hs.90786	ATP-binding cassette, sub-family C	ABC_tran,ABC_membrane;TM=	2.7
•	417880	BE241595	Hs.82848	selectin L (lymphocyte adhesion mol	EGF,lectin_c,sushi;TM;S	2.7
	432074	AA525248	Hs.149723		Y_phosphatase	2.6
	402154			NM_031896*:Homo sapiens calcium cha	PMP22_Claudin;TM;SS	2.6
70	431222	X56777	Hs.273790	zona pellucida glycoprotein 3A (spe	zona_pellucida;TM;SS	2.6 2.6
70	419913	AW270040	Hs.34455	ESTs	EPH_lbd,fn3,pkinase, MIP;TM;SS	2.6
	412802	U41518	Hs.74602	aquaporin 1 (channel-forming integr gb:CM2-NN0010-100300-111-e09 NN0010	7tm_2,HRM	2.6
	412070 422676	AW893260 D28481	Hs.1570	histamine receptor H1	7tm_1;TM;SS	2.6
	422311	AF073515	Hs.114948		fn3;TM;	2.6
75	444381	8E387335	Hs.283713		Collagen; TM; SS	26
	419972	AL041465	Hs.182982	golgin-67	-	2.6
	418526	BE019020	Hs.85838	solute carrier family 16 (monocarbo	TM;SS	2.6
	421997	R66740	Hs.110613	KIAA0220 protein	aa_permeases,pyridoxal_de	2.6 2.5
90	430181	AF065314	Hs.234785		cNMP_binding.ton_trans;TM	2.5 2.5
80	426318	AA375125	Hs.147112 Hs.256150		EPH_lbd,pkinase,fn3,SAM,n TM:	2.5
	434808	AF 155 108 AJ 25 1016	Hs.250150	NY-REN-41 antigen potassium intermediate/small conduc	CaMBD,SK_channel;TM;SS=	2.5
	418843 410290	AA402307	Hs.322844		Sema, PSI, TIG, integrin_B:T	2.5
	410290	<b>10111111</b>	,		200	-

		\$78187 R38438 Al064813	He 182575 5	ell division cycle 258 SLC15A2 Solute carrier family 15 (H Horno sapiens amino acid transport s	Rhodanese;SS PTR2;TM; Aa_trans;TM;	2.5 2.5 2.5				
5	TABLE 328 Pkey: CAT number Accession:	Uniqu er: Gene	e Eos probeset cluster number ank accession n	identifier number numbers	·					
10	Pkey 438993 412070	CAT Number 2580163_1 287551_1		134879 AA828995 V890808 BF904755 AW893260 BI03468	4 BF963423 BF961550 M85689					
15	TABLE 32C: Pkey: Unique number corresponding to an Eos probeset Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.									
	Strand: Nt_position	Indic	ates DNA strant	from which exons were predicted. positions of predicted exons.						
20	Pkey 402154	Ref 8516165	Strand Minus	Nt_position 125299-125494						
25	Table 33/	Lists about 798	genes up-regul d "averane" kidt	164 CHILDEL IO SACLODE LIGHTIC SCOTT		I from 59680 probesets on the Affymetrix/Eos Hu03 Geni. The "average" bidney cancer level was set to the 90th ongst various non-malignant tissues. In order to remove g ssues was subtracted from both the numerator and the	eChip gene-			
30	percentile enerific h	amongst various ackground level ator before the r Uni Exe	is iddney cance is of non-specifi atio was evalua and Foe probes	c hybridization, the 15th percentile value	amongst the various non-malignant t	ingst various not manginal society was subtracted from both the numerator and the				
35	Unigene R1:	Title: Uni	gene gene title tio of turnor to n		Ri					
40	Pkey 421471 445178 452401 421727	ExAccn U90545 AI792241 NM_00711 Y13153	UniGenelD Hs.104635 Hs.129614 5 Hs.29352 Hs.107318	solute carrier family 17 (sodium phosp kidney-specific membrane protein turnor necrosis factor, alpha-induced	ha 100 438 oro 336 enine 3 323	.0 .4 .6				
	440304 436878 452795	BE159984 BE465204 AW392555	Hs.125395 Hs.47448 Hs.18878	ESTs ESTs hypothetical protein FLJ21620	295 256 250 250 250	i.8 i.6				
45	421155 426471 421478 424086	M22440 AI683243	Hs.102267 Hs.170009 Hs.97258 Hs.102267	transforming growth factor, alpha ESTs Nsvf oxidase	40					
50	428296 426890 441031 411642	NM_00305 AA393167 A1110684	58 Hs.183577 Hs.41294 Hs.7645	solute carrier family 22 (organic cation ESTs fibrinogen, 8 beta polypeptide neuroligin 1	18 17 17	3.4 4.0 2.4				
55	452838 42598 43896	8 U65011 4 AW83627 6 AW97907	Hs.30743 7 Hs.16563	preferentially expressed antigen in n hypothetical protein DKFZp761C071 gb:EST391184 MAGE resequences	21 15 , MAGP Homo 15 mayan 15	1.4 11.0 15.0 14.8				
	45316 45316 45243 42350	0 Al263307 1 U88879	Hs.14622 Hs.29499 Hs.12971	8 ESTs 1 toll-like receptor 3 1 toll-like receptor 3	1 1 1	92.6 90.6 20.4 12.6				
60	40797 43170	5 X89426 8 Al698136	Hs.41710 Hs.1088	<ul> <li>endothelial cell-specific molecula 1</li> <li>ESTs</li> </ul>	(NO 1	11.8 09.8 03.6				
65	4424	50 N66045 55 AI75370 38 AA9959	Hs.1335 Hs.1524	29 ESTs 84 ESTs gb:as26b03.s1 NCI_CGAP_Kid5 H	omo sapiens	03.0 01.4 8.8 8.5				
70	4334 4403 4150 4371 4533 4470	11 AI73307 76 NM_000 57 BE0488 19 AI98536	9 Hs.1254 857 Hs.7789 60 Hs.1206 19 Hs.2011	07 ESTs, Moderately similar to ALUE, 10 guanylate cyclase 1, soluble, beta 155 ESTs 17 ESTs	3	88.2 97.0 94.4 91.4 90.2				
75	4391 4318	69 Al91212 870 AW449 993 AA8289 879 R41900	12 Hs.4109 902 Hs.1059 195 Hs.222	500 ESTs gb:od77508.s1 NCI_CGAP_0v21 45 ESTs 897 ESTs	tomo sapiens	84.4 83.8 82.4 79.4				
80	4225 423	966 AV648 109 M5930 989 Al2677 544 AB018	119 Hs.122 5 Hs.123 00 Hs.111 259 Hs.118 806 Hs.380	613 dimethylglycine dehydrogenase p 655 natriuretic peptide receptor Clgua 128 ESTs 1140 (AA0716 gene product ESTs, Wealdy similar to putative	nylate	78.8 78.0 77.0 74.8 74.8 73.0				
		352 AK001	512 Hs.200	hypothetical protein FLJ10650	383	•				

	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	72.2
	441665	Al301355	Hs.151285	ESTs	71.6
	435094	AI560129	Hs.277523	EST	71.2 69.6
5	403345	X52599	U- 2661	nerve growth factor, beta polypeptide	69.0
,	430440 440482	AA886658	Hs.2561 Hs.50873	ESTs	67.6
	457100	AA417878	Hs.48401	ESTs, Wealty similar to ALU8_HUMAN ALU S	67.0
	420637	AW976153		gb:EST388262 MAGE resequences, MAGN Homo	65.2
10	407905	AW103655	Hs.252905	ESTS	63.2 61.8
10	422998 432267	AK000588 AK000872	Hs.122939 Hs.274227	hypothetical protein FLJ 20581 Homo sapiens cDNA FLJ 10010 fis, clone HE	61.2
	449448	D60730	Hs.57471	ESTs	60.6
	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone CO	59.8
1.5	419752	AA249573	Hs.152618	ESTs	58.4 58.2
15	449579 408609	AW207260 AA330431	Hs.134014 Hs.640	prostate cancer associated protein 6 calcitonin receptor	57.4
	451009	AA013140	Hs.115707	ESTs	57.2
	435610	AI862767	Hs.114157	ESTs, Wealty similar to putative p150 [H	56.4
20	411893	R82845	Hs.273789	ESTs .	56.2 55.2
20	415227 433859	AW821113 AW896758	Hs.72402 Hs.163925	ESTs ESTs	55.0
	450459	A1697193	Hs.299254	ESTs	54.4
	400302	N48056	Hs.1915	folate hydrolase (prostate-specific memb	53.4
25	421831	AA298836	Hs.22026	ESTs	52.8 52.1
25	438817	A1023799 AA205847	Hs.163242 Hs.23016	ESTs G protein-coupled receptor	52.0
	449101 410025	BE220489	Hs.113592	ESTs	51.8
	423685	BE350494	Hs.49753	Homo sapiens mRNA for KIAA1561 protein,	48.0
20	436751	AA732217	Hs.294054	ESTs	46.6 45.4
30	445424	AB028945	Hs.12696 Hs.75442	cortactin SH3 domain-binding protein albumin	44.8
	444059 442671	R69743 Al005668	Hs.134779	EST	44.4
	445657	AW612141	Hs.279575	ESTs	44.3
2.5	452891	N75582	Hs.212875	ESTs, Weakly similar to KIAA0357 (H.sapi	44.0
35	423735	AA330259	Un 171466	gb:EST33963 Embryo, 12 week II Homo sapi	43.8 43.6
	422553 452461	AI697720 N78223	Hs.171455 Hs.108106	ESTs transcription factor	42.8
	408430	S79876	Hs.44926	dipeptidy/peptidase IV (CD26, adenosine	42.6
40	452240	AI591147	Hs.61232	ESTs	41.7
40	445186	AW614544	Hs.123641	protein tyrosine phosphatase, receptor t	41.4 41.4
	452788 419287	AW294571 X91906	Hs.136040 Hs.89872	ESTs chloride channel 5 (nephrolithiasis 2, X	40.6
	428822	W28418	Hs.301148	potassium voltage-gated channel, lsk-rel	40.2
	412359	AW837985		gb:QV3-LT0048-140200-083-e05 LT0048 Homo	40.0
45	434208	T92641	Hs.127648	hypothetical protein PRO2176	39.2 38.8
	442168 400792	AI253165 AA635062	Hs.146022 Hs.50094	ESTs Homo sapiens mRNA; cDNA DKFZp43400515 (f	38.6
	445900	AF070526	Hs.13429	Homo sapiens clone 24787 mRNA sequence	38.4
	444743	AA045648	Hs.11817	nudix (nucleoside diphosphate linked moi	38.4
50	428795	R45503	Hs.97469	ESTs, Wealthy similar to 149698 alpha-1,3	37.6 37.6
	406411 423657	AL045128	Hs.1691	glucan (1,4-alpha-), branching enzyme 1	37.5
	417218	AA005247	Hs.285754	met proto-oncogene (hepatocyte growth fa	37.2
	448788	A1570286	Hs.107070		37.2
55	441826	AW503603	Hs.129915		37.0 36.8
	409263 425577	AA069573 BE464496	Hs.50319 Hs.280977	ESTs ESTs	36.2
	452249	8E394412	Hs.61252	ESTs	34.8
	435986	AA703158	Hs.187848		34.4
60	417236	AI908497	Hs.170737		33.8 33.8
	440234 435334	AW117264 R94223	Hs.126252 Hs.117747		33.2
	410153	BE311926	Hs.15830	Homo sapiens cDNA FLJ12691 fis, clone NT	33.1
	424871	NM_004525			32.8
65	420908	AL049974	Hs.100261 Hs.137206		32.4 32.4
	423992 451050	AW898292 AW937420	Hs.69662	ESTs	32.0
	449034	AI624049		gb:ts41a09x1 NCI_CGAP_Ut1 Homo sapiens	31.6
70	434539	AW748078	Hs.214410	ESTs	31.0
70	431595	AA508196	Hs.23796	gb:nh60f07.s1 NCI_CGAP_Pr8 Homo sapiens odz (odd Oz/ten-m, Drosophila) homolog 1	30.6 30.5
	449625 448243	NM_014253 AW369771	Hs.77496	small nuclear ribonucleoprotein polypept	30.4
	413573		Hs.149089		30.2
76	421037	A1684808	Hs.197653		30.2 30.2
75	449353		Hs.271369	B ESTs gb:yr47f06.r1 Soares fetal liver spleen	30.2 29.6
	416548 423020		Hs.1608	replication protein A3 (14kD)	29.6
	422420		Hs.1524	tumor necrosis factor (ligand) superfami	29.6
00	459508		Hs.205956		29.2 28.8
80	414245 424565		Hs.75850 Hs.75295		28.6
	424505 445925		Hs.14566		28.4
	412616				28.0
				384	
				23.	

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				_	22.0
				Homo sapiens cDNA FLJ11663 fis, clone HE	27.6 27.6
				KIAA1603 protein RU2S	27.4
	410247 406414	AF181721	ns.01343	NOZO	27.2
5	435951	AF269162		c21orf7 form A-D	27.2 27.0
	458680	N73773		ESTs	26.4
	419948 423276	AB041035 AC003034		NADPH oxidase 4 Homo sapiens Chromosome 16 BAC clone CIT	26.3
	427457	AW779105	Hs 164682	ESTs. Weakly similar to ORF2 consensus s	26.0
10	446346	AI290205		gb:ql79g06.x1 Soares_NhHMPu_S1 Homo sapi	26.0 25.8
	448595	AB014544	Hs.21572	KIAA0644 gene product	25.6
	419569	AI971651 AB040938	Hs.91143 Hs.113940	jagged 1 (Alagitte syndrome) KIAA1505 protein	25.6
	433242 453118	AW195849	Hs.252757	FSTs	25.6
15	412209	AW901456		gb:RC0-NN1012-270300-031-c07 NN1012 Homo	25.2 25.2
_	429710	Al337113	Hs.146025	Homo sapiens cDNA: FLJ23594 fis, clone L	23.2 24.6
	444783	AK001468 AA766908	Hs.62180 Hs.259047	anitlin (Drosophila Scraps homolog), act ESTs	24.4
	436788 427660	AI741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone C	24.4
20	419172	AW338625	Hs.22120	ESTs	24.3
	436061	A1248584	Hs.190745	Homo sapiens cDNA: FLJ21326 fis, clone C	24.2 24.0
	413623	AA825721	Hs.246973	ESTs gb:PM1-CT0247-151299-005-a03 CT0247 Homo	23.8
	407615 452466	AW753085 N84635	Hs.29664	Human DNA sequence from clone 682J15 on	23.8
25	432809	AA565509	Hs.131703	ESTs	23.7 23.6
	440102	AI672443	Hs.131190	ESTs	23.6 23.2
	451559	AL119980	Hs.128857	ESTs ESTs	23.0
	410811 416778	AWB05687 M16505	Hs.300648 Hs.79876	steroid sutfatase (microsomal), arylsutf	23.0
30	453628	AW243307	Hs.170187	ESTs	22.8
	401352				22.6 22.6
	451561	N52812	Hs.177403	ESTs	22.4
	401976 410658	AW105231	Hs.192035	ESTs	22.4
35	416220	N49776	Hs.121773	ESTs	22.2
	424073	U03493	Hs.138959	gap junction protein, alpha 7, 45kD (con	22.0 22.0
	444575	AI264847	Hs.22545	Homo sapiens cDNA FLJ12935 fis, clone NT hypothetical protein	21.8
	444144 438504	BE159397 AW665281	Hs.7736 Hs.224625		21.2
40	439157	AA912737	Hs.20160	ESTs	20.8
	429006	AA443143	Hs.50929	Homo sapiens cDNA FLJ13842 fis, clone TH	20.5 20.2
	442006	AW975183	Hs.292663		19.8
	409569	AW573153 AL080215	Hs.256216 Hs.102301		19.8
45	421160 404200	ALUOVZIS	(15.102301	Tionio dopona tina a que a ser	19.6
7.5	446591	H44186	Hs.15456	PDZ domain containing 1	19.2 18.9
	420218	AW958037	Hs.22437	Homo sapiens cDNA: FLJ23366 fis, clone H	18.8
	408390	AA054222 AW134509	Hs.40400 Hs.135077	ESTs ESTs	18.8
50	444038 446443	AV659082	Hs.134228		18.8
•	442204	AI635450	Hs.21914		18.4 18.2
	451177	AI969716	Hs.13034	ESTs	18.1
	453931 437212	AL121278 AI765021	Hs.25144 Hs.210775	ES7s 5 ESTs	18.1
55	437212	AF186114	Hs.270737	7 himor necrosis factor (ligand) superfami	18.0
-	451659	BE379761	Hs.14248	ESTs, Weakly similar to ALU8_HUMAN ALU S	17.8 17.6
	423909	AJ223183	Hs.135194		17.6
	441082		Hs.20265 Hs.42278		17.6
60	446259 423609		Hs.21828	9 ESTs	17.4
00	428301	*******	Hs.98440	ESTs	17.4
	446364	AB006624	Hs.14912	KIAA0286 protein	17.4 17.0
	419983		Hs.94030 Hs.22498		17.0
65	424929 425695				17.0
05	449122		Hs.19695	5 ESTs	17.0
	409519	AA075368		gb:zm86h10.r1 Stratagene ovarian cancer	16.8 16.8
	410947			5 hypothetical protein FLJ20298 gb:zn55d06.s1 Stratagene muscle 937209 H	16.8
70	418053 433225				16.8
70	44320			Homo sapiens cDNA FLJ13103 fis, clone NT	16.6
	42100	2 AF116030	Hs.10093	32 transcription factor 17	16.5 16.2
	41929		Hs.12071		16.2
75	42165		59 Hs.1065 Hs.1391		16.0
13	41758 44605		Hs.1493		15.8
	43463	6 AA083764	l Hs.2413	34 ESTs	15.6 15.6
	44679	7 AI682536			15.6 15.4
80	44371				15.2
30	40974 44321			55 ESTs	15.0
	42891	1 Z43846	Hs.1944	78 Homo sapiens mRNA; cDNA DKFZp434O1572 (f	14.9
	44469		2 Hs.1450	147 ÉSTs	14.8

	445436	AI224105	Hs.151408	ESTs	14.6
	408684	R61377	Hs.12727	hypothetical protein FLJ21610	14.5 14.4
	405943				14.4
5	406291 458679	AW975460	Hs.143563	ESTs	14.4
,	450152	Al138635	Hs.22968	ESTs	14.4
	403899	A1130000	15.22500		14.2
	454490	AW797778		gb:CM2-UM0041-250200-104-d02 UM0041 Homo	14.2
	451807	W52854	Hs.27099	DXFZP564J0863 protein	14.0
10	452453	AI902519		gb:QV-8T009-101198-051 BT009 Homo sapien	13.8
	447499	AW262580	Hs.147674	KIAA1621 protein	13.8
	406598				13.6
	430939	AI269471	Hs.187018	ESTs	13.4
16	443316	AJ478463	Hs.18443	ESTs	13.4
15	408034	N26639	Hs.42192	Human EST clone 251800 mariner transposo	13.2
	428508	BE252383	Hs.184668	SBBI31 protein	13.2
	447934	AW631440	Hs.165596	ESTS	13.2 13.1
	406671 438199	AA129547 AW016531	Hs.285754 Hs.122147	met proto-oncogene (hepatocyte growth fa ESTs	13.0
20	415511	A1732617	Hs.182362	ESTs ESTs	12.9
20	426920	AA393351	Hs.132121	ESTs	12.8
	447311	R37010	Hs.33417	Homo sapiens cDNA: FLJ22806 fis, clone K	12.6
	423321	AB013885	Hs.126926	beta-ureidopropionase	12.5
	403622			, ,	12.4
25	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	12.4
	422317	NM_001147	Hs.115181	angiopoletin 2	12.2
	428637	AW979268		gb:EST391378 MAGE resequences, MAGP Homo	12.2
	445717	AW664658	Hs.149332	ESTs	12.2
20	418413	R95735	Hs.117753	ESTs, Weakly similar to antigen of the m	12.1
30	405336	41704070	11- 44505	Management of the Company of the same is	12.0
	437100	AI761073	Hs.14535	Homo sapiens cDNA: FLJ22314 fis, clone H	12.0 12.0
	428227 414923	AA321649 AW445008	Hs.2248 Hs.77637	small inducible cytokine subfamily B (Cy homeo box A4	11.9
	432009	AL137424	11037	gb:Homo sapiens mRNA; cDNA DKFZp761G2123	11.8
35	433326	AL379486	Hs. 159430	ESTs	11.8
	453955	AW579207		ab:RC1-DT0029-120100-011-h01 DT0029 Homo	11.8
	407510	U96191		gb:Human trophoblast hypoxia-regulated f	11.6
	433231	A8040926	Hs.143552	KIAA1493 protein	11.6
	451651	AI097337	Hs.88977	hypothetical protein dJ511E16.2	11.6
40	443672	AA323362	Hs.9667	butyrobetaine (gamma), 2-oxoglutarate di	11,4
	405609				11.4
	418912	NM_000685	Hs.89472	angiotensin receptor 1	11.4 11.4
	421306	AA806207	Hs.125889	ESTs	11.4
45	428721 419255	X02158 AA235672	Hs.2303 Hs.87491	erythropoietin ESTs	11.4
43	450006	AI241555	Hs.60171	ESTs	11.3
	435420	AI928513	Hs.59203	ESTs	11.2
	449802	AW901804	Hs.23984	hypothetical protein FLJ20147	11.2
	424647	W67751	Hs.137308	ESTs	11.0
50	435758	AI242163	Hs.22670	chromodomain helicase DNA binding protei	11.0
	404347				10.8
	438664	AI911173	Hs.213722		10.8
	429125	AA446854	Hs.271004	ESTs	10.7
55	416560	R02818	Hs.14102	ESTs	10.6
23	429945	NM_006729	Hs.226483		10.6 10.6
	435085	AW130284	Hs.192752 Hs.129544		10.6
	442409 450644	BE208843 AW505496	Hs.281215		10.6
	448298	AW137134	Hs.187203		10.4
60	404115	,			10.2
	406242				10.2
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	10.2
	452588	AA889120	Hs.110637		10.2
	457233	A1355009	Hs.221698		10.2
65	416185	AW975861	Hs.291995		10.2
	446152	A1292036	Hs.150028		10.1
	44629B	AF187813	Hs.14637	kidney- and liver-specific gene	10.1
	423637	AL137279	Hs.130187		10.0 9.9
70	442405	BE465247	Hs.129530	ESTs gb:PM0-BT0340-170100-004-e03 BT0340 Homo	9.8
70	419213 420840	AW749146 AJ915836	Hs.294008		9.8
	423355	AA324856	Hs.257510		9.8
	444929	AI685841	Hs.161354		9.8
	423811	AW299598	Hs.50895	homeo box C4	9.8
75	433527	AW235613	Hs.133020		9.6
	429975		Hs.165538	S ESTs	9.6
	439979		Hs.6823	hypothetical protein FLJ 10430	9.5
	433703		Hs.3532	nemo-like kinase	9.2
80	417404			pleckstrin homology-like domain, family	9.2 9.2
οU	451621		Hs.26770	fatty acid binding protein 7, brain	9.2
	406992 419699		Hs.31246	gb:beta-pol≈DNA polymerase beta (exon a ESTs	9.2
	443740		Hs.21062	ESTs	9.2
				386	
				146	

		A1402702C	u_ 102252 F	STs	9.2
				STs	9.2
	431385	BE178536	Hs.11090	igh affinity immunoglobulin epsiton rec	9.1 9.1
_	411411			STs, Weakly similar to KIAA1330 protein	9.0
5	424115 402045	AA335497	Hs.293965	ESTs	9.0
	433426	H69125		ESTs	9.0
	425493	AW363582	Hs.75323	prohibitin	9.0 9.0
10	447641	BE619186	,	gb:601472933F1 NIH_MGC_68 Homo sapiens c	8.8
10	403095 407942	AA378608	Hs.5894	hypothetical protein FLJ10305	8.8
	423126	AA322245	Hs.290165	ESTs	8.8 8.7
	408134	AK000184		acid sphingomyelinase-like phosphodieste a disintegrin and metalloproteinase doma	8.6
15	450375 443647	AA009647 AV653846	Hs.8850 Hs.126261	Homo sapiens Chromosome 16 BAC clone CIT	8.6
1,5	401439	71100010			8.6 8.6
	449532	W74653		ESTs ESTs, Weakly similar to ALU5_HUMAN ALU S	8.6
	453197 448450	AI916269 BE612490	Hs.109057	gb:601451884F1 NIH_MGC_66 Homo sapiens c	8.5
20	425176	AW015644	Hs.301430	ESTs, Moderately similar to TEF1_HUMAN T	8.4
	407721	Y12735	Hs.38018	dual-specificity tyrosine-(Y)-phosphoryl	8.4 8.4
	402921	A18/467707	Hs.11873	ESTs	8.4
	428133 419503	AW167727 AA243642	Hs.137422	ESTs	8.4
25	452644	AW452616	Hs.212481	ESTs (harmely	8.4 8.4
	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo gb:EST112514 Adrenal gland tumor Homo sa	8.3
	409695 418076	AA296961 R61388	Hs.6724	ESTs	8.3
	402696	1101000			8.3 8.3
30	423099	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor t	8.2
	413998 410008	AW103807 AA079552	Hs.243933	ESTs gb:zm20h12.s1 Stratagene pancreas (93720	8.2
	416623	N74925	Hs.38761	Homo sapiens cDNA: FLJ21564 fis, clone C	8.2
	450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitte	8.1 8.0
35	435496	AW840171	Hs.265398 Hs.246973	ESTs, Wealdy similar to transformation-r ESTs	8.0
	413627 415713	BE182082 AW968573	113.240310	gb:EST380649 MAGE resequences, MAGJ Homo	8.0
	426695	AW118191	Hs.112729	ESTs	8.0 8.0
40	452284	AW451426	Hs.252740	ESTs gb:QV0-HT0101-061099-032-c04 HT0101 Homo	8.0
40	454933 426269	BE141714 H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	8.0
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	8.0 7.9
	444107	T46839	Hs.10319	UDP glycosyltransferase 2 family, polype Homo sapiens clone 25181 mRNA sequence	7.9
45	445740 433190	T78281 M26901	Hs.13226 Hs.3210	renin	7.8
73	432777	AA564991	Hs.269477	ESTs	7.8
	449444	AW818436	Hs.23590	solute carrier family 16 (monocarboxytic	7.7 7.7
	444042	NM_004915 AW009951	Hs.10237 Hs.206892	ATP-binding cassette, sub-family G (WHIT ESTs	7.7
50	434032 419750	AL079741	Hs.183114		7.6
-	439024	R96696	Hs.35598	ESTs	7.6 7.4
	437205		Hs.13544	gb:Homo sapiens mRNA; cDNA DKFZp564D2071 Homo sapiens clone 24850 mRNA sequence	7.4
	446030 446311	AW007294			7.4
55	452883		Hs.150318		7.4 7.4
	448253		Hs.201591	ESTs	7.4
	406030 437084		Hs.127811	ESTs .	7.3
	435013	H91923	Hs.11002		7.3 7.3
60	432143		Hs.123484	ESTs, Weakly similar to The KIAA0149 gen gb:zm18e06.s1 Stratagene pancreas (93720	7.2
	409594 425151		Hs.29867		7.2
	448582		Hs.94812	ESTs	7.2 7.2
45	455068		Hs.27910	centrosomal protein 2	7.2
65	406504 428395		Hs.10488	5 ESTs, Weakly similar to zinc finger prot	7.2
	42110		Hs.89217	ESTs	7.2 7.1
	42316			6 Homo sapiens mRNA; cONA DKFZp564N1116 (f gb:QV0-NN1071-280400-207-g07 NN1071 Homo	7.1
70	41053- 41508		8 Hs.77899		7.0
,,	41027		Hs.61762	hypoxia-inducible protein 2	7.0 6.9
	43941	6 W58294	Hs.56254		6.8
	42003 42334		Hs.52792 Hs.12742	28 homeo box A9	6.8
75	42334	O AA126770	5	gb:zn88c11.s1 Stratagene lung carcinoma	6.8
	44936	1 AW20789	0 Hs.2019		6.8 6.8
	45930 40877				6.8
_	40877 41646			gb:zh80f05.r1 Soares_fetal_liver_spleen_	6.8
80	44783	5 AW59162	3 Hs.1641	29 ESTs	6.7 6.7
	40356		113 Hs.1810	60 apelin; peptide ligand for APJ receptor	6.6
	42789 42200			gb:QV0-HT0368-040100-082-c05 HT0368 Homo	6.6

	40 0075	A1407700C		gb:EST389810 MAGE resequences, MAGO Horno	6.6
	455275 441350	AW977806 A8020690		paraneoplastic antigen MA2	6.6
	445575	Z25368		titin	6.6
_	446075	AW451457		ESTs	6.6
5	405963				6.6
	423049	X59373	Hs.188023	ESTs	6.6 6.5
	436456	AW292677	Hs.65909	ESTs	6.5
	420273	A1652864	Hs.197257	ESTs ESTs	6.4
10	420831	AA280824 AA398155	Hs.190035 Hs.97600	ESTs	6.4
10	423739 441559	AA938448	Hs.259733	ESTs	6.4
	433999	AA778212	Hs.191869	ESTs	6.4
	439703	AF086538	Hs.196245	ESTs	6.4
	433757	AI949974	Hs.152670	ESTs	6.3
15	422095	AI868872	Hs.288966	ceruloptasmin (ferroxidase)	6.3
	415138	C18356	Hs.78045	tissue factor pathway inhibitor 2	6.3
	448515	H68441	Hs.13528	Homo sapiens cDNA FLJ14054 fis, clone HE	6.3
	443595	AF169312	Hs.9613	PPAR(gamma) angiopoietin related protein	6.3
20	429357	AA779725	Hs.164589	ESTs	6.3 6.3
20	404939	1150000	14- 035433	cor.	6.2
	417071	N58820	Hs.275133	ESTs	6.2
	436209	AW850417	Hs.254020	ESTs, Moderately similar to unnamed prot	6.2
	403111 448796	AA147829	Hs.33193	ESTs, Highly similar to AC007228 3 BC372	6.2
25	442353	BE379594	Hs.49136	ESTS	6.2
	451110	A1955040	Hs.301584	ESTs	6.1
	420092	AA814043	Hs.88045	ESTs	6.1
	441801	AW242799	Hs.211874	ESTs	6.0
	407500	U43279		gb:Human nucleoporin nup 36 mRNA, comple	6.0
30	450864	R64139	Hs.205225	ESTs	6.0
	455711	BE069465		gb:RC2-BT0388-290100-012-a11 BT0388 Homo	6.0
	405394				6.0
	436476	AA326108	Hs.53631	ESTs. Weakly similar to enhancer-of-spli	6.0 6.0
25	454392	BE260893	U- 205222	gb:601150677F1 NIH_MGC_19 Homo sapiens c	5.9
35	414575	H11257	Hs.295233 Hs.117874	ESTs ESTs	5.9
	435767 445495	H73505 BE622641	Hs.38489	ESTs	5.9
	428372	AK000684	Hs.183887	hypothetical protein FLJ22104	5.9
	436464	AI016176	Hs.269783	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.9
40	415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	5.9
	402421	•••••			5.8
	417038	T85230		ģb:yd33f02.r1 Soares fetal liver spieen	5.8
	436461	AW511956	Hs.293261	ESTs	5.8
	440870	AI687284	Hs.150539	Homo sapiens cDNA FLJ13793 fis, clone TH	5.8
45	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	5.8
	417280	AW173116	Hs.262206	ESTs	5.7 5.7
	437259	AI377755	Hs.120695	ESTs	5.7
	425717	X07282	Hs.171495	retinoic acid receptor, beta fibrinogen, 8 beta polypeptide	5.7
50	443614 450625	AV655386 AW970107	Hs.7645	gb:EST382188 MAGE resequences, MAGK Homo	5.6
50	425305	AA363025	Hs.155572	Human clone 23801 mRNA sequence	5.6
	430371	D87466	Hs.240112	KIAA0276 protein	5.6
	430499	AW969408	Hs.231991	ESTs	5.6
	427920	Z11502	Hs.181107	annexin A13	5.6
55	449318	AW236021	Hs.108788	ESTs, Weakly similar to zeste [D.melanog	5.6
	407864	AF069291	Hs.40539	chromosome 8 open reading frame 1	5.5
	410754	T63840		gb:yc16b10.s1 Stratagene lung (937210) H	5.5
	415286	AW249540	Hs.72548	ESTs	5.5
۲0	443297	AI049864	Hs.133029	ESTs	5.5 5.5
60	440138	AB033023	Hs.6982	hypothetical protein FLJ10201	5.4
	441006	AW605267	Hs.7627 Hs.146090	CGI-60 protein ESTs	5.4
	409348 449679	AI401535 AI823951	Hs.296668	Homo sapiens cDNA FLJ11846 fis, clone HE	5.4
	408938	AA059013	Hs.22607	ESTs	5.4
65	456411	AA603305	1.5.22501	gb:np12d11.s1 NCI_CGAP_Pr3 Homo sapiens	5.4
•	443756	AW089799	Hs.153665		5.4
	422232	D43945	Hs.113274	transcription factor EC	5.4
	424574	BE408518	Hs.150748	matonyl-CoA decarboxylase	5.3
~~	424834	AK001432	Hs.153408		5.3
70	440589	BE397763	Hs.194478		5.3
	425782	U66468	Hs.159525		5.3 5.3
	450236	AW162998		KIAA1376 protein	5.3 5.3
	418110	R43523	Hs.217754		5.3
75	427061	AB032971	Hs.173392 Hs.75576	KIAA1145 protein plasminogen	5.3
,,	413841 432358	M34276 A1093491	Hs.72830	ESTs	5.2
	416805	F13271	Hs.79981	Human clone 23560 mRNA sequence	5.2
	438475	W03856	Hs.13188	ESTs, Highly similar to Gene product wit	5.2
	443305	AI050693	Hs.133318		5.2
80	413930		Hs.75618	RAB11A, member RAS oncogene family	5.1
	451859	H44491	Hs.252938		5.1
	429826		Hs.40747	ESTs	5.1 5.1
	436032	AA150797	Hs.109276	i latexin protein	3.1

				aternium inwanth metifican channel 5	5.1
			Hs.17287 P Hs.258238 E	otassium inwardly-rectifying channel, s ESTs, Moderately similar to ALU1_HUMAN A	5.1
				nsufin-like growth factor binding prote	5.1 5.1
_		AW451970		paired box gene 2	5.0
5				nuclear receptor subfamily 1, group H, m ESTs, Weakly similar to hypothetical pro	5.0
	425813 432328			5-phosphofructo-2-kinase/fructose-2,6-bi	5.0
	430682		He 201252	FSTs	5.0 5.0
	410049	AW579475		gb:RC0-DT0076-110100-031-d10 DT0076 Homo	5.0
10	429222			ESTs ESTs	5.0
	446317 409506	AI287367 NM_006153		NCK adaptor protein 1	5.0
	407768	AW002841	Un 20175	ESTs	5.0 5.0
	437938	A1950087		gb:wq05c02.x1 NCI_CGAP_Kid12 Homo sapien	4.9
15	430403	AF039390	Hs.241382 Hs.155223	tumor necrosis factor (ligand) superfami stanniocalcin 2	4.9
	426215 448570	AW963419 AJ923944	Hs.30913	ESTs	4.9
	445034	AW293376	Hs.160323	ESTs	4.9 4.8
20	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon- Homo sapiens mRNA full length insert cDN	4.8
20	453891	AB037751 AW340048	Hs.36353 Hs.293188	ESTs	4.8
	438492 446417	A1299050	115.233100	chign14d12.x1 NCI_CGAP_Lu5 Homo sapiens	4.8
	409578	BE041386		gb:hk88c02.x1 NCI_CGAP_Lu21 Homo sapiens	4.8 4.8
0.5	447269	NM_004861	Hs.17958	cerebroside (3-phosphoadenylylsulfate:9	4.8
25	413795	AL040178	Hs.142003 Hs.115418	ESTs cadherin 16, KSP-cadherin	4.8
	422357 452208	AF016272 AA024792	Hs.31895	ESTs Weakly similar to B9 [H.sapiens]	4.7
	422711	D60641	Hs.21739	Homo sagiens mRNA; cDNA DKFZp586i1518 (f	4,7 4,7
	441392	AW451831	Hs.222119	ESTs, Wealthy similar to K1CQ_HUMAN KERAT	4.7
30	439221	AA737106	Hs.32250 Hs.272245	ESTs Homo sapiens cDNA FLJ11170 fis, clone PL	4.7
	431956 417355	AK002032 D13168	Hs.82002	endothelin receptor type B	4.7
	414700	H63202	Hs.38163	ESTs	4.7 4.6
	402739				4.6
35	403170	NIM 002429	Hs.9450	zinc finger protein 84 (HPF2)	4.6
	443486 408380	NM_003428 AF123050	Hs.44532	diubiquitin	4.6
	427899	AA829286	Hs.181062	serum armyloid A1	4.5 4.5
40	446302	A1285848	Hs.149757	ESTs monokine induced by gamma interferon	4.4
40	414812	X72755	Hs.77367 Hs.138671	fms-related tyrosine kinase 1 (vascular	4.4
	424063 413384	NM_002019 NM_000401	Hs.75334	exostoses (multiple) 2	4.4
	421298	AW172431	Hs.13012	ESTs	4.4 4.4
	420789	AI670057	Hs.199882		4.4
45	453558	Al417023	Hs.40478	ESTs Homo sapiens HSPC316 mRNA, partial cds	4.4
	453745 451762	AA952989 AF222980	Hs.63908 Hs.26985	disrupted in schizophrenia 1	4.4
	410334	AW979261	Hs.291993	ESTS	4.4 4.4
	457030	Al301740	Hs.173381		4.3
50	452194	Al694413	Hs.298262 Hs.63287	carbonic anhydrase IX	4.3
	410407 401157	X66839	15.03201	-	4.3
	432004	BE018302	Hs.2894	placental growth factor, vascular endoth	4.3 4.3
	426866		Hs.172810		4.3
55	446115		Hs.29268 Hs.15209		4.2
	424704 446619			secreted phosphoprotein 1 (osteopontin,	4.2
•	433578		Hs.3416	adipose differentiation-related protein	4.2 4.2
<b>60</b>	407065		11- 22015	gh:H.sapiens DAT1 gene, partial, VNTR.	4.2
60	407182 416565		Hs.23015 Hs.44970		4.2
	442230		Hs.27954	7 FSTs	4.2
	440680	) AA903098		gb:ok46f08.s1 NCI_CGAP_Lei2 Homo sapiens	4.2 4.2
45	41380				4.2
65	438370 43273		Hs.28782	20 fibronectin 1	4.2
	40974			gb:7B14E12 Chromosome 7 Fetal Brain cDNA	4.2
	44148	4 AA935481	Hs.5897	2 ESTs	4.2 4.2
70	41121				4.2
70	45304 40799			3 FSTs. Wealdy similar to HYPOTHETICAL PRO	4.2
	40799		6	gb:UI-HF-BR0p-aji-c-12-0-UI.r1 NiH_MGC_5	4.1
	44985	6 AA20315	5 Hs.1820	O ESTs	4.1 4.1
75	43080		Hs.2479	78 T-cell acute lymphocytic leukemia 2 gb:RC2-BN0127-240300-011-b05 BN0127 Homo	4.1
75	41287 43071			96 ESTs	4.1
	4307			7 Homo sapiens mRNA; cONA DKFZp434K0621 (f	4.1
	41469	96 AF00202	0 Hs.7691	8 Niemann-Pick disease, type C1	4.1 4.1
0.0	4446		Hs.3749		4.1
80	) 4480: 4088:			13 hynothetical protein FLJ10847	4.1
	4190		3 Hs.774	small nuclear ribonucleoprotein polypept	4.1 4.1
	4166		13 Hs.794	28 BCL2/adenovirus E1B 19kD-interacting pro	9,1

	436772	AW975688	Hs.250867	zona pellucida glycoprotein 3A (sperm re	4.1
	442556	AL137761	Hs.8379	Homo sapiens mRNA; cDNA DKFZp586L2424 (I	4.1
	459595	AL040421	Un 154073	gb:DXFZp434B0714_r1 434 (synonym: htes3)	4.1 4.0
5	438859 423279	AI559626 AW959861	Hs.164973 Hs.290943	ESTs, Weakly similar to AF231024 1 proto ESTs	4.0
•	441592	AW137071	Hs.127211	ESTs	4.0
	411836	AW901879		gb:QV0-NN1021-280400-212-110 NN1021 Homo	4.0
	426384 412494	A1472078 AL133900	Hs.792	gb:tj85h03.x1 Soares_NSF_F8_9W_OT_PA_P_S ADP-ribosylation factor domain protein 1	4.0 4.0
10	413583	AL120806	Hs.5888	ESTs	4.0
	415610	L44319		gb:HUMEST1D10 Human thymus NSTH II Homo	4.0
	430009	AA894564	Hs.22242	ESTs	4.0
	449539 438929	W80363 AW195515	Hs.58446 Hs.253177	ESTs ESTs	4.0 4.0
15	416000	R82342	Hs.79856	ESTs	4.0
	429616	AI982722	Hs.120845	ESTs	4.0
	458471	AV648609	Hs.194240	ESTs	4.0 4.0
	453195 459046	BE241876 AA910339	Hs.32352 Hs.26216	hypothetical protein DKFZp434K1210 Homo sapiens cDNA: FLJ22811 fis, clone K	3.9
20	438177	BE327015	Hs.281391	ESTs	3.9
	422438	AA445925	Hs.270896	ESTs	3.9
	450382 449611	AA397658 AI970394	Hs.60257 Hs.197075	Homo sapiens cDNA FLJ13598 fis, clone PL ESTs	3.9 3.9
	452030	AL137578	Hs.27607	Homo sapiens mRNA; cDNA DKFZp564N2464 (f	3.9
25	452881	AW135220	Hs.241921	ESTs	3.9
	414729	8E466928	Hs.281901	ESTs	3.9 3.9
	428816 405908	AA004986	Hs.193852	ATP-binding cassette, sub-family C (CFTR	3.8
	445452	H92975	Hs.246046	ESTs, Weakly similar to RET1_HUMAN RETIN	3.8
30	447961	W32791	Hs.170405	ESTs	3.8
	446639	AI016826	Hs.132501	ESTs	3.8 3.8
	401189 429548	AW138872	Hs.135288	ESTs	3.8
	431523	N55759	Hs.163674	ESTs	3.8
35	430014	H59354	Hs. 182485	actinin, alpha 4	3.8
	429250 451988	H56585 AF263928	Hs.198308 Hs.27410	tryptophan rich basic protein papillomavirus regulatory factor PRF-1	3.8 3.8
	437939	AW298600	Hs.141840	ESTs, Weakly similar to S59501 Interfero	3.8
40	427510	Z47542	Hs.179312	small nuclear RNA activating complex, po	3.8
40	433522	AI821730	Hs.116524	ESTs	3.8 3.7
	443843 407305	AW878864 AA715284	Hs.13528	Homo sapiens cDNA FLJ14054 fis, clone HE gb:riv35f03.r1 NCI_CGAP_Br5 Homo sapiens	3.7
	434613	AI821826	Hs.187786	ESTs, Moderately similar to ALUB_HUMAN!	3.7
45	410276	A1554545	Hs.68301	ESTs	3.7
45	422504	AA311407	Lb. 1245	gb:EST182167 Jurkat T-cells V Homo sapie	3.7 3.7
	421013 437949	M62397 U78519	Hs.1345 Hs.41654	mutated in colorectal cancers ESTs	3.7
	431840	AA534908	Hs.2860	POU domain, class 5, transcription facto	3.7
50	409446	AI561173	Hs.67688	ESTs	3.7
50	415263 450206	AA948033 AJ796450	Hs.130853 Hs.201600	ESTs ESTs	3.7 3.7
	439444	AI277652	Hs.54578	ESTs	3.7
	437828	AW976806	Hs.291805	ESTs	3.7
55	453238	AA033991 AB005142	Hs.269234	ESTs Natio	3.7 3.7
55	420041 448458	AW614367	Hs.94592 Hs.171054	ESTs	3.7
	435080	AI831760	Hs.155111	ESTs	3.7
	444249	T87398	Hs.205816	ESTs	3.7
60	426595 417715	AW971980 AW969587	Hs.62402 Hs.86366	p21/Cdc42/Rac1-activated kinase 1 (yeast ESTs	3.7 3.7
-	432579	AF043244	Hs.278439	nucleolar protein 3 (apoptosis repressor	3.6
	440048	AA897461	Hs.158469	ESTs, Wealthy similar to envelope protein	3.6
	430091 438030	AB032958 X98427	Hs.233023 Hs.122634	KIAA1132 protein	3.6 3.6
65	453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	3.6
	446636	AC002563	Hs.15767	citron (rho-interacting, serine/threonin	3.6
	417860	AW408557	Hs.235498	Homo sapiens cDNA FLJ14075 fis, clone HE	3.6
	435794 449695	H72108 AA164569	Hs.13704 Hs.34550	ESTs ESTs	3.6 3.6
70	411485	AW848125	110.01000	gb:IL3-CT0214-301299-048-G04 CT0214 Homo	3.6
	426274	D38122	Hs.2007	tumor necrosis factor (tigand) superfami	3.6
	458201	AI989961 AA911705	Hs.233477 Hs.130229	ESTs, Moderately similar to A Chain A, S ESTs	3.6 3.6
_	440987 425178	H16097	Hs.161027		3.6
75	419080	AW150835	Hs.18878	hypothetical protein FLJ21620	3.6
	436091	AA704705	Hs.181044		3.6
	452671 437222	AW861074 AL117588	Hs.225833 Hs.299963		3.6 3.6
^^	437809	AL137723	Hs.5855	Homo sapiens mRNA; cDNA DKFZp434D0818 (f	3.5
80	411545	AW850818		gb:IL3-CT0220-091199-026-A03 CT0220 Homo	3.5
	414799 439882	A1752416 AA847856	Hs.77326 Hs.124565	insufin-like growth factor binding prote ESTs	3.5 3.5
	419229	AI827237	Hs.282884		3.5
	-				

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					26
				STs Tetra	3.5 3.5
				STs STs	3.5
			Hs.13281 E	ESTs	3.5
5		AW934714	(	b:RC1-DT0001-031299-011-a11 DT0001 Homo	3.5 3.5
				ESTs ESTs	3.5
	453365 452355			G protein-coupled receptor 34	3.5
	423246			ESTs	3.5 3.5
10	434131	AI858275		ESTs	3.5 3.5
	425304	AA463844		fibroblast growth factor 11 replication factor C (activator 1) 4 (37	3.4
	453775	NM_002916 AB001914		paired basic amino acid cleaving system	3.4
	426559 456311	AA225632	Hs.190016	ESTs	3.4
15	420737	L08096		tumor necrosis factor (ligand) superfami	3.4 3.4
	448733	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte	3.4
	401811 404021				3.4
	447175	Al365208	Hs.293606	ESTs	3.4
20	453743	AL120480		gb:DKFZp761K098_r1 761 (synonym: hamy2)	3.4 3.4
	455070	AW854675		gb:MR1-CT0258-290300-206-a01 CT0258 Homo gb:nc06c05.s1 NCI_CGAP_Pr1 Homo sapiens	3.4
	419546 449441	AA244199 AI656040	Hs.196532	ESTs	3.4
	441606	R37263	Hs.21065	ESTs	3.4 3.4
25	446594	Al311917	Hs.16292	ESTs	3.4
	424664	AJ432572	Hs.164221	ESTs small inducible cytokine subfamily A (Cy	3.4
	413719 427914	BE439580 AA417350	Hs.75498 Hs.20575	ESTs	3.4
	438257	AW474419	Hs.224794	ESTs	3.4
30	412642	BE244598	Hs.809	hepatocyte growth factor (hepapoietin A:	3.4 3.3
	454690	AW854639	U= 455301	gb:MR1-CT0258-140100-203-d10 CT0258 Homo ESTs, Moderately similar to 138022 hypot	3.3
	428046 407331	AW812795 AI570416	Hs.155381 Hs.99910	phosphofructokinase, platelet	3.3
	440472	AA886169	Hs.169071	ESTs	3.3
35	421893	NM_001078	Hs.109225	vascular cell adhesion molecule 1	3.3 3.3
	403797	44 1033034	u. 02022	cyclin D1 (PRAD1: parathyroid adenomatos	3.3
	417924 410623	AU077231 AW958932	Hs.82932 Hs.293833	ESTs	3.3
	449338	H73444	Hs.394	adrenomedullin	3.3 3.3
40	441024	AW081530	Hs.137088	ESTs	3.3
	405257	411077000	Hs.24950	regulator of G-protein signalling 5	3.3
	450396 416892	AU077002 L24498	Hs.80409	growth arrest and DNA-damage-inducible,	3.3
	444471	AB020684	Hs.11217	KIAA0877 protein	3.3 3.3
45	431689	AA305688	Hs.267695	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	3.3
	452093	AA447453	Hs.27860	Homo sapiens mRNA; cDNA DKFZp586M0723 (f stanniocatcin 2	3.3
	425236 428824	AW067800 W23624	Hs.155223 Hs.173059		3.2
	450101	AV649989	Hs.24385	Human hbc647 mRNA sequence	3.2 3.2
50	425260	L47726	Hs.1870	phenylalanine hydroxylase	3.2
	443830	A1142095	Hs.143273 Hs.27252	ESTs ESTs	3.2
	415245 405953		115.21232		3.2
	430812		Hs.247992		3.2 3.2
55	418946		Hs.132103		3.2
	424750		Hs.152818 Hs.163270		3.2
	435342 458860			· ===-	3.2
	430172	AA468591	Hs.16188	9 ESTs	3.2 3.2
60	431842				3.2
	451221 436211		Hs.21058 Hs.80961		3.2
	433727		Hs.11260	8 ESTs	3.2
	424897		Hs.15368	4 frizzled-related protein	3.2 3.1
65	41482		Hs.77424		3.1
	41803 41791		Hs.83321 Hs.86379		3.1
	43043		Hs.16994		3.1
	40966				3.1 3.1
70					3.1
	42498 42163		Hs.15407 Hs.10620		3.1
	43600		Hs.1209	67 FSTs	3.1
	43768	2 AA47665	2 Hs.9495	2 Homo sapiens cDNA: FLJ23371 fis, clone H	3.1 3.1
75	43945	1 AF08627		heterochromatin-like protein 1 gb:PM3-BN0176-100400-001-g04 BN0176 Homo	3.1
	43018		8 Hs.1845		3.1
	42847 44128			microtubule-associated protein 2	3.1
	45638			gb:47e1 Human retina cDNA randomty prime	3.1
80	45113	30 AI762250			3.1 3.1
	4397				3.1
	4533: 4288				3.1

	449899	AI610700	Hs.103280	ESTs	3.1
	436009	H57130	Hs.120925	ESTs	3.1 3.1
	448966	AW372914	Hs.287452	Homo sapiens cDNA FLJ11875 fis, clone HE	3.1
5	408239	AA053401	Hs.271827 Hs.85838	ESTs, Moderately similar to ALU7_HUMAN A solute carrier family 16 (monocarboxylic	3.1
,	418526 401260	BE019020	115.05050	South Carles Idiay to (Indiaca south	3.1
	450705	U90304	Hs.25351	iroquois-class homeodomain protein	3.1
	447233	AW246333	Hs.17901	Homo sapiens cDNA: FLJ21974 fis, clone H	3.1
10	424415	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	3.0 3.0
10	403346	4145007500	Un 160711	ESTs	3.0
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15	434398	AA121098	Hs.3838	serum-inducible kinase	3.0
	440113	AI916532	Hs.188272	ESTs	3.0 3.0
	424539	L02911 AW192803	Hs.150402 Hs.98974	activin A receptor, type I ESTs	3.0
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20	424405	AI076838	Hs.12967	ESTs	3.0
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	459065	AI373532 AI754443	Hs.157910 Hs.185951	ESTs	3.0
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	406117	7400.020			3.0
	415492	R41674	Hs.16491	ESTs	3.0
	419854	AW664873	Hs.87836	Homo sapiens PAC clone RPS-1087M19 from	3.0 3.0
30	453688	AW381270 W26213	Hs.194110	Homo sapiens mRNA; cDNA DKFZp434C0814 (f qb:22d10 Human retina cDNA randomly prim	3.0
30	408119 438358	W20213 AL035992	Hs.210278	ESTs	3.0
	412372	R65998	Hs.118615	ESTs	3.0
	431984	AL080239	Hs.272284	Human DNA sequence from clone GS1-256O22	3.0
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40	432596	AJ224741	Hs.278461	matrilin 3	3.0
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	448592	N69546	Hs.141706	ESTs	3.0 3.0
	421477	AI904743	Hs.104650	hypothetical protein FLJ10292 proline-serine-threonine phosphatase Int	3.0
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55	449547	H93543	Hs.117963	ESTs gb:MR3-SN0009-180400-110-c12 SN0009 Homa	3.0
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	401707				3.0
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	406007	MACAAA	Un 42457	ECTA	3.0 3.0
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	406506		,,		3.0
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                                                 Hs.156294
                                                                  ESTs
                                                                  ESTs
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AW905138 AW753008 R13818 Z43519
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AW835544 AW835613 AW835711 AW835697 AW835703 BE092535 BE092199 411485 1247181_1AW848125 AW848124 AW848203 AW848695
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Ref:
                             Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
                             Indicates DNA strand from which exons were predicted.
          Strand:
                             Indicates nucleotide positions of predicted exons.
          Nt position:
15
                                    Strand
                                                 Nt position
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          401157
                     9690246
                                                 90815-90929
           401189
                                    Minus
20
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                                                 86008-86355
26064-26208
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                     9931258
                                    Minus
                                                 92993-94026
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             406291
                                                   9562-9867
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                                      Minus
             406506
                       7711374
                                                   56373-56849
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                        8248614
             TABLE 34A: ABOUT 197 GENES UP-REGULATED IN KIDNEY CANCER
  70
             Table 34A lists about 197 genes up-regulated in kidney cancer compared to normal adult tissues that are likely to be extracellular or cell-surface proteins. These were selected as for
             Table 33A and the predicted protein contained a structural domain that is indicative of extracellular localization (e.g. ig, In3, egf, 7tm domains). Predicted protein domains are noted.
             Pkey:
                                Unique Eos probeset identifier number
                                Exemplar Accession number, Genbank accession number
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                                Unigene number
                                Unigene gene title
             Unigene Title:
                                Protein Structural Domain
             PSDomain:
                                Ratio of tumor to normal tissue
  80
                                                                             PSDomain
                                                   UnigeneTitle
                                       UnigenelD
             Pkey
                        ExAcon
                                                                                                                                 1007.4
             421471
                        U90545
                                       Hs.104635
                                                   solute carrier
                                                                             TMLSS
                                                                             TM,SS,XIink,CUB
                                                                                                                                 336.4
              452401
                        NM_007115
                                       Hs.29352
                                                   turnor necrosis
                                                   kynurenine 3-mo
                                                                              TM,SS,Monooxygenase
                                                                                                                                 323.6
                        Y13153
                                       Hs. 107318
             421727
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					THE PO ECE	224.6
	426471		Hs.170009	transforming gr fibrinogen, 8 b	TM,SS,EGF fibringen_C	174.0
	441031		Hs.7645 Hs.71132	neuroligia 1	TM.SS.COesterase	172.4
	411642 452838		Hs.30743	preferentially	TM	161.4
5	425984		Hs.165636	hypothetical pr	TM	151.0 134.8
	453165	S74727	Hs.32042	aspartoacylase	TM TM.SS.TIR.LRRCT	130.6
	452431	U88879	Hs.29499	toll-like recep hepatitis A vir	TM,SS,Ig	120.4
	423508 407975	AW604297 X89426	Hs.129711 Hs.41716	endothelial cel	SS,IGFBP	111.8
10	415076	NM_000857	Hs.77890	guanylate cycla	TM.guanylate_cyc	97.0 90.2
•	447046	AA326187	Hs.17170	G protein-coupl	TM,7tm_1	78.0
	423109	M59305	Hs.123655	natriuretic pep	TM,SS,ANF_receptor TM	74.8
	422544	AB018259	Hs.118140 Hs.200097	KIAA0716 gene p hypothetical pr	TM	73.0
15	429352 453392	AK001512 U23752	Hs.32964	SRY (sex determ	TM,HMG_box	72.2
13	403345	023132	, 5.52.22		TM,alpha-amylase	69.6 69.0
	430440	X52599	Hs.2561	nerve growth fa	TM,SS,NGF	57.4
	408609	AA330431	Hs.640	calcitonin rece	TM,SS,7tm_2 TM,7tm_1	52.0
20	449101	AA205847	Hs.23016 Hs.49753	G protein-coupl Homo sapiens mR	TM,Myosin_tail	48.0
20	423685 452891	BE350494 N75582	Hs.212875	ESTs, Weakly si	SS	44.0
	408430	S79876	Hs.44926	dipeptidylpepti	TM,SS,DPPIV_N_term,Peptidase_S9	42.6 40.6
	419287	X91906	Hs.89872	chloride channe	TM,CBS,voltage_CLC	40.2
~ ~	428822	W28418	Hs.301148	potassium volta	TM TM,SS	39.2
25	434208	T92641	Hs.127648 Hs.50094	hypothetical pr Homo sapiens mR	TM,BIR,CARD,zf-C3HC4	38.6
	400792 444743	AA635062 AA045648	Hs.11817	nudix (nucleosi	TM,mutT	38.4
	405411	74101010			TM,vwa,FG-GAP	37.6 37.5
	423657	AL045128	Hs.1691	glucan (1,4-alp	TM,alpha-amylase	32.8
30	424871	NM_004525	Hs.153595		TM,SS,EGF,Idl_recept_a,Idl_recept_b SH2,EGF	30.5
	449625	NM_014253	Hs.23796 Hs.1608	odz (odd Oz/ten replication pro	TM	29.6
	423020 422420	AA383092 U03398	Hs.1524	tumor necrosis	TM_TNF	29.6
	414245	8E148072	Hs.75850	WAS protein fam	TM,WH2	28.8 27.4
35	410247	AF181721	Hs.61345	RU2S	TM	27.2
	406414			A. m A	TM,vwa,FG-GAP TM	27.2
	435951	AF269162	Hs.41267	c21orf7 form A- NADPH oxidase 4	TM,SS,Ferric_reduct	26.4
	419948	AB041035 AB014544	Hs.93847 Hs.21572	KIAA0644 gene p	TM.SS.LRRCT.LRR	25.8
40	448595 419569	AB014344 AI971651	Hs.91143	jagged 1 (Alagi	TM,SS,DSL,EGF	25.6
70	433242	AB040938	Hs.113940		SS	25.6 23.0
	416778	M16505	Hs.79876	steroid sulfata	TM, Sulfatase	22.6
	401352				TM SS	19.6
45	404200	1144400	Hs.15456	PDZ domain cont	TM,PDZ	19.2
43	446591 431806	H44186 AF186114	Hs.27073		TM,SS	18.0
	423909		Hs.13519		TM,SS,ig	17.6 17.4
	446364		Hs.14912		TM	17.0
60	425695		Hs.15923		TM,Band_41,Y_phosphatase TM	16.8
50	410947		Hs.67055 Hs.10093		TM, KRAB, zf-C2H2	16.5
	421002 421659				TM,SS,cadherin	16.0
	458679				SS	14.4 13.6
	406598				SS TMPX	13.2
55	428508		Hs.18460 Hs.12692		TM,SS,CN_hydrolase	12.5
	423321 422317				fibrinogen_C	12.2
	42822			small inducible	IL8	12.0 11.9
	41492				TM,homeobox	11.6
60	43323				SS TM	11.4
	44367		Hs.9667	butyrobetaine (	TM, Myosin_tail, myosin_head	11.4
	40560 41891		35 Hs.8947	2 angiotensin rec	TM,7tm_1	11.4
	44980				TM	11.2
65	40434				SS	10.8 10.6
	42994					10.6
	43508		4 Hs.1927	752 ESTs, Moderate	SS	10.2
	40411 42075		Hs.999	15 androgen recep	make the company of CA	10.2
70	44629				TM, Acetyltransi	10.1
. •	43370		3 Hs.353			9.2 9.2
	41740				TM TM,SS,lipocalin	9.2
	4516		Hs.267	70 fatty acid bind	TM,SS	9.0
75	4020- 4030				SS,PAX,homeobox	8.8
, ,	4014				TM	8.6
	4077		Hs.380	18 dual-specificit	TM.pkinase	8.4 8.4
	4029	21		100 CCT-	TM TM	8.4
80	4195				·	8.4
O	J 4522 4026		H 113.401	o. agrica sociocino	TM	8.3
	4500		044 Hs.406		TM,SS,SNF	8.1 7.8
	4331		Hs.321	10 renin	SS,asp	1.0
					205	

	440444	A18/01042C	14- 22500		THUCT	7.7
	449444 444042	AW818436 NM_004915	Hs.23590 Hs.10237	solute carrier ATP-binding cas	TM,MCT TM.ABC_tran	7.7
						7.4
	452883	X80031	Hs.150318	EST's	TM,C4,Collagen TM	7.2
5	425151	AA351814	Hs.298678	ESTs		7.2 7.2
,	455068	A1807894	Hs.27910	centrosomal pro	TMSS	7.2 7.2
	406504	4.4204003	41- 64760	h	TM	7.2
	410274	AA381807	Hs.61762	hypoxia-inducib	SS	
	423349	AF010258	Hs.127428	homeo box A9	TM,homeobox	6.8
10	408771	AW732573	Hs.47584	potassium volta	TM,K_tetra.ion_trans	6.8
10	445575	<b>Z25368</b>	Hs.172004	titin	TM	6.6
	415138	C18356	Hs.78045	tissue factor p	Kunitz_BPTI,G-gamma	6.3
	443595	AF169312	Hs.9613	PPAR(gamma) ang	TM,SS,fibrinogen_C	6.3
	404939				TM	6.3
	436209	AW850417	Hs.254020	ESTs, Moderatel	TMLSS	6.2
15	403111			•	TM	6.2
	405394				TM	6.0
	454392	BE260893		gb:601150677F1	TMLSS	6.0
	415910	U20350	Hs.78913	chemokine (C-X3	TM,7tm_1	5.9
	402421	020000	15.70313	Cicionio (OA)	TM	5.8
20	425717	X07282	Hs.171495	retinoic acid r	TM_hormone_rec.zf-C4	5.7
20						5.6
	427920	Z11502	Hs.181107	annexin A13	TM, annexin	5.5
	407864	AF069291	Hs.40539	chromosome 8 op	TM,FHA,BRCT	5.4
	441006	AW605267	Hs.7627	CGI-60 protein	TM	
26	422232	D43945	Hs.113274	transcription (	TMHLH	5.4
25	425782	U66468	Hs.159525	cell growth reg	SS	5.3
	450236	AW162998	Hs.24684	KIAA1376 protei	TM,SS	5.3
	413841	M34276	Hs.75576	plasminogen	SS,trypsin,kringle,PAN	5.3
	436032	AA150797	Hs.109276	tatexin protein	TM	5.1
	447081	Y13896	Hs.17287	potassium inwar	TM,IRK	5.1
30	421126	M74587	Hs.102122	insulin-like gr	SS,thyroglobulin_1,IGFBP	5.1
•	426651	AU076646	Hs.171683	nuclear recepto	TM.zf-C4.hormone_rec	5.0
	432328	AI572739	Hs.195471	6-phosphotructo	TM,6PF2K,PGAM	5.0
	409506	NM_006153	Hs.54589	NCK adaptor pro	TM,SH2,SH3	5.0
		BE391804	Hs.62661	guanylate bindi	TM,SS,GBP	4.8
35	410361				TM	4.8
22	453891	AB037751	Hs.36353	Homo sapiens mR		4.8
	447269	NM_004861	Hs.17958	cerebroside (3	TM,SS	4.8
	422357	AF016272	Hs.115418	cadherin 16, KS	TM,cadherin	
	417355	D13168	Hs.82002	endothelin rece	TM,SS,7tm_1,zf-C3HC4	4.7
40	402739				SS	4.6
40	443486	NM_003428	Hs.9450	zinc finger pro	TM,KRAB,zf-C2H2	4.6
	408380	AF123050	Hs.44532	diubiquitin	TM.ubiquitin,7tm_3,ANF_receptor,sushi,7tm_1	4.6
	414812	X72755	Hs.77367	monokine induce	SS,IL8	4.4
	424063	NM_002019	Hs.138671	fms-related tyr	TM,SS,pkinase,ig	4.4
	413384	NM_000401	Hs.75334	exostoses (mult	TM	4.4
45	457030	Al301740	Hs.173381	dihydropyrimidi	TM,SS,Dihydroorotase	4.4
	410407	X66839	Hs.63287	carbonic anhydr	TM,SS,carb_anhydrase	4.3
	401157	7,0000	113.00201	om out to the you	TM_citrate_synt	4.3
	432004	BE018302	Hs.2894	placental growt	SS,PDGF	4.3
		AI263293			SS,p450	4.2
50	424704		Hs.152096	cytochrome P450		4.2
30	407065	Y10141		gb:H.sapiens DA	TM,SS,SNF	4.2
	411213	AA676939	Hs.69285	neuropilin 1	TM,CUB,F5_F8_type_C,MAM	
	430806	\$69377	Hs.247978	T-cell acute ly	TMHLH	4.1
	414596	AF002020	Hs.76918	Niemann-Pick di	TM,SS,Patched	4.1
	408830	AK001709	Hs.48403	hypothetical pr	TM,UPF0013	4.1
55	416655	AW968613	Hs.79428	BCL2/adenovirus	TM	4.1
	412494	AL133900	Hs.792	ADP-ribosylatio	TM,arf,zf-B_box,zf-C3HC4	4.0
	453195	BE241876	Hs.32352	hypothetical pr	TM	4.0
	428816	AA004986	Hs.193852	ATP-binding cas	TM_ABC_membrane,ABC_tran,COX15-ClaA	3.9
	401189			<u>-</u>	TM,SET,PHD,HMG_box	3.8
60	451988	AF263928	Hs.27410	papillomavirus	TM	3.8
	421013	M62397	Hs.1345	mutated in coto	TM	3.7
	420041	AB005142	Hs.94592	klotho	TM,SS,Glyco_hydro_1	3.7
	432579	AF043244	Hs.278439	nucleolar prote	TM	3.6
		AA442103	Hs.33084	solute carrier	TM,SS,sugar_tr	3.6
65	453496		Hs.15767		TM,CNH,DAG_PE-bind,PH,pkinase,pkinase_C	3.6
UJ	446636	AC002563		citron (rho-int		3.6
	426274	D38122	Hs.2007	tumor necrosis	TM,TNF	3.5
	452355	N54926	Hs.29202	G protein-coupt	TM,7tm_1	3.4
	453775	NM_002916		replication fac	TM,SS,AAA	
	426559	AB001914	Hs.170414		TM,Pepfidase_S8,P	3.4
70	420737	L08096	Hs.99899	tumor necrosis	TM,TNF	3.4
	448733	NM_005629			TM, SNF, ABC_tren, isodh, pkinase, Ribosomal_L18a	
	413719	BE439580	Hs.75498	small inducible	SS,IL8	3.4
	427914	AA417350	Hs.20575	ESTs	TM,GAS2	3.4
_	412642	BE244598	Hs.809	hepatocyte grow	kringle,PAN,trypsin	3.4
75	421893	NM_001078			TM,SS,ig	3.3
. •	417924	AU077231	Hs.82932	cyclin D1 (PRAD	TM,cyclin	3.3
	405257			-,	TM	3.3
	450396	AU077002	Hs.24950	regulator of G-	TM.RGS	3.3
	416892	L24498	Hs.80409	growth arrest a	TM,Ribosomal_L7Ae	3.3
80		AW067800	Hs.155223		SS S	3.3
JU	425236				TM,SS	3.2
	430812	L10405	Hs.247992			3.2
	431842	NM_005764			TM,SS	3.2
	424897	D63216	Hs.153684	frizzted-relate	TM,Fz,NTR	J.2

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41482 41803						
					mu ocia	3.1
41003	21 M6		Hs.77424	Fc fragment of	TM,SS,ig	3.1
41003			Hs.83321	neuromedin B	SS	3.1
42163			Hs.106260	sorting nexin 1	TM,PX SS,tubutin-binding	3.1
_ 44128			Hs.167	microtubule-ass	TM,MCT	3.1
5 41852		019020	Hs.85838	solute carrier	TM,SS	3.1
40126				Incomela alega	TM,horneobox	3.1
45070		0304	Hs.25351	iroquois-class	TMLSS,enolase	3.0
4244		J_001975	Hs.146580	enolase 2. (gam	TM,alpha-amylase	3.0
4033				PRO0806 protein	TM	3.0
10 4327		113013	Hs.278919	serum-inducible	TM pkinase,POLO_box	3.0
4343		A121098	Hs.3838	activin A recep	TM, Activin_recp, pkinase	3.0
4245		)2911	Hs.150402	acutili v lecch	SS	3.0
4061		m.n.a		gb:22d10 Human	TMSS	3.0
15 4081 4319		/26213 L080239	Hs.272284	Human DNA seque	TM	3.0
		LU0U239	NS.21 2204	Homan Divisoras	TM	3.0
4037		00010	Hs.20019	hemochromatosis	TM,SS,ig,MHC_I,histone,SPRY,zf-B_box,zf-C3HC4	3.0
4479		92910 F008192	Hs.194283	putative GR6 pr	SS	3.0
4288			Hs.278461	matrilin 3	SS	3.0
20 4325		J224741 W085781	Hs.26270	Homo sapiens cD	TM	3.0
20 4533		11003701	149.20210	( to the copies to	TM_SS_ABC_membrane,ABC_tran	3.0
4055		91963	Hs.129700	tolloid-like 1	TM,SS,EGF,CUB,Astacin	3.0
		131303	15.125100		SS	3.0
	1707				TM,ion_trans,K_tetra	3.0
	3144 B375 N	4M_003081	Hs.84389	synaptosomal-as	TM,NA	3.0
		AF016833	Hs.122785		TM,Glyco_hydro_31,trefoil	3.0
		41010000	115.122100	Hillians Brasser.	TM	3.0
	6506	BE242870	Hs.75379	solute carrier	TM,SDF	3.0
413	3472 E	BE24201U	15.75075	301000 4011101		
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	18119	1040172 1	W26213 H	08055 Z44031 AW954559	R17434	
- 408		1040172_1	W26213 H BE260893	108055 Z44031 AW954559 1 AA078319 R85057 AW803	R17434 3024 H85811 AA078293	
- 408		1040172_1 115882_1	W26213 H BE260893	108055 Z44031 AW954559 1 AAQ78319 R85057 AWB03	R17434 3024 H85811 AA078293	
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. 408 454 40 Pk	54392 ABLE 34C: key: kef: Strand:	115882_1 Uni Sec sec Ind	BE260893  que number c  quence source  quence of hum  instes DNA st	AA078319 R85057 AW800 orresponding to an Eos pro	ibeset is column are Genbank Identifier (GI) numbers. "Dunhar arn, et al. (1999) <u>Nature</u> 402:489-495. e predicted.	n, et al.* refers to the publication entitled *The DNA
40 40 Pk	54392 ABLE 34C: Rey: Ref:	115882_1 Uni Sec sec Ind	BE260893  que number o quence source quence of hum icates DNA st icates nucleof	orresponding to an Eos prog. The 7 digit numbers in the an chromosome 22" Dunharrand from which exons were ide positions of predicted e	ibeset is column are Genbank Identifier (GI) numbers. "Dunhar arn, et al. (1999) <u>Nature</u> 402:489-495. e predicted.	n, et al.* refers to the publication entitled *The DNA
40 Pk	54392 ABLE 34C: key: kef: Strand:	115882_1 Uni Sec sec Ind	BE260893  que number c quence source quence of hum icates DNA st icates nucleot  Strand	orresponding to an Eos pro  . The 7 digit numbers in th  and chromosome 22 Dunha  rand from which exons wer  ide positions of predicted e  Nt_position	abeset iss column are Genbank Identifier (GI) numbers. "Dunhar am, et al. (1999) <u>Nature</u> 402:489-495. e predicted. xons.	n, et al.* refers to the publication entitled *The DNA
40 45 45 45 45 45 45 Pi	54392 ABLE 34C: key: tef: strand: t_position:	115882_1 Uni Sec sec Ind	BE260893  que number c quence source quence of hum icates DNA st icates nucleof  Strand Minus	orresponding to an Eos pro  . The 7 digit numbers in the an chromosome 22" Dunka rand from which exons were ide positions of predicted e  Nt_position 114133-114247,11456	abeset iss column are Genbank Identifier (GI) numbers. "Dunhar am, et al. (1999) <u>Nature</u> 402:489-495. e predicted. xons.	n, et al." refers to the publication entitled "The DNA
40 45 TA 40 Pk Re Nt 45	54392 ABLE 34C: key: kef: strand: It_position: Pkey	115882_1 Uni Sec sec Ind	ge number of que number of quence source quence of hum icates DNA st icates nucleof Strand Minus Minus	orresponding to an Eos prog. The 7 digit numbers in the an chromosome 22" Dunhar rand from which exons were ide positions of predicted et Nt_position 114133-114247,11456 90815-90929	abeset iss column are Genbank Identifier (GI) numbers. "Dunhar am, et al. (1999) <u>Nature</u> 402:489-495. e predicted. xons.	n, et al.* refers to the publication entitled *The DNA
40 45 TA 40 Pk Re N1 45	54392 ABLE 34C: key: kef: Strand: It_position: Pkey 101157	115882_1 Uni Sec sec Ind Ind Ref 9438289 9690246 8076883	gue number of quence source quence source quence of hum icates DNA stricates nucleof Strand Minus Minus Minus	orresponding to an Eos prog. The 7 digit numbers in than chromosome 22 Dunharrand from which eositions of predicted e. Nt. position 114133-114247,11456 90815-90929 86008-86355	abeset iss column are Genbank Identifier (GI) numbers. "Dunhar am, et al. (1999) <u>Nature</u> 402:489-495. e predicted. xons.	n, et al.* refers to the publication entitled *The DNA
40 45 40 Pk Re St Ni 45 Pi 44 44 44 44	54392  ABLE 34C: Rey: Ref: Strand: R_position: Pkey 101157	115882_1 Uni Sec sec Ind Ref 9438289 9690246 8076883 9931258	gue number of que number of quence source quence of hum icates DNA st icates nucleof Strand Minus Minus Minus Minus Minus	orresponding to an Eos pro 2. The 7 digit numbers in that an chromosome 22" Dunhar and from which exons were ide positions of predicted et Nt_position 114133-114247,11456 98815-9929 86008-86355 26064-26208	abeset iss column are Genbank Identifier (GI) numbers. "Dunhar am, et al. (1999) <u>Nature</u> 402:489-495. e predicted. xons.	n, et al." refers to the publication entitled "The DNA
40 45 TA 40 PR Re NI 45 PR 45 A45 A45 A45 A45 A45 A46	54392 ABLE 34C: key: kef: Strand: kt_position: Pkey 101157 101189 301260	Uni See sec Ind Ind Ref 9438289 9690246 8076883 9931258 8246737	que number o que number o quence source quence of hum icates DNA st icates nucleot Strand Minus Minus Minus Minus Plus	orresponding to an Eos pro 2. The 7 digit numbers in the control of the control o	abeset iss column are Genbank Identifier (GI) numbers. "Dunhar am, et al. (1999) <u>Nature</u> 402:489-495. e predicted. xons.	n, et al." refers to the publication entitled "The DNA
40 45 TA 40 PR Re St Nt 45 PH 445 44 44 44 44 44 44 44 44 44 44 44 44	ABLE 34C: key: tef: Strand: lt_position: Pkey 101157 101159 101260 101352 101439 101707	115882_1 Uni See sec Ind Ind Ref 9438289 9690246 8076883 9931258 8246737 2951946	que number o quence source quence of hum icates DNA st licates nucleof Strand Minus Minus Minus Plus Plus	orresponding to an Eos prog. The 7 digit numbers in the can chromosome 22" Dunhar rand from which exons were ide positions of predicted et Nt_position 114133-114247,11456 90815-90929 86008-86355 26064-26208 92933-94026 21972-22104	abeset iss column are Genbank Identifier (GI) numbers. "Dunhar am, et al. (1999) <u>Nature</u> 402:489-495. e predicted. xons.	n, et al.* refers to the publication entitled *The DNA
40 45 TA 40 Pk Re NI 45 Pi 44 44 44 44 44 44 44 44 44 44 44 44 44	ABLE 34C: key: ker: krand: kt_position: Pkey 101157 101189 101260 401352 401439 401707 402045	115882_1  Uni See sec Ind Ind Ref 9438269 9690246 8076883 9931258 6226732 9251946 7923943	gue number o quence source quence of hum icates DNA st icates nucleof Strand Minus Minus Minus Minus Plus Plus	orresponding to an Eos prog. The 7 digit numbers in the control of	obeset is column are Genbank Identifier (GI) numbers. "Ounhar arn, et al. (1999) <u>Nature</u> 402:489-495. e predicted. xons. 67-114645	
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40 45 TA 40 Pr. Re St. NI 40 40 40 40 40 40 40 40 40 40 40 40 40	ABLE 34Ckey: lef: ltposition: lkey: lef: ltposition: lkey: lo1157 l01189 l01352 l01439 l01352 l01439 l01352 l01439 l01352 l01439 l01352 l01439 l01352 l01439 l01352 l014139 l01352 l01439 l015539 l0345 l034	115882_1  Uni See Ind Ind Ref 9438289 9690246 8076883 9931258 8246737 2951946 7923943 9796341 7328818 9212192 7981303 8954339 8954349 8569726 8569726 8569726 8569726 8569726 8569726 65621489 6010176 9638195 6682697 7329310 6624740	que number o quence source quence source quence of hum icates DNA st licates nucleof Strand Minus Minus Minus Minus Plus Plus Plus Plus Plus Plus Plus Pl	AA078319 R85057 AW803  a. The 7 digit numbers in that and chromosome 22 Dunhar and from which exons were ide positions of predicted et Nt_position of predicted et Nt_posi	3024 H85811 AA078293  ibbeset is column are Genbank Identifier (GI) numbers. "Dunhar arn, et al. (1999) <u>Nature</u> 402:489-495. e predicted. xons.  57-114645  46811,86293-86346,89776-89829,90048-90101,102817- 55858,57124-57309,59633-59761,59957-60123 i64-151690	102924
40 45 TA 40 Pr. Re St. NI 40 40 40 40 40 40 40 40 40 40 40 40 40	ABLE 34C: key: lef: Strand: lt_position: Pkey 101157 101189 101250 101352 101439 101707 102045 102421 102696 102739 102921 103345 10344 103345 10344 10344 10344 10344 10344 10344 10344 10345 10440 10440 10440 10440 10440 1045257 105394	115882_1  Uni Sec Sec Ind Ind Ref 9438289 9650248 967883 9931258 8246737 7923943 9796341 7328818 9212192 7981303 8954339 8954339 8954339 601076 9838195 6862897 7328310 6624123	que number o quence source con l'uence of hum irates DNA st licates nucleof Minus Minus Minus Minus Plus Plus Minus Plus Plus Plus Plus Plus Plus Plus Pl	AA078319 R85057 AW803  a. The 7 digit numbers in that and chromosome 22 Dunhar and from which exons were ide positions of predicted et Nt_position of predicted et Nt_posi	3024 H85811 AA078293  ibbeset is column are Genbank Identifier (GI) numbers. "Dunhar arn, et al. (1999) <u>Nature</u> 402:489-495. e predicted. xons.  57-114645  46811,86293-86346,89776-89829,90048-90101,102817- 55858,57124-57309,59633-59761,59957-60123 i64-151690	102924
40 45 TA 40 Pr. Re St. NI 40 40 40 40 40 40 40 40 40 40 40 40 40	54392  ABLE 34C: key: lef: ltrand: lt_position: Pkey 101157 101189 101260 401352 401439 401707 402045 402421 402696 402739 402921 403095 403111 403345 403346 403782 404115 404200 404347 404939 405257 405394 405547 405609	115882_1  Uni See sed Ind Ind Ref 9438289 9650248 9931258 8246737 293943 9796341 7328818 27981303 8954339 8954339 8954339 8954339 601078 96858976 8078608 9621489 601078 601078 6026977 7328310 6624123 1054740 5757553	que number o quence source juence of hum icrates DNA st licates nucleot Minus Minus Minus Minus Plus Plus Plus Plus Plus Plus Plus Pl	AA078319 R85057 AW803  orresponding to an Eos pro  . The 7 digit numbers in than chromosome 22 Dunhar and from which exons were received positions of predicted et   Nt_position 114133-114247,11456 90815-90929 86008-86355 26064-26208 92933-94026 21972-22104 5964-6128 46609-46662,46758-4 23600-23731 60456-61019 52242-52384,55599-1 150025-150240,1515 175012-175159 166200-166628 77890-78069 92752-93015 41326-41633 232707-232982 7066-7210 74493-74829 175318-175476 73121-73273 31900-32373 124361-124520,124 42814-43010,43585 55601,57111-57307	3024 H85811 AA078293  ibbeset iss column are Genbank Identifier (GI) numbers. "Dunhar am, et al. (1999) <u>Nature</u> 402:489-495. e predicted. xons.  57-114645  46811,86293-86346,89776-89829,90048-90101,102817- 55858,57124-57309,59633-59761,59957-60123 664-151690	102924
40 45 TA 40 Pr. Re St. NI 40 40 40 40 40 40 40 40 40 40 40 40 40	S4392  ABLE 34C: key: lef: Strand: luposition: luposit	115882_1  Uni See Ind Ind Ref 9438289 9690248 9690248 9931258 8246737 2951946 97923943 9796341 7328819 2712192 7981303 8954339 8959726 8569726 8569726 8569726 8569726 6562439 9621489 6010176 9638195 6862697 7329310 6624740 5757553	gue number of quence source quence source quence of hum irrates DNA st licates nucleof Strand Minus Minus Minus Minus Plus Plus Minus Plus Plus Plus Plus Plus Plus Plus Pl	AA078319 R85057 AW803  a. The 7 digit numbers in than chromosome 22" Dunhar and from which exons were ide positions of predicted et Nt. position 114133-114247,11456 90815-90929 86008-86355 26064-26208 92933-94026 21972-22104 5964-6128 46609-46662,46758-4 23500-23731 60456-6109 52242-52384,55599-1 50025-150240,1515 175012-175159 166200-166628 77890-78069 92752-393015 41326-41633 232707-232982 7066-7210 74493-74829 175318-175476 73121-73273 31900-32273 124361-124520,124 42814-43010,43583 55601,57111-57307 54344-54584	3024 H85811 AA078293  ibbeset is column are Genbank Identifier (GI) numbers. "Dunhar arn, et al. (1999) <u>Nature</u> 402:489-495. e predicted. xons.  57-114645  46811,86293-86346,89776-89829,90048-90101,102817- 55858,57124-57309,59633-59761,59957-60123 i64-151690	102924
40 45 PR Re St. Nt. 45 PR 44 44 44 44 44 44 44 44 44 44 44 44 44	ABLE 34C: key: lef: strand: lt_position: Pkey 101157 101189 101352 401439 401707 402421 402696 402421 402696 402421 403395 402345 40344 403346 403782 404115 404200 4040399 405257 405394 405609	115882_1  Lini See Sec Lind  Ref 9438289 9690246 807683 973623 9931258 8246737 2951943 9796341 7328818 9212192 7981303 8954339 8954339 8954339 8954339 8954339 8954339 8954339 6010176 983815 662489 6010176 983815 6624123 1054740 1054740 105475553 9142932 9256407	gue number of quence source quence source quence of hum icates DNA st licates nucleof Strand Minus Minus Minus Minus Plus Plus Minus Plus Plus Plus Plus Plus Plus Plus Pl	AA078319 R85057 AW803  a. The 7 digit numbers in the control of th	3024 H85811 AA078293  ibbeset is column are Genbank Identifier (GI) numbers. "Dunhar arn, et al. (1999) <u>Nature</u> 402:489-495. e predicted. xons.  57-114645  46811,86293-86346,89776-89829,90048-90101,102817- 55858,57124-57309,59633-59761,59957-60123 i64-151690	102924
40 45 TA 40 Pr. Re St. NI 40 40 40 40 40 40 40 40 40 40 40 40 40	54392  ABLE 34C: key: lef: strand: lt_position: Pkey 101157 101189 101269 101352 401439 401707 4020421 402696 402739 402421 403095 403111 40344 403345 403346 403782 404105 404105 404200 404347 404909 405257 405394 40517 4056019	115882_1  Uni See sec Inde  Ref 9438289 9690246 8076883 8246737 2951946 7923943 895931258 8246737 2951946 7923943 8959339 8989970 9454649 9521493 9569726 8569726 8569726 8578689 9610176 9638195 68624123 1054740 5757553 9142932 9256407 9256407	que number o quence source quence source quence of hum icates DNA st icates nucleot Minus Minus Minus Minus Minus Minus Minus Minus Plus Plus Minus Plus Plus Plus Plus Plus Plus Plus Pl	AA078319 R85057 AW803  a. The 7 digit numbers in than chromosome 22 Dunhar and from which exons were ide positions of predicted et Nt_position of 114133-114247,11456-90815-90929-9939-90929-2014-2014-2014-2014-2014-2014-2014-2014	3024 H85811 AA078293  ibbeset is column are Genbank Identifier (GI) numbers. "Dunhar arn, et al. (1999) <u>Nature</u> 402:489-495. e predicted. xons.  57-114645  46811,86293-86346,89776-89829,90048-90101,102817- 55858,57124-57309,59633-59761,59957-60123 i64-151690	102924
40 45 PR Re St. Nt. 45 PR 44 44 44 44 44 44 44 44 44 44 44 44 44	ABLE 34C: key: lef: Strand: luposition: Pkey 101157 101189 1011352 401439 401707 402045 402421 402696 402739 402921 403091 403144 403346 403346 403346 404200 404347 404939 405547 405609	115882_1  Uni See ser Ind Ind Ref 9438289 9690248 9690248 8246737 923943 9796341 732881 9796341 732881 9796341 8569726 856976 856976 8078608 9621489 601016 9624123 1054740 5757553	que number o quence source source quence of hum icates DNA st licates nucleot Strand Minus Minus Minus Plus Plus Minus Plus Plus Plus Plus Plus Plus Plus Pl	AA078319 R85057 AW803  a. The 7 digit numbers in than chromosome 22 Dunhar and from which exons were ide positions of predicted et al. (1975)  Nt. position 114133-114247,11456 90815-90929 86008-86355 26064-26208 92933-94026 21972-22104 5964-6128 46609-46662,46758-4 23600-32731 60456-61019 52242-92384,55599-1 150025-150240,1515 175012-175159 166200-166628 77890-78007 92752-393015 41326-41633 232707-232982 7066-7210 74493-74829 175318-175476 73121-73273 31900-32373 124361-124520,124 42814-43010,43583 55601,57111-57307 54304-54584 7400-7527 49533-43850 107068-107277	3024 H85811 AA078293  ibbeset is column are Genbank Identifier (GI) numbers. "Dunhar arn, et al. (1999) <u>Nature</u> 402:489-495. e predicted. xons.  57-114645  46811,86293-86346,89776-89829,90048-90101,102817- 55858,57124-57309,59633-59761,59957-60123 i64-151690	102924
40 45 PR Re St. Nt. 45 PR 44 44 44 44 44 44 44 44 44 44 44 44 44	54392  ABLE 34C: key: lef: strand: lt_position: Pkey 101157 101189 101269 101352 401439 401707 4020421 402696 402739 402421 403095 403111 40344 403345 403346 403782 404105 404105 404200 404347 404909 405257 405394 40517 4056019	115882_1  Uni See sec Inde  Ref 9438289 9690246 8076883 8246737 2951946 7923943 895931258 8246737 2951946 7923943 8959339 8989970 9454649 9521493 9569726 8569726 8569726 8578689 9610176 9638195 68624123 1054740 5757553 9142932 9256407 9256407	gue number of quence source quence source quence of hum icates DNA st licates nucleof Strand Minus Minus Minus Minus Plus Plus Minus Plus Plus Plus Plus Plus Plus Plus Pl	AA078319 R85057 AW803  a. The 7 digit numbers in than chromosome 22 Dunhar and from which exons were ide positions of predicted et Nt_position of 114133-114247,11456-90815-90929-9939-90929-2014-2014-2014-2014-2014-2014-2014-2014	3024 H85811 AA078293  ibbeset is column are Genbank Identifier (GI) numbers. "Dunhar arn, et al. (1999) <u>Nature</u> 402:489-495. e predicted. xons.  57-114645  46811,86293-86346,89776-89829,90048-90101,102817- 55858,57124-57309,59633-59761,59957-60123 i64-151690	102924

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TABLE 35A: ABOUT 532 GENES UP-REGULATED IN KIDNEY CANCER
Table 35A lists about 532 genes up-regulated in kidney cancer compared to normal kidney. These were selected as for Table 33A except using an "average" of the 70th pecentile for both the numerator and the denominator and using non-malignant kidney specimens in determining the denominator value.

	Pkey:	Uniqu	e Eas probese	t identifier number	
	ExAcon:	Exem	plar Accession	number, Genbank accession number	
	UnigenelD:	•	ne number		
5	Unigene Ti R1:		ne gene title of turnor to no	mal tissue	
	Pkey	ExAcon	UnigenelD	UnigeneTide	R1
	424704	AI263293	Hs.152096	cytochrome P450, subfamily IU (arachido	40.9
10	426559 458079	AB001914 Al796870	Hs.170414 Hs.54277	paired basic amino acid cleaving system ESTs	35.6 34.6
10	433447	U29195	Hs.3281	neuronal pentraxin ()	32.0
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	29.3
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	25.9 25.4
15	435359 450152	T60843 AI138635	Hs.189679 Hs.22968	ESTs ESTs	25.2
13	452401	NM_007115	Hs.29352	turnor necrosis factor, atpha-induced pro	24.8
	440304	BE159984	Hs.125395	ESTs	24.5
	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	23.4 22.4
20	421155 452795	H87879 AW392555	Hs. 102267 Hs. 18878	hysyl oxidase hypothetical protein FLJ21620	22.2
	414812	X72755	Hs.77367	monokine induced by gamma interferon	22.1
	426471	M22440	Hs.170009	transforming growth factor, aipha	21.3
	427897	NM_017413	Hs.181060	apelin; peptide ligand for APJ receptor	21.3 20.7
<b>25</b>	449523 436961	NM_000579 AW375974	Hs.54443 Hs.156704	chemakina (C-C motif) receptor 5 ESTs	20.5
	447499	AW262580	Hs.147674	KIAA1621 protein	20.4
	438817	AI023799	Hs.163242	ESTs	20.4
	430630	AW269920	Hs.2621	cystatin A (stefin A)	19.8 19.5
30	428227 424086	AA321649 Al351010	Hs.2248 Hs.102267	small inducible cytokine subfamily B (Cy tysyl oxidase	18.7
50	425289	AW139342	Hs.155530	interferon, gamma-inducible protein 16	18.7
	436476	AA326108	Hs.53631	ESTs, Weakly similar to enhancer-of-spli	18.7
	415286	AW249540	Hs.72548	ESTs	18.2 18.1
35	428157 456804	A1738719 A1421645	Hs.298668 Hs.139851	ESTs caveolin 2	17.8
-	429490	AI971131	Hs.293684	ESTs, Weakly similar to atternatively sp	17.5
	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	17.1
	433757	A1949974	Hs.152670	ESTS	16.8 16.4
40	400419 428046	AF084545 AW812795	Hs.81800 Hs.155381	chondroitin sulfate proteoglycan 2 (vers ESTs, Moderately similar to 138022 hypot	16.3
	411642	NM_014932	Hs.71132	neuroligin 1	16.2
	444381	BE387335	Hs.283713	ESTs, Weakly similar to CA54_HUMAN COLLA	16.0
	435767	H73505	Hs.117874	ESTs	15.7 15.6
45	427581 448019	NM_014788 AW947164	Hs.179703 Hs.195641	KIAA0129 gene product ESTs	15.6
43	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	15.5
	447835	AW591623	Hs.164129	ESTS	15.4
	448520	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	14.8 14.8
50	417308 432731	H60720 R31178	Hs.81892 Hs.287820	KIAA0101 gene product fibronectin 1	14.7
-	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	14.6
	419235	AW470411	Hs.288433	neurotrimin	14.6
	426490	NM_001621	Hs. 170087	anyl hydrocarbon receptor hypothetical protein FLJ10134	14.4 14.4
55	421485 422603	AA243499 BE242587	Hs.104800 Hs.118651	hematopoietically expressed homeobox	14.4
	418110	R43523	Hs.217754		14.2
	425984	AW836277	Hs.165636		14.2
	432606	NM_002104 AW975688	Hs.3066 Hs.250867	granzyme K (serine protease, granzyme 3; zona pellucida glycoprotein 3A (sperm re	14.1 14.0
60	436772 444969	A1203334	Hs.160628	ESTs	13.9
••	426890	AA393167	Hs.41294	ESTs	13.8
	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	13.8
	458809	AW972512 AI973016	Hs.20985	sin3-associated polypeptide, 30kD hypothetical protein SBBI48	13.7 13.6
65	446627 452960	AK001335	Hs.15725 Hs.31137	Homo sapiens cDNA: FLJ22681 fis, clone H	13.3
00	417280	AW173116	Hs.262206		13.1
	422173	BE385828	Hs.250619		13.0
	420552	AK000492	Hs.98806	hypothetical protein hypothetical protein FLJ11190	13.0 12.6
70	425188 427871	AK002052 AW992405	Hs.155071 Hs.59622	ESTs, Weakly similar to unknown (H.sapie	12.6
. •	446152	AI292036	Hs.150028		12.5
	426560	AA381661	Hs.119878		12.4
	419034	NM_002110	Hs.89555 Hs.123469	hemopoietic cell kinase ESTs, Weakly similar to AF208855 1 BM-01	12.3 12.3
75	456508 452281	AA502764 T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	12.3
. 5	442932	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma	12.3
	426075	AW513691	Hs.270149		12.2
	434398	AA121098	Hs.3838	serum-inducible kinase	12.2 12.1
80	450506 425782	NM_004460 U66468	Hs.418 Hs.159525	fibroblast activation protein, alpha cell growth regulatory with EF-hand doma	12.0
	426108	AA522037	Hs.166468		11.9
	416000	R82342	Hs.79856	ESTs	11.8
	450236	AW162998	Hs.24684	KIAA1376 protein	11.7
				222	

						11.6
				Homo	sapiens cDNA FLJ11846 fis, clone HE coplastic antigen MA2	11.4
			Ur 175437	<b>FSTs</b>		11.4
	414004		Hs.7155	ESTs.	Weakly similar to 2115357A TYKi pr	11.4 11.3
5	447056			ESTs	•	11.3
	444863		Hs.301323 Hs.30743	ESTs prefer	entially expressed antigen in mela	11.2
	452838 426780	BE242284	Hs.172199		Nate cyclase 7	11.1 11.1
_	453160	AI263307	Hs.146228	ESTS		11.1
10	449539	W80363	Hs.58446	ESTs	ophil cytosolic factor 2 (65kD, chr	11.0
	415323 423508	BE269352 AW604297	Hs.949 Hs.129711	hepa	titis A virus celtular receptor 1	11.0
	408380	AF123050	Hs.44532	diubi	quitin	11.0 11.0
	448410	AK000227	Hs.21126	hypo	thetical protein FLJ20220	10.8
15	451277	AK001123	Hs.26176 Hs.32042	nypo	thetical protein FLJ10261 rtoacylase (aminoacylase 2, Canavan	10.8
	453165 435380	S74727 AA679001	Hs.192221	EST		10.7
	447183	AI554733	Hs.173182	EST		10.7 10.6
••	438330	AW450572	Hs.257316	EST	s s, Weakly similar to K1CQ_HUMAN KERAT	10.5
20	441392	AW451831 Z37976	Hs.222119 Hs.83337	later	nt transforming growth factor beta b	10.5
	418036 452862	AW378065	Hs.8687	EST	s	10.4 10.3
	431512	BE270734	Hs.2795		ate dehydrogenase A	10.3
26	421478	A1683243	Hs.97258 Hs.212533	ESI	s no sapiens cDNA: FLJ22572 fis, clone H	10.3
25	413879 411800	AA132961 N39342	Hs.5184	TH	drosophila homotog	10.3
	433862	D86960	Hs.3610		A0205 gene product	10.3 10.2
	440594	AW445167	Hs.126036	ES.	is is, Wealty similar to transformation-r	10.2
20	414504	AW069181	Hs.293523 Hs.5566	car	iunction protein, beta 2, 26kD (conn	10.2
30	431211 437682	M86849 AA476652	Hs.94952	Ho	no sapiens cDNA: FLJ23371 fis, clone H	10.1
	430097	AI523245	Hs.127638	ES	Ts	10.1 10.0
	432579	AF043244	Hs.278439		deolar protein 3 (apoptosis repressor mo sapiens HSPC285 mRNA, partial cds	9.9
35	434927	H46612 AI743880	Hs.293815 Hs.12876	ES		9.9
33	424113 439981	A1348408	Hs.124675		Te Weakly similar to unnamed protein	9.9 9.9
	411937	AW876626		gb	RC3-PT0028-120200-013-d08 PT0028 Homo	9.9
	439653	AW021103	Hs.6631 Hs.2316	hy	pothetical protein FLJ20373 (Y (sex-determining region Y)-box 9 (ca	9.8
40	428862 424623	NM_000346 AW963062	Hs.165809		STS	9.8
40	410762	AF226053	Hs.66170	H	SKM-B protein	9.8 9.7
	433285	AW975944	Hs.237396		STs	9.6
	413795	AL040178	Hs.14200 Hs.26805	_	STs STs	9.6
45	434392 435542	AW983709 AA687376	Hs.26953	. F	STe	9.6 9.5
73	430887	N66801	Hs.26028		STs, Weakly similar to ALU7_HUMAN ALU S	9.5
	410339		Hs.29825		STs #-like receptor 3	9.5
	452431 405121	U88879 AB028989	Hs.29499 Hs.88500	) п	ritogen-activated protein kinase 8 inter	9.5
50	408134		Hs.42945		cid sobingomyelinase-like phosphodieste	9.4 9.4
• •	438966	AW979074		. 9	b:EST391184 MAGE resequences, MAGP Homo dz (odd Oz/ten-m, Drosophila) homolog 1	9.4
	449629			22 5	:STe	9.3
	441024 445900			9 H	tomo sapiens ctone 24787 mRNA sequence	9.2 9.2
55	43300	AF217513		05 (	lone HQ0310 PRO0310p1 STs, Weakly similar to T00050 hypotheti	9.2
	440074	AAB63045			cotocadherin 17	9.2
	421659 43454			n i	rynothetical protein FLJ13164	9.1
	42728		Hs.1741	85	ectonucientide pyrophosphatase/phosphodi	9.1 9.1
60	42882		4 11- 3743		integrin, alpha M (complement component Homo sapiens mRNA; cDNA DKFZp586I1524 (f	9.0
	41944			175	nhosphorrotein associated with GEMs	9.0
	40785 43194			227	Homo sapiens cDNA FLI 20099 fis, clone CO	9.0 8.9
	44646	0 AW01399	9 Hs.1501	164	ESTs ESTs, Weakly similar to ALU7_HUMAN ALU S	8.9
65			Hs.6864 Hs.417		endothetial cett-specific molecule 1 (NO	8.9
	40797 43725				ESTs	8.7
	4202		6 Hs.311	78	ESTS	8.7 8.7
	4369	59 AL13307			hypothetical protein FLJ12716	8.6
70					secretogranin II (chromogranin C) ESTs	8.6
	4358 4186				thrombospondin 1	8.6 8.6
	4257	70 NM_014	363 Hs.159	492	spastic ataxia of Charlevoix-Saguenay (s	8.6
	4562	49 Al20614			HRIHFB2206 protein flavohemoprotein b5+b5R	8.6
75					hypothetical grotein FLJ20730	8.5
	4302 4172				Homo saniens cDNA FLJ12649 fis, clone N1	8.5 8.4
	4357	266 AK0019	42 Hs.486	63	Homo sapiens cONA FLJ11080 fis, clone PL gb:yi64b03.s1 Soares placenta Nb2HP Homo	8.4 8.4
0/	4479			822	SEC24 (S. cerevisiae) related gene famili	8.4
80	) 4471 429				actoriscleoside triphosphate diphosphohyd	8.3
	435	717 AF2279	05 Hs.10	5794	UDP-glucose:glycoprotein glucosyltransfe	8.3 8.3
	445		55 Hs.14	<b>6065</b>	ESTs	
					300	3

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	454024 443885	AA993527 H91806	Hs.16281	hypothetical protein FLJ23403	8.3
	403713	U31000	Hs.15284	ESTs	8.3 8.3
•	433376	A1249361	Hs.74122	caspase 4, apoptosis-related cysteine pr	8.2
5	419490 444670	NM_006144 H58373	Hs.90708	granzyma A (granzyma 1, cytotoxic T-lymp	8.2
	408761	AA057264	Hs.37494 Hs.238936	ESTs ESTs	8.2 8.2
	453033	AA325869	Hs.31463	KIAA0281 gene product	8.2
10	441224 441689	AU076964	Hs.7753	catumenin	8.1
10	440283	AI123705 AI732892	Hs.106932 Hs.190489	ESTs ESTs	8.1 8.1
	429598	AA811257	Hs.269710	ESTs	8.1
	424775	AB014540	Hs.153026	SWAP-70 protein	8.1
15	451292 453951	AB037716 Al676235	Hs.26204 Hs.24789	KIAA1295 protein ESTs	8.0 8.0
	416200	Al188972	Hs.44257	Homo sapiens mRNA; cDNA DKFZp762O2215 (f	8.0
	431087	H12723	Hs.290791	ESTs	8.0
	432328 419474	AI572739 AW968619	Hs.195471 Hs.155849	6-phosphofructo-2-kinase/fructose-2,6-bi ESTs	7.9 7.9
20	418342	BE002723	Hs. 293504	ESTs, Moderately similar to ALU1_HUMAN A	7.9
	408088	AW157022	Hs.4947	Homo sapiens cDNA: FLJ22584 fis, clone H	7.9
	413719 440987	8E439580 AA911705	Hs.75498 Hs.130229	small inducible cytokine subfamily A (Cy ESTs	7.9 7.9
25	412448	L12964	Hs.73895	tumor necrosis factor receptor superfami	7.9
25	415737	AA167626	Hs.118743	ESTs	7.9
	412959 424247	D87458 X14008	Hs.75090 Hs.234734	KIAA0282 protein lysozyme (renal amyloidosis)	7.8 7.8
	453331	AI240665	Hs.8895	ESTs	7.8
30	421991	NM_014918	Hs.110488	KIAA0990 protein	7.8
30	443450 431876	N66045 AA521183	Hs.133529 Hs.269678	ESTs ESTs	7.8
	432582	AI623817	Hs.168457	ESTs	7.8 7.7
	445800	AA126419	Hs.301632	ESTs	7.7
35	424636 432134	AA453734 AI816782	Hs.10198 Hs.122583	ESTs Homo sapiens cDNA: FLJ21934 fis, clone H	7.7
-	446873	AI554439	Hs.30724	ESTs	7,7 7,7
	400793	AA635062	Hs.50094	Homo sapiens mRNA; cDNA DKFZp43400515 (I	7,7
	436061 442028	AI248584 AI239437	Hs.190745 Hs.48945	Homo sapiens cDNA: FLJ21326 fis, clone C	7.7
40	442760	BE075297	Hs.10067	ESTs ESTs, Weakly similar to KIAA1205 protein	7,7 7,7
	442152	R39246	Hs.239666	Homo sapiens cDNA FLJ13495 fis, clone PL	7.7
	427944 414646	AA417878 AA353776	Hs.48401	ESTs, Weakly similar to ALUS_HUMAN ALU S	7.6
	407634	AW016569	Hs.901 Hs.301280	CD48 antigen (B-cell membrane protein) ESTs, Highly similar to AF241831 1 intra	7.6 7.6
45	418372	AA311833	Hs.84318	replication protein A1 (70kD)	7.6
	434666 442432	AF151103	Hs.112259	T cell receptor gamma locus	7.6
	408418	8E093589 AW963897	Hs.38178 Hs.44743	Homo sapiens cDNA: FLJ23468 fis, ctone H KIAA1435 protein	7.6 7.6
50	418805	AI829520	Hs.227513	ESTs	7.5
50	425354 408743	U62027 AL110246	Hs.155935	complement component 3a receptor 1	7.5
	444836	ALT10246 AI589825	Hs.47367 Hs.173504	hypothetical protein from EUROIMAGE 7836 ESTs, Weakly similar to JC5238 galactosy	7.5 7.5
	421810	AK001718	Hs.108530	hypothetical protein FLJ 10856	7.4
55	432753 420061	NM_014075 AW024937	Hs.278915 Hs.29410	PRO0593 protein	7.4
-	432865	A1753709	Hs.152484	ESTs ESTs	7.4 7.4
	419070	AW979068	Hs.182503	ESTs	7.4
	430172 446343	AA468591 AW771414	Hs.161889 Hs.8314	ESTs	7.4
60	424125	M31669	Hs.1735	ESTs Inhibin, beta B (activin AB beta polypep	7.4 7.4
	453818	BE256832	Hs.10711	Homo sapiens cDNA FLJ13449 fis, clone PL	7.4
	447046 410577	AA326187 X91911	Hs.17170 Hs.64639	G protein-coupled receptor 4	7.4
	452240	AI591147	Hs.61232	glioma pathogenesis-related protein ESTs	7,4 7.3
65	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	7.3
	422631 450205	BE218919 AI219748	Hs.118793	hypothetical protein FLJ10688 ESTs	7.3
	437212	AI765021	Hs.11356 Hs.210775	ESTs	7.3 7.3
70	440193	AW902312	Hs.7037	pallid (mouse) homotog, patlidin	7.2
70	417022	NM_014737 AJ819018	Hs.80905	Ras association (RalGDS/AF-6) domain fam	7.2
	451818 453013	AA031407		gb:ts54f01.x1 NCI_CGAP_Kid8 Homo sepiens gb:zk15g12.r1 Soares_pregnant_uterus_NbH	7.2 7.2
	430105	X70297	Hs.2540	cholinergic receptor, nicotinic, alpha p	7.2
75	451621 442438	AJ879148 AA995998	Hs.26770	fatty acid binding protein 7, brain gb:os26b03.s1 NCI_CGAP_Kid5 Homo sapiens	7.2
	415138	C18356	Hs.78045	gitos20003.81 NCI_CGAP_Rido Homo sapiens tissue factor pathway inhibitor 2	7.2 7.2
	407305	AA715284		gb:nv35f03.r1 NCI_CGAP_Br5 Homo sapiens	7.2
	452814 426028	AI092790 NM_001110	Hs.55016 Hs.172028	hypothetical protein FLJ21935	7.2
80	443462	AI064690	Hs. 171176	a disintegrin and metalloproteinase doma ESTs	7.2 7.2
	422060	R20893	Hs.75613	CD36 antigen (collagen type I receptor,	7.2
	434096 443161	AW662958 AI038316	Hs.75825	pleiomorphic adenoma gene-like 1 gb:ox48c08.x1 Soares_total_fetus_Nb2HF8_	7.1
					7.1
				400	

					7.1
			Hs.171942	ras responsive eternent binding protein 1 single-stranded-DNA-binding protein	7.1
	426423 412783		Hs.169833 (	singre-strandeo-DNA-diriding process DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	7.1
	435664	AI032087		ESTs	7.0
5	431708	AI698136		ESTs	7.0
-	426501	AW043782		ESTs	7.0 7.0
	453548	AL079983		albumin	7.0 7.0
	426595	AW971980	Hs.62402	p21/Cdc42/Rec1-activated kinase 1 (yeast Homo sapiens cDNA: FLJ22528 fis, clone H	7.0
10	412490	AW803564 AF016028	Hs.268850 Hs.260039	sarcospan (Kras oncogene-associated gene	6.9
10	431556 420018	U56387		proprotein convertase subtilisin/kexin t	6.9
	418986	Al123555		ESTs	6.9
	430290	AI734110	Hs.136355	ESTs	6.9
	427472	AA522539		transposon-derived Buster3 transposase-I	6.9 6.9
15	444042	NM_004915	Hs.10237	ATP-binding cassette, sub-family G (WHIT	6.9
	414737	A1160386	Hs.125087	ESTs ESTs	6.9
	420479 432656	AW183695 NM_000246	Hs.186572 Hs.3076	MHC class II transactivator	6.9
	414217	Al309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	6.9
20	431870	AW449902	Hs.105500	ESTs	6.9
	415788	AW628686	Hs.78851	KIAA0217 protein	6.9
	430066	AI929659	Hs.237825	signal recognition particle 72kD	6.9 6.8
	437156	A1916600	Hs.121194	Homo sapiens cDNA: FLJ21569 fis, clone C	6.8
25	401539	A1400211	Hs.173044	ESTs	6.8
23	412782 416058	AI189211 L08895	Hs.78995	MADS box transcription enhancer factor 2	6.8
	437205	AL110232		gb:Homo sapiens mRNA; cDNA DKFZp564D2071	6.7
	458814	AI498957	Hs.170861	ESTs	6.7
	452106	A1141031	Hs.21342	ESTs	6.7 6.7
30	413249	AF167160	Hs.75251	DEAD/H (Asp-Glu-Ala-Asp/His) box binding	6.7
	420910	AL049437	Hs.100292	Homo sapiens mRNA; cDNA DKFZp588E1120 (f ESTs	6.7
	445527	W39694 NM_002019	Hs.83286 Hs.138671	fms-related tyrosine kinase 1 (vascular	6.7
	424063 421977	W94197	Hs.110165	ribosomal protein L26 homolog	6.7
35	430280	AA361258	Hs.237868	Interleukin 7 receptor	6.7
	415989	AI267700	Hs.111128	ESTs	6.7
	418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	6.6 6.6
	425295	AA431366	Hs.37251	ESTs	6.6
40	438619	AB032773	Hs.6341 Hs.23096	TU12B1-TY protein	6.6
40	424916 429697	AW867440 AW296451	Hs.24605	ESTs ESTs	6.6
	429097	M73720	Hs.646	carboxypeptidase A3 (mast cell)	6.6
	403549	MITOTEG	1.5.5 15		6.6
	449008	AW578003	Hs.22826	tropomodulin 3 (ubiquitous)	6.6
45	435798	BE395289	Hs.12720	elF4E-transporter	6.6 6.6
	447217	BE465754	Hs.17778	neuropilin 2	6.6
	453070	AK001465	Hs.31575 Hs.68301	SEC63, endoptasmic reticutum translocon ESTs	6.6
	410276 435391	A1554545 AA704588	Hs.58934	ESTS	6.6
50	421878	AA299652	Hs.111496		6.6
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	6.5
	448789	BE539108	Hs.22051	Homo sapiens mRNA; cDNA DKFZp434O119 (fr	6.5 6.5
	425331	AW962128		gb:EST374201 MAGE resequences, MAGG Homo	6.5
55	431956	AK002032	Hs.272245		6.5
55	444880	AW118683 AI858275	Hs.154150 Hs.143659		6.5
	434131 446658	AI440137	Hs.164989		6.5
	408150	BE620274	Hs.43112	Homo sapiens mRNA; cDNA DKFZp434B1620 (f	6.5
	403790				6.5
60	417129	AI381800	Hs.143275		6.5 6.4
	452119	AI656378	Hs.33461	ESTs	6.4
	437396		Hs.21621	hypothetical protein OKFZp7620076 ESTs	6.4
	458946 452110		Hs.42311 Hs.28005		6.4
65	449318				6.4
05	408308		Hs.44197		6.4
	402474				6.4
	430712				6.4 6.4
70	418299				6.4
70	432683				6.4
	423764 409571				6.4
	401600				6.4
	415076				6.4
75	43292	5 AA878324	Hs.19273	M ESTs	6.4 6.4
	42752				6.4
	45389				6.3
	43033		Hs.23949 Hs.18235		6.3
80	45337 42132				6.3
	45065			5 Kruppel-type zinc finger protein	6.3
	41349	7 BE17766	1	gb:RC1-HT0598-020300-011-h02 HT0598 Homo	6.3
	44527	9 R41900	Hs.2224	5 ESTs	6.3

	429747	M87507	Hs.2490	caspase 1, apoptosis-related cysteine pr	6.3
	421252	AA765930	Hs.130878	ESTs .	6.3
	432140	AK000404	Hs.272688	hypothetical protein FLJ20397	6.3
5	434203 419436	BE262677 AA991639	Hs.283558 Hs.15036	hypothetical protein PRO1855	6.2
9	430287	AW182459	Hs.125759	ESTs, Highly similar to AF161358 1 HSPC0 ESTs, Weakly similar to tumor suppressor	6.2 6.2
	409690	W45393	Hs.94642	ESTs, Highly similar to ATFa [H.sapiens]	6.2
	420101	AW500529	Hs.95180	Homo sapiens mRNA; cDNA DKFZp434A205 (tr	6.1
10	435889 417259	AI249107	Hs.269901	ESTs	6.1
10	448030	AW903838 N30714	Hs.81800 Hs.20161	chondroitin sulfate proteoglycan 2 (vers HDCME31P protein	6.1 6.1
	442571	C06338	Hs.165464	ESTs	6.1
	421202	AF193339	Hs.102506	eukaryotic translation initiation factor	6.1
15	415558	AA885143	Hs.125719	ESTs .	6.1
13	408042 438086	AL049233 AA336519	Hs.42244 Hs.301167	Homo sapiens mRNA; cDNA DKFZp564A023 (fr Homo sapiens cDNA: FLJ21545 fis, clone C	6.1 6.1
	427390	AJ432163	Hs.268231	Homo sapiens cDNA: FLJ23111 fis, clone L	6.0
	440749	W22335	Hs.7392	Homo sapiens mRNA; cDNA DKFZp761E0323 (1	6.0
20	448822	BE149845	Hs.289038	Homo sapiens cDNA: FLJ20994 fis, clone C	6.0
20	424806 435185	AA382523 AA669490	Hs.105689	ESTs	6.0
	452235	AL039743	Hs.289109 Hs.28514	dimethylarginine dimethylarninohydrolase Homo sapiens mRNA; cDNA DKFZp434H092 (fr	6.0 6.0
	432415	T16971	Hs.289014	ESTs .	6.0
25	436345	AA873008	Hs.121572	ESTs	6.0
25	439451	AF086270	Hs.278554	heterochromatin-like protein 1	6.0
	434674 429653	AA831879 NM_005955	Hs.136985 Hs.211581	ESTs metal-regulatory transcription factor 1	6.0 6.0
	446822	AB037794	Hs.16229	KIAA1373 protein	6.0
	423590	AW952412	Hs.65874	ESTs	6.0
30	424026	AI798295	Hs.123218	ESTs	5.9
	423246	AL119114	Hs.23107	ESTs	5.9
	420982 435008	AW576160 AF150262	Hs.100729 Hs.162898	KIAA0692 pratein ESTs	5.9 5.9
	420092	AA814043	Hs.88045	ESTs	5.9
35	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	5.9
	410193	AJ132592	Hs.59757	zinc finger protein 281	5.9
	450534	AI570189	Hs.25132	KIAA0470 gene product	5.9
	440146 425361	AW014231 AA355933	Hs.90790 Hs.132221	Homo sapiens cDNA: FLJ22930 fis, clone K Homo sapiens cDNA FLJ12401 fis, clone MA	5.9 5.9
40	425174	D87450	Hs.154978	KIAA0261 protein	5.9
	458287	AA987556	Hs.12867	ESTs	5.9
	433793	AW975959	Hs.107513	ESTs, Moderately similar to KIAA 1058 pro	5.8
	443228	W24781	Hs.293798	ESTS	5.8
45	419983 410361	W55956 BE391804	Hs.94030 Hs.62661	Homo sapiens mRNA; cDNA DKFZp586E1624 (f guanyfate binding protein 1, interferon-	5.8 5.8
	415714	NM_002290	Hs.76672	laminin, alpha 4	5.8
	421689	N87820	Hs.106826	hypothetical protein	5.8
	431176	AI026984	Hs.293662	ESTs	5.8
50	443837 410623	AI984625 AW958932	Hs.9884 Hs.293833	spindle pole body protein ESTs	5.8 5.8
50	421298	AW172431	Hs.13012	ESTS	5.8
	449052	AW029507	Hs.161102	ESTs	5.8
	433043	W57554	Hs.125019	ESTs, Highly similar to KIAA0886 protein	5.8
55	439444	AI277652	Hs.54578	ESTs	5.7
33	428698 411928	AA852773 AA888624	Hs.297939 Hs.19121	ESTs, Weakly similar to T17344 hypotheti adaptor-related protein complex 2, alpha	5.7 5.7
	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	5.7
	417315	AI080042	Hs.180450	ribosomal protein S24	5.7
60	422544	AB018259	Hs.118140	KIAA0716 gene product	5.7
UU	412584 433505	X54870 AW504027	Hs.74085 Hs.15301	DNA segment on chromosome 12 (unique) 24 Homo sapiens NY-REN-25 antigen mRNA, par	5.7 5.7
	410425	BE278367	Hs.63510	KIAA0141 gene product	5.7
	457292	Al921270	Hs.214178	Homo sapiens cDNA FLJ14251 fis, clone OV	5.7
65	457100	AA417878	Hs.48401	ESTs, Wealdy similar to ALU8_HUMAN ALU S	5.7
05	436995 426283	AI160015 NM 003937	Hs.118112 Hs.169139	ESTs kynureninase (L-kynurenine hydrolase)	5.7 5.7
	441518	AW161697	Hs.294150	ESTs	5.7
	448807	AI571940	Hs.7549	ESTs	5.7
70	449656	AA002008	Hs.188633	ESTs	5.7
70	439211	A1890347	Hs.271923 Hs.2561	Homo sapiens cDNA: FLJ22785 fis, clone K	5.7 5.7
	430440 413551	X52599 BE242639	Hs.75425	nerve growth factor, beta polypeptide ubiquitin associated protein	5.7 5.7
	441633	AW958544	Hs.112242		5.7
75	427093	AA398118	Hs.97579	ESTs	5.6
75	418250	U29926	Hs.83918	adenosine monophosphate deaminase (isofo	5.6
	432267 419839	AK000872 U24577	Hs.274227 Hs.93304	Homo sapiens cDNA FLJ10010 fis, clone HE	5.6 5.6
	430253	AK001514	Hs.235844	phospholipase A2, group VII (platelet-ac hypothetical protein FLJ10652	5.6
	450447	AF212223	Hs.25010	hypothetical protein P15-2	5.6
80	434623	AB023163	Hs.4014	KIAA0946 protein; Huntingtin interacting	5.6
	420642	AK001520	Hs.99545	Homo sepiens cDNA FLJ10658 fis, clone NT	5.6 s.c
	414020 420825	NM_002984 AI656727	Hs.75703	small inducible cytokine A4 (homologous gb:tl53f12.x1 NCI_CGAP_GC6 Homo sapiens	5.6 5.6
				A	0.0

	422262	T55979	Hs.115474 n	eplication factor C (activator 1) 3 (38	5.6
	422363 452046		Hs.27657 H	QAA0802 protein	5.6 5.6
	408911			formo sapiens cDNA FLJ14103 fis, clone MA	5.6
5	414844		Hs.77494 d Hs.79351 (	leoxyguanosine kinase otassium channel, subfamily K, member 1	5.6
,	416498 430512		Hs.241578	J6 snRNA-associated Sm-like protein LSm8	5.6
	430339	W28608		ntegral membrane protein 28	5.6 5.6
	420153			nypothetical protein FLJ13910 nuclear phosphoprotein similar to S. cer	5.6
10	420892 441568	AW975076 AI733322		ESTs	5.5
10	414575	H11257	Hs.295233	ESTs	5.5
	419929	U90268	Hs.93810	cerebral cavernous malformations 1	5.5 5.5
	438613	C05569	Hs.243122 Hs.301395	hypothetical protein FLJ13057 similar to Homo sapiens cDNA: FLJ21204 fis, clone C	5.5
15	453064 433409	R40334 A1278802	Hs.25661	ESTs	5.5
13	407094	AF000574	Hs.22405	leukocyte immunoglobulin-like receptor,	5.5 5.5
	425234	AW152225	Hs.165909	ESTS	5.5
	447644	AW861622 AF070578	Hs.108646 Hs.71168	Homo sapiens cDNA FLJ12534 fis, clone NT Homo sapiens clone 24674 mRNA sequence	5.5
20	411653 446534	A1307356	Hs.175225	ESTs	5.5
20	452355	N54926	Hs.29202	G protein-coupted receptor 34	5.5 5.5
	434715	BE005346	Hs.116410	ESTs hypothetical protein PP1044	5.5
	440486 444825	BE243513 AW167613	Hs.7212 Hs.248	mitogen-activated protein kinase kinase	<b>5</b> .5
25	419172	AW338625	Hs.22120	ESTS	5.4
	444931	AV652066	Hs.75113	general transcription factor IIIA	5.4 5.4
	413940	AI633205	Hs.159914	ESTs cadherin 13, H-cadherin (heart)	5.4
	410480 447072	R97457 D61594	Hs.63984 Hs.17279	tyrosytorotein sulfotransferase 1	5.4
30	434361	AF129755	Hs.117772	ÉSTS	5.4
•	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	5.4 5.4
	445175	AV652851	Hs.300846	ESTs neuropilin 1	5.4
	411213 412530	AA676939 AA766268	Hs.69285 Hs.266273	Homo sapiens cDNA FLJ13346 fis, clone OV	5.4
35	422667	H25642	Hs.133471	ESTs	5.4
-	434064	AL049045	Hs.180758	hypothetical protein PRO0082	5.4 5.4
	429688	BE245169	Hs.211610	CUG triplet repeat, RNA-binding protein ATP-binding cassette, sub-family F (GCN2	5.4
	452060 419093	W26980 AI804054	Hs.153612 Hs.112885	ESTs	5.4
40	436267	AW450938	Hs.180115	ESTs	5.4 5.4
	405257			FOT	5.4
	431154	AW971228	Hs.290259 Hs.182362	ESTs ESTs	5.4
	415511 419175	AI732617 AW270037	Hs.179507	KIAA0779 protein	5.3
45	454117	BE410100	Hs.40368	adaptor-related protein complex 1, sigma	5.3 5.3
	423720	AL044191	Hs.23388	Homo sapiens cDNA: FLJ21310 fis, clone C	5.3 5.3
	409995	AW960597 NM_000107	Hs.30164 Hs.77602	ESTs damage-specific DNA binding protein 2 (4	5.3
	414911 455716	BE070263	15.77002	gb:QV4-BT0407-280100-090-e07 BT0407 Homo	5.3
50	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	5.3 5.3
	419985	H66373	Hs.15973	ESTs, Highly similar to bA393J16.3 [H.sa hypothetical protein FLJ20251	5.3
	428753 423099		Hs.192927 Hs.123641		5.3
	404176			•	5.3 5.3
55	431475	AI567669	Hs.287316		5.3
	406625		Hs.119597	stearoyi-CoA desaturase (deta-5-desatur	5.3
	405475 430180		Hs.75456	A kinase (PRKA) anchor protein 10	5.3
	446183	AA354991	Hs.14222	Homo sapiens mRNA; cDNA DKFZp761P019 (fr	5.3 5.3
60	417381		Hs.82042	solute carrier family 23 (nucleobase tra	5.3
	433029		2 Hs.279926 Hs.50492	opsin 3 (encephalopsin) ESTs	5.3
	442837 437140		Hs.28368		5.3
	408989		Hs.49500	KIAA0746 protein	5.3 5.3
65	417355		Hs.82002		5.3
	40736				5.3
	437734 45223				5.3
	42305	7 AW961597	Hs.13081		5.3 5.3
70	43959				5.3
	44650 41640		Hs.15081 Hs.79299		5.2
	42716		Hs.17387	1 KIAA1300 protein	5.2
~-	41681	5 U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	5.2 5.2
75	44821		Hs.73853	gb:tc87d07.x1 NCI_CGAP_CLL1 Homo sapiens bone morphogenetic protein 2	5.2
	41242 41697			granzyme B (granzyme 2, cytotoxic T-lymp	5.2
	40681	5 AA833930	Hs.2880	36 (RNA isopentenytpyrophosphate transferas	5.2 5.2
00	45141	18 BE387790			5.2 5.2
80			Hs.1556 Hs.2320	· . •	5.2
	45115 41591		Hs.7891	3 chemokine (C-X3-C) receptor 1	5.2
	4230				5.2
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428593
                      AW207440
                                     Hs.185973
                                                   degenerative spermatocyte (homolog Droso
                                                                                                                       5.2
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          451149
                      AL047586
                                      Hs.10283
                                                   ESTs
          429458
                      BE161832
                                      Hs.292689
                                                   ESTs
                                                   protein tyrosine phosphatase, receptor t
Homo sapiens cDNA FLJ20137 fis, clone CO
CD69 antigen (p60, early T-cell activati
          422241
                       Y00062
                                      Hs.170121
 5
          432383
                      AK000144
                                      Hs.274449
          417696
                      RF241624
                                      Hs.82401
                                                   hypothetical protein FLJ20424
          442991
                      BE281238
                                      Hs.8886
                                                   conserved gene amplified in osteosarcoma
          426711
                      AA383471
                                      Hs.180669
           438995
                       A1277986
                                      Hs.164875
                                                   ESTs
                                                   ESTs, Weakly similar to ALUS_HUMAN ALU S
10
           438582
                      AI521310
                                      Hs.283365
                                                    Homo sapiens pTM5 mariner-like transposo
          424859
                                      Hs.153527
                      U92014
           445563
                      AW873606
                                      Hs.149006
                                                    ESTs
                       AF283776
                                      Hs.80285
                                                    Homo sapiens mRNA; cDNA DKFZp586C1723 (f
           416852
                                                    similar to proline-rich protein 48
           420567
                       AK000812
                                      Hs.98874
                                                    Homo sapiens mRNA; cDNA DKFZp43400921 (I
15
                      AL133101
AA422029
                                      Hs.99508
           420630
           455510
                                                    ESTs, Weakly similar to hyperpolarizatio
                                      Hs.143640
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5.1
           412676
                       NM_000165
                                      Hs.74471
                                                    gap junction protein, atpha 1, 43kD (con
           438146
                       Z36842
                                      Hs.57548
                                                    FSTs
                                      Hs.128501
           423430
                       AF112481
                                                    RAD54, S. cerevisiae, homolog of, B
20
                                                    sorting nexin 10
           421633
                       AF121860
                                      Hs.106260
                                                    gb:yh88b01.s1 Soares placenta Nb2HP Homo
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5.1
           447197
                       R36075
                       AA773838
                                      Hs.5353
                                                        spase 10, apoptosis-related cysteine p
            436943
                                                    ESTs
                                      Hs.156875
Hs.273789
           456210
                       N49729
                                                    ESTs
                       RR2845
           411893
                                                    Homo sapiens mRNA; cDNA DKFZp586I1524 (f
                                                                                                                         5.1
25
                       W37862
                                       Hs.274368
           432331
            414696
                       AF002020
                                       Hs.76918
                                                    Niemann-Pick disease, type C1
            426822
                       W78950
                                       Hs.220823
                                                    ESTs
                                       Hs 146220
                       AI590346
           444269
                                                    ESTs
                                                    ESTs
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                       AL110216
                                       Hs.12285
           437204
30
            443180
                        R15875
                                       Hs.70945
                                                                                                                         5.0
            431510
                        AA580082
                                       Hs.112264
                                                    ESTs
                                                     gb:QV1-BT0681-290400-181-h05 BT0681 Homo
                       BE087853
            446312
                                                                                                                         5.0
5.0
                                       Hs.15423
                                                     hypothetical protein HDCMC04P
                        AI672487
            449870
            430462
                        AI584156
                                       Hs.105640
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35
            457452
                        AW972675
                                                     gb:EST384766 MAGE resequences, MAGL Homo
            420397
                        NM_007018
                                       Hs.97437
                                                     centrosomal protein 1
                                                     hypothetical protein FLJ10512
                                                                                                                         5.0
                        BE294069
                                       Hs.93581
            408750
                                                                                                                         5.0
                        N67325
                                       Hs.247132
                                                     ESTs
            426874
                                                                                                                         5.0
                                                     Homo sapiens cONA FLJ13465 fis, clone PL
            419746
                        AW867943
                                       Hs.127216
                                                     hypothetical protein PRO2955
 40
            434237
                        AF119908
                                       Hs.235516
                                                                                                                         5.0
                                                     hypoxia-inducible protein 2
            410274
                        AA381807
                                       Hs.61762
            TABLE 358:
                                 Unique Eos probeset identifier number
            Pkey:
 45
            CAT number.
                                 Gene cluster number
                                 Genbank accession numbers
             Accession:
                        CAT number
                                        AW876626 AW876622 AW876624
             411937
                         1266219_1
 50
                                        BE177661 H06215 BE144709 BE144829
                                        BE177001 RU0213 BE1447U9 BE144829
AI656727 AI697687 AI802122 AA910877 Z28718 T16711 AA651731 AL047264 BE000621 R68736 AW992695 AI768764 AW271284 AW974653
AI308951 AW055146 R93609 AW467031 AI096866 AI371871 AI126182 AI564756 AI361460 AI358914 AI419231 AW439733 R87059 AA628064
AW088970 AW008695 R68682 AI719136 R97752 AW196262
                         1373771_1
             413497
                         196769 1
             420825
                                        AW962128 AA355353 AA427363
AL110232 N94765
             425331
                        250199_1
43463_1
 55
             437205
                                        AW979074 AA834841 AA828650
AA995998 AI916584 R61781 T77332 F07756 F08149 F07647
AI038316 AI344631 AI261653
                         467435_1
             438966
             442438
                         542469_1
             443161
                         561305_1
                                        BE087853 AI286184
             446312
                         671114 1
  60
                                         R36075 Al366546 R36167
             447197
                         711623_1
                                         R76886 AI453674 R77049
             447974
                         745643_1
                                        AI475858 AW969013
             448212
                         755099_1
                                         AI819018 R05492 W27615
             451818
                         887271 1
                                         AA031407 N85751 AW974119 AA031408 AA572965
             453013
                         94390 1
                                         BE070263 BE070195 BE070265 BE070202 BE070233 BE070399 BE070203
  65
                         1352695_1
             455716
                         339381_1
             457452
                                         AW972675 AA541366 AA523039
                                         AA715284
             407305
                         312657
             TABLE 35C:
                                  Unique number corresponding to an Eos probeset Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA
  70
             Pkey:
             Ref:
                                  sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
                                  Indicates DNA strand from which exons were predicted.
              Strand:
                                  Indicates nucleotide positions of predicted exons.
              Nt_position:
  75
                                                       Nt position
                                         Strand
                         8072433
              401539
                                         Minus
                                                       53526-53628,55755-55920,57530-57757
              402474
                          7547175
                                         Minus
                                                       137150-137362
              403549
                          8081591
                                         Minus
   80
                                                       152769-153155
              403713
                          6573831
                                         Minus
                          8084957
                                                       87826-87947,89835-90002
              403790
                                         Minus
                          9931122
                                                        52685-52800
              404176
                                         Plus
                                                       73121-73273
              405257
                          7329310
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PCT/US02/29560 WO 03/025138

405475 1931025 Plus 1548-1702

TABLE 36A: ABOUT 169 GENES UP-REGULATED IN KIDNEY CANCER
Table 36A lists about 169 genes up-regulated in kidney cancer compared to normal kidney that are likely to be extracellular or cell-surface proteins. These were selected as for Table 35A and the predicted protein contained a structural domain that is indicative of surface or extracellular localization (e.g. ig, fn3, egf. 7tm domains). Predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number Exacor: Exemplar Accession number, Genbank accession number UnigenelD: Unigene number Unigene gene title: Unigene gene title: Protein Structural Domain R1: Ratio of tumor to normal tissue 5

10 R1:

Unigene gene title Protein Structural Domain Ratio of turnor lo normal tissue

1.5   Proy   Carbon   All Car						DOD-main	Rt
42470 A/85233 htts.17014 performer 430 stages of the 17014 performer 430 s	15				Unigene Title	PSDomain	
ASSIST							
20 45897 AM012113 Hs. 15530 small inducible Ms. 144821 Ms. 2539 Ms. 2549 Ms							34.6
20 63201 NH, (007115 Hz, 2935) Lumror necrosis Hz, 7424 Fragment of Hz, 14812 X7755 Hz, 7424 Fragment of Hz, 14812 X7755 Hz, 7424 Mz, 14812 X7755 Hz, 7427 Mz, 14812 X7755 Hz, 7427 Mz, 14812 X7755 Hz, 7427 Mz, 14812 XZ, 148560 Hz, 14812 XZ, 1							
14421   Missas   145,7724	20						
144812   X7755   Ns. 7785   monofinine indicase   Ns. 10009   Ns. 5443   Ms. 10009   Ms. 1000	20						
Application							
25 449523 NM, 000379 Hs.244 456804 AL/21645 411642 NM, 014932 Hs.71920 477581 NM, 014798 Hs.719703 AURISON AB002367 Hs.719305 477581 NM, 014788 Hs.719703 AURISON AB002367 Hs.719305 AURISON AB002367 Hs.719305 AURISON AB01628 Hs.719305 AURISON AB002367 Hs.719305						TM,SS,EGF	
255 428227 AV221695 Hz.248 Hz.3955 Hz.3955 Hz.3956 Nz.248 Hz.3956				Hs.54443		TM,7tm_1	
465804 AV21645 NB, 100399 Hs, 179703 AV2650 NB, 100399 Hs, 18950 AV2650	25						
411642 NM, Ol4992 Hs.71122 neuroligin 1 MLSS (Obesterase 1.55) 448520 AB002367 Hs.186127 double-cords an MLAO1073 perception an MLAO1074 perception and MLAO10	20			Hs.139851	caveolin 2		
April				Hs.71132			
48520 AB002367 Hs. 1893   421566 NM, 000399 Hs. 19856   422594 AW832677 Hs. 155536   425984 AW832677 Hs. 155536   425984 AW832677 Hs. 155536   425984 AW832677 Hs. 155536   425980 AW972512 Hs. 20985   425980 AW972512 Hs. 20985   425980 AW071335 Hs. 11172   425980 AW071335 Hs. 11172   425188 AW020252 Hs. 15071   425188 AW020252 Hs. 155071   425188 AW020252 Hs. 155071   44398 AV12098 Hs. 3808   447912 AA57711 Hs. 8838   447912 AA57711 Hs. 8839   447912 Hs. 8439   447912 AA57711 Hs. 84			NM_014788	Hs.179703			
417308 H00720 H217308 H217308 H22597 H21805 H22597 H22503 BE242597 H22504 AW836277 H22506 MM 002104 H2306 H22506 AW00135 H231137 H20552 AW000492 H25808 H22597 H20552 AW000492 H25808 H22597 H22505 AW000292 H25807 H22506 H22507			AB002367				
422803 BEZ42587 Hs.18551 hypothetical pr grazyme K (ser all 3256 Mx	30	417308					
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35   383809   AW972512   15 20985   5   13,7   466627   A973016   Ks 15725   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6   13,6							14.1
A6627   A973016	25						13.7
45960 AX00033 Hs.31137 Homo sapiens cD hypothetical pr hypothe	33						
420552 AK000492 Hs. 15071 40 41934 NM.002110 Hs. 39555 hempoletical pr hypothetical pr 1M. 123 homodomain adj 1M. promodomain print 1M. planase, POLO, box 122 homodomain adj 1M. promodomain print 1M. planase, POLO, box 122 homodomain adj 1M. promodomain print 1M. planase, POLO, box 122 homodomain print 1M.							
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40 419394 NM, 002110 Hs 99555 hemopoietic cel 42932 AA457211 Hs 8838 hemopoietic cel 542932 AA457211 Hs 8838 hemopoietic cel 542938 AA72108 Hs 3838 hemopoietic cel 545566 NM, 004460 Hs 418 A18 455566 Hs 48632 AR23037 Hs 166468 hs 5566 Hs 3310 A33662 A8602103 Hs 55631 Hs 3493 A872103 AR2303 AW02103 Hs 27843 Hs 1729 Hs 27843 AR2303 AW02103 Hs 27843 Hs 27843 Hs 1729 A860213 AR2303 AW02103 Hs 27843 Hs 27843 Hs 27843 AR2303 AW02103 Hs 27843 Hs 27843 Hs 27843 AR2303 AW02103 Hs 27843 Hs 27843 AR2303 AW02103 Hs 27843 Hs 27843 AR2303 AW02103 Hs 27843 Hs 38879 Hs 27843 AR2303 AR2303 AW02103 Hs 27843 Hs 38879 Hs 27843 AR2303 AR2303 AW02103 Hs 27843 Hs 38879 Hs 27843 AR2303 AR2303 AR2303 AW02103 Hs 27843 AR2303						TM	
Add	<b>4</b> 0					TM,pkinase,SH2,SH3	
A3398	70						
## 150506 NM_004460 Hs. 418 fibroblast acti cell growth reg S\$ 12.0  ## 450108 AA622037 Hs.166468 Hs. 159525 cell growth reg S\$ 12.0  ## 450238 AV162998 Hs.24684 Hs. 172199 adenylate cycla meutrophil cyto aneutrophil cyto meutophil cyto meutophil cyto meutophil cyto meutophil cyto fibrobletical pr Massay AF123050 Hs. 44532 Hs. 21126 hs. 44532 Hs. 21126 hs. 44532 Hs. 21126 hs. 44532 Hs. 21126 hs. 45127 AK001123 Hs. 25176 hs. 33105 S74727 Hs. 32042 sagartacs/dasc fibrobletical pr Massay Hs. 23112 hs. 25176 Hs. 33105 S74727 Hs. 32042 sagartacs/dasc fibrobletical pr Massay Hs. 25176 hs. 33105 S74727 Hs. 32042 sagartacs/dasc fibrobletical pr Massay Hs. 25176 hs. 33105 S74727 Hs. 32042 sagartacs/dasc fibrobletical pr Ms. 33862 De6690 Hs. 3310 sagartacs/dasc fibrobletical pr Ms. 33862 De6990 Hs. 3510 sagartacs/dasc fibrobletical pr Ms. 3510 sa					serum-inducible		
45787 US6468 Hs. 159525 cell growth reg programmed cell 17. MDUF122 11.9 426108 AA522037 Hs. 166468 programmed cell 17. MDUF122 11.9 426780 BE242284 Hs. 177199 and preferentially 18. MASS 11.2 11.2 11.2 11.2 11.2 11.2 11.2 11				Hs.418	fibroblast acti		
456 42618 AAV62937 Hs. 166468 programmed cell MA.01376 protein M.052038 U65011 Hs. 30743 preferentially adentylate cycla hs. 172199 adentylate cycla hs. 172199 adentylate cycla hs. 172190 adentylate cycla hs. 172190 adentylate cycla hs. 172190 adentylate cycla hs. 172190 adentylate cycla hs. 172104 adentylate cycla hs. 172190 adentylate cycla hs. 172104 adentylate cycla hs. 172105 adentylate cycla hs. 172105 adentylate cycla hs. 172107 hp. 172107				Hs.159525			
450236 AW162998 Hs.24894 NJA0137 protes 426780 BE242284 Hs.30743 perferentially to the specific cycle and representally to the	45			Hs.166468			
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48410 AK000227 Hs.21126 hypothetical pr 451277 AK001123 Hs.26176 hypothetical pr 1 M 10.8 453165 S74727 Hs.32042 sapartaos/Jase 1 M 10.8 453165 S74727 Hs.32042 sapartaos/Jase 1 M 10.8 453165 S74727 Hs.32042 sapartaos/Jase 1 M 10.8 453165 Z37976 Hs.83337 latent transfor SS.TB.EGF 10.5 M 10.3 433852 D86960 Hs.3510 KlAA02025 gene p 1 M,SS 10.3 433852 D86960 Hs.3510 KlAA02025 gene p 1 M,SS 10.3 432579 AF043244 Hs.278439 nucleolar prote hypothetical pr 1 M,Connexin 10.0 439653 AW021103 Hs.6631 Hs.2316 SRY (sex-determ 1 M,MMC box 9.8 410762 AF226053 Hs.66170 HSKM-B protein SS.zHAYND 9.8 425431 U88879 Hs.89500 milogen-activat odd color broad 49625 NM, 014253 Hs.23795 odd (odd Ozhen 405121 AB028989 Hs.816501 hlikier ecep 1 M,SS.TRLRRCT 9.5 427283 AL119796 Hs.174185 ectonucleolide score to protectivat odd helidical cel score to protectivat odd helidical protectivat odd hel	50					TM ubiquitin 7tm 3 ANF receptor sushi.7tm_1	
451277 AK001123 Hs.26176 hypothetical pr							11.0
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String							
431512   BEZ70734   Hs.2795   Beddendro   Hs.3610   KIAA0205 gene p   TM,SS   10.3	55					SS,TB,EGF	
433862   D86960   Hs.3810   KIAA0205 gene p gap junction pr   TM,SS   TM, Connexin   TM, Conne	75					TM,ldh	
431211 M86849 Hs.5566 gap junction pr mucleotar prote mucleotar prote mucleotar prote TM, SS, SS, AW021103 Hs.6631 hypothetical pr TM, SS 9.9 MS, WILLIAM MS, SS, TM, WILLIAM MS, WILLIAM MS, WILLIAM MS, SS, TM, WILLIAM MS, WILLIAM							
A					gap junction pr		
439653 AW021103 Hs.6631 hypothetical pr 1M,SS 3.3 AV021103 Hs.2316 SRY (sex-determ 1M,HMG,box 9.8 Hs.2316 AF226053 Hs.66170 Hs.82409 milogen-activat SS,zx-MYND 9.8 Hs.23431 U88879 Hs.29499 milogen-activat SS,zx-MYND 9.5 Hs.82507 milogen-activat SS,zx-MYND 9.5 Hs.82507 milogen-activat SS,zx-MYND 9.5 Hs.82507 MM_014459 Hs.106511 protocadherin 1 milogen-activat SS,zx-MYND 9.5 Hs.107675 X89426 Hs.117186 endomicleoidde Hs.174185 ectonucleoidde Hs.174185 Hs.75426 secretogranin 1 mrombospondin Hs.75426 Secretogranin 1 mrombospondin Hs.75427 Hs.				Hs.278439	nucleolar prote		
428862 NM_000346 Hs.2316 SRY (sex-determ IM,HMS_00X 9.8 Hs.66170 H	60		AW021103				
410762 AF226053 Hs.2949 hs.8610 milogen-activat odz (odd Oz/ten odz Odd Oz/ten odz Oz/ten odz Odd Oz/ten odz Odd Oz/ten odz Oz/ten odz Oz/ten odz Oz/ten odz Oz/ten odz Odd Oz/ten odz	-		NM_000346				
452431							
4965 NM_014253 Hs.23796 odz (odd Ozhen 11							
421659 NM_014459 Hs.106511 protocadherin 1 TM,SS,cacherin SE,Cacherin TM,SS,cacherin SE,Cacherin TM,SS,cacherin SE,Cacherin TM,SS,cacherin SE,Cacherin TM,SS,cacherin TM,SS	15						
477283 AL119796 Hs.174185 ectonucleotide endothelial cel endot	00						9.2
407975 X89426 Hs.41716 endotheliat cel SS.IGFBP TM,SS.Granin 1 1 14,3554 A319145 Hs.57426 secretogranin 1 1 14,3554 A319145 Hs.57431 flavohemoprotei TM,SS.Granin 86 14,30268 AK000737 Hs.237480 hypothetical pr 437672 AV748265 Hs.5741 flavohemoprotei TM,heme_1.oxidored_fad,Cy1_reductase 86 14,30268 AK000737 Hs.237480 hypothetical pr 435717 AF227905 Hs.105794 UDP-glucose:gly TM,SS 8.5 14,33376 Al249361 Hs.74122 caspase 4, apop 433376 Al249361 Hs.74122 caspase 4, apop 4333376 Al249361 Hs.97078 granzyme A (gra 433033 A325869 Hs.31463 KJAA0281 gene p TM,SS.bytpsin 8.2 14,3238 AJ572739 Hs.195471 Hs.95471 H					protocauncini i	TM SS Phosphodiest Somatomedin B	9.1
70 418693 AJ319145 Hs.75426 secretogramin 1 TM,SS,Gramin 8.6 437672 AW748265 Hs.5741 flavohemoprotei TM,heme_1_oxidored_fad,Cy1_reductase 8.6 430268 AK000737 Hs.237480 hypothetical pr 447850 AB018298 Hs.19822 SEC24 (S. cerev 1M, heme_1_oxidored_fad,Cy1_reductase 8.5 437671 AF227905 Hs.105794 UDP-glucose:gly TM,SS 8.5 433376 AJ249361 Hs.74122 caspase 4, apop 453333 AA325869 Hs.31463 KIAA0281 gene p 433333 AA325869 Hs.31463 KIAA0281 gene p 433238 AJ572739 Hs.195471 6-phosphofructo 5MC 1M, heme_1_oxidored_fad,Cy1_reductase 8.6 432424 Kj.4008 Hs.75498 small inducible SIA IM, heme_1_oxidored_fad,Cy1_reductase 8.6  TM,SS,Gramin 8.6 EGF,TSPN,tsp_1,tsp_3,vwc 8.6 TM,heme_1_oxidored_fad,Cy1_reductase 8.6 TM,heme_1_oxidored_fad,Cy1_red							8.9
70 418693 A1750878 Hs.87409 thrombospondin 437672 AVV748265 Hs.5741 flavohemoprotei TM,heme_1.oxidored_fad,Cyt_reductase 8.6 Ms.74850 A8018298 Hs.19822 SEC24 (S. cerev TM 8.4 Ms.74870 A5217905 Hs.105794 UDP-glucose:gly TM,Cs)vo_transf_8 8.3 Ms.74122 caspase 4, apop TM,Cs_p20,ICE_p10,CARD 8.2 Ms.74122 hs.74122 caspase 4, apop TM,Cs_p20,ICE_p10,CARD 8.2 Ms.74122 hs.74122 caspase 4, apop TM,Sc,bryskin 8.2 Ms.74124 hs.98708 granzyme A (grant Ms.74125 hs.74125 hs							
A37672	70			Hs 87409	thrombospondin	EGF,TSPN,tsp_1,tsp_3,vwc	
ASD	70				flavohemoprotei	TM,heme_1,oxidored_fad,Cyt_reductase	
447850 AB018298 Hs.19822 SEC24 (S. cerev TM 35717 AF227905 Hs.105794 UDP-glucose:gly TM,Gtyco_transf_8 8.2 435717 AF227905 Hs.105794 UDP-glucose:gly TM,Gtyco_transf_8 8.2 432376 AI249361 Hs.7422 caspase 4, apop TM,ICE_p20,ICE_p10,CARD 8.2 439337 AA325869 Hs.31463 KIAA0281 gene p TM,SS,trypsin 8.2 432328 AI572739 Hs.195471 6-phosphofructo TM,GFF2K,PGAM 7.9 413719 BE439580 Hs.75498 small inducible SS,ILB 7.9 80 412448 L12964 Hs.73895 tymor necrosis TM,SS,TNFR_c6 7.9 424247 X14008 Hs.234734 lysozyme (renal SS,lys 7.8 421991 NM_014918 Hs.110488 KIAA0990 protei SS 7.8						TM,SS .	
A35717							
75 433376 AI249361 Hs.74122 caspase 4, apop TM,CE_pAU,ICE_bTU,CARU 0.2 43903 MM_006144 Hs.90708 granzyme A (gra TM,SS,tyrpsin 8.2 453033 AA325869 Hs.31463 KIAA0281 gene p TM 432718 BE439580 Hs.75498 small inducible SS,IL8 7.9 413719 BE439580 Hs.75498 small inducible SS,IL8 7.9 412448 L12964 Hs.73895 tmmor necrosis TM,SS,TNFR_c6 7.9 424247 X14008 Hs.234734 lysozyme (renal 421991 NM_019918 Hs.110488 KIAA0990 protei SS 7.8	-						
419490 NM, 006144 Hs.90708 granzyme A (gra 1M,SS,TypSin 6.2 435033 AA325869 Hs.31463 KIAA0281 gene p TM 8.2 432328 AI572739 Hs.195471 6-phosphofucto TM,6PF2K,PGAM 7.9 413719 BE439580 Hs.75498 small inducible SS,IL8 7.9 412448 L12954 Hs.73895 tumor necrosis TM,SS,TNFR_c6 7.9 424247 X14008 Hs.234734 hysozyme (renal SS,bys 7.8 421991 NM_01918 Hs.110488 KIAA0990 protei SS 7.8	75		6 Al249361	Hs.74122			
453033 A325869 Hs.31463 KIAA0281 gene p TM 432328 A1572739 Hs.195471 6-phosphofructo TM,6PF2K,PGAM 7.9 413719 BE439580 Hs.75498 small inducible SS,IL8 7.9 41248 L12964 Hs.73895 tmror necrosis TM,SS,TNFR_c6 7.9 424247 X14008 Hs.234734 lysozyme (renal SS,bys 7.8 421991 NM_014918 Hs.110488 KIAA0990 protei SS 7.8							
#3.7328 AI5/27.99 Hs.19947/ Spitishiototo #5.18 7.9  #4.3719 BE439580 Hs.75498 small inducible SS,ILB 7.9  #4.13719 BE439580 Hs.73895 tumor necrosis TM,SS,TNFR_c6 7.9  #4.24247 X14008 Hs.234734 lysozyme (renal SS,lys 7.8  #4.21991 NM_014918 Hs.110488 KIAA0990 protei SS 7.8		45303	3 AA325869				
80 41248 L12964 Hs.73895 tumor necrosis TM,SS,TNFR_c6 7.9 424247 X14008 Hs.234734 lysozyme (renal SS,bys 7.8 421991 NM_01998 Hs.110488 KIAA0990 protei SS 7.8							
412448 L12994 Hs.1393 Hs.234734 hsporyme (renal SS.lys 7.8 421991 NM_014918 Hs.110488 KIAA0990 protei SS 7.8 7.8 7.8 7.8 7.8 7.8 7.8 7.8 7.8 7.8	00						
424247 X14008 153.234734 1930211118 (16108 SS 7.8 421991 NM_014918 Hs.110488 KIAA0990 protei SS 7.8	80						
421991 RM 019310 13.11000 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1100 10.1							
400/50 MADDANIA HS.JOUGH HARRA SEPTEMBER 1001							7.7
		400/9	N ANDUU	. 13.3003	, rance supreme to	405	

	*****	25275				7.6
	414646	AA353776 AA311833	Hs.901	CD48 antigen (B	TM,ig TM	7.6 7.6
	418372 408418	AW963897	Hs.84318 Hs.44743	replication pro KIAA1435 protei	TM_WD40,FYVE	7.6
	425354	U62027	Hs.155935	complement comp	TM,7tm_1	7.5
5	432753	NM_014075	Hs.278915	PRO0593 protein	TM pkinase	7.4
•	447046	AA326187	Hs.17170	G protein-coupl	TM,7tm_1	7.4
	410577	X91911	Hs.64639	giorna pathogen	TM,SCP	7.4
	422631	BE218919	Hs.118793	hypothetical pr	TM	7.3
10	417022	NM_014737	Hs.80905	Ras association	TM,RA	7.2
10	430105	X70297	Hs.2540	cholinergic rec	TM,neur_chan	7.2
	451621	AI879148	Hs.26770	fatty acid bind	TM, SS, lipocatin	7.2
	415138	C18356	Hs.78045	tissue factor p	Kunitz_BPTI,G-gamma	7.2 7.2
	426028	NM_001110	Hs.172028	a disintegrin a	TM, SS, disintegrin, Reprolysin	7.2 7.1
15	434096	AW662958 NM_012446	Hs.75825 Hs.169833	pleiomorphic ad	TM,zI-C2H2 TM	7.1
13	426423 412783	BE276738	Hs.74578	single-stranded DEAD/H (Asp-Glu	TM.dsrm,helicase_C	7.1
	431556	AF016028	Hs.260039	saroospan (Kras	TM	6.9
	420018	U56387	Hs.94376	proprotein conv	TM,SS,Peptidase_S8,P	6.9
	444042	NM_004915	Hs.10237	ATP-binding cas	TM_ABC_tran	6.9
20	432656	NM_000246	Hs.3076	MHC class II tr	TMLRR	6.9
	430066	AI929659	Hs.237825	signal recognit	TM,TPR	6.9
	401539			• •	TM,SS,zf-B_box,zf-C3HC4,Lysyl_oxidase	6.8
	416058	L08895	Hs.78995	MADS box transc	tm,srf-tf	6.8
25	413249	AF167160	Hs.75251	DEAD/H (Asp-Glu	TM,SAP	6.7
25	424063	NM_002019	Hs.138671	fms-related tyr	TM,SS,pkinase,ig	6.7
	418026	BE379727	Hs.83213	fatty acid bind	TM, SS, fipocafin	6.6
	438619	AB032773	Hs.6341	TU12B1-TY prote	TM	6.6
	408741	M73720	Hs.646	carboxypeptidas	SS,Zn_carbOpept,Propep_M14	6.6 6.6
30	403549	000000	Un 40700	alC4C terrored	TM,pkinase	6.6
30	435798 453070	BE395289 AK001465	Hs.12720 Hs.31575	elF4E-transport SEC63, endoptas	TM TM,SS,DnaJ	6.6
	452092	BE245374	Hs.27842	hypothetical pr	TM,SS,Acyltransferase	6.5
	437396	BE140396	Hs.21621	hypothetical pr	TM	6.4
	402474	50.40030	113.21021	nypourous pr	TM,Peptidase_C1	6.4
35	401600	BE247275	Hs.151787	U5 snRNP-specif	TM,SS,HECT	6.4
	415076	NM_000857	Hs.77890	quanylate cycla	TM,guanylate_cyc	6.4
	430335	D80007	Hs.239499	KIAA0185 protei	TM,S1	6.3
	434203	BE262677	Hs.283558	hypothetical pr	TM	6.2
40	430287	AW182459	Hs.125759	ESTs, Wealtly si	TM,SS	6.2
40	417259	AW903838	Hs.81800	chondroitin sul	TM,Xlink,lectin_c,sushi,EGF.ig	6.1
	421202	AF193339	Hs.102506	eukaryotic tran	TM,SS	6.1
	452235	AL039743	Hs.28514	Homo sapiens mR	TM	6.0 6.0
	429653	NM_005955	Hs.211581	metal-regulator	TM,zf-C2H2 TM	5.9
45	444484 410193	AK002126 AJ132592	Hs.11260 Hs.59757	hypothetical pr zinc finger pro	TM,zI-C2H2	5.9
72	425361	AA355933	Hs.132221	Homo sapiens cD	TM	5.9
	410361	BE391804	Hs.62661	guanylate bindi	TM,SS,GBP	5.8
	415714	NM_002290	Hs.78672	laminin, alpha	TM,SS,taminin_G,taminin_EGF	5.8
	421689	N87820	Hs.106826	hypothetical pr	TM,SS,PHD	5.8
50	443837	AI984625	Hs.9884	spindle pale bo	SS	5.8
	422544	A8018259	Hs.118140	KIAA0716 gene p	TM	5.7
	412584	X54870	Hs.74085	DNA segment on	TM,lectin_c	5.7
	410425	BE278367	Hs.63510	KIAA0141 gene p	TM	5.7
<i></i>	426283	NM_003937	Hs.169139	kynureninase (L	TM	5.7
55	430440	X52599	Hs.2561	nerve growth fa	TM,SS,NGF	5.7
	413551	BE242639	Hs.75425	ubiquitin assoc	TM,SS,UBA	5.7
	418250	U29926	Hs.83918	adenosine monop	TM.A_deaminase	5.6 5.6
	419839	U24577 AK001514	Hs.93304 Hs.236844	phospholipase A	SS TM	5.6
60	430253 450447	AF212223	Hs.25010	hypothetical pr hypothetical pr	TM_ANF_receptor.guanylate_cyc.pkinase	5.6
U	414020	NM_002984		small inducible	SS,IL8	5.6
	414844	AA296874	Hs.77494	deoxyguanosine	SS,dNK	5.6
	416498	U33632	Hs.79351	potassium chann	TM	5.6
	430512	AF182294	Hs.241578		SS .	5.6
65	419929	U90268	Hs.93810	cerebral cavern	SS,ank,Band_41	5.5
	407094	AF000574	Hs.22405	leukocyte immun	TM,SS,ig	5.5
	411653	AF070578	Hs.71168	Homo sapiens cl	TM,SS,Aa_trans	5.5
	452355	N54926	Hs.29202	G protein-coupl	TM,7tm_1	5.5
70	440486	BE243513	Hs.7212	hypothetical pr	TM	5.5
70	444825	AW167613	Hs.248	mitogen-activat	TM,SS,pkinase	5.5
	447072	D61594	Hs.17279	tyrosylprotein	SS THANKS have	5.4 5.4
	453392	U23752	Hs.32964	SRY (sex determ	TM,HMG_box	5.4 5.4
	411213	AA676939	Hs.69285	neuropilin 1	TM,CUB,F5_F8_type_C,MAM TM.rrm	5.4 5.4
75	429688	BE245169	Hs.211610	CUG triplet rep	IM,rm TM	5.4 5.4
15	405257	NM_000107	Hs.77602	damage-specific	TM,WD40	5.3
	414911 430598	AK001764	Hs.247112		TM	5.3
	428753	AW939252	Hs.192927		TM,SS	5.3
	406625	Y13647	Hs.119597		TM,Desaturase	5.3
80	405475			• == ==	TM,sugar_tr	5.3
	430180	AA331406	Hs.75456	A kinase (PRKA)	TM	5.3
	417381	AF164142	Hs.82042	sotute carrier	TM.xan_ur_permease	5.3
	433029	NM_014322	Hs.279926	opsin 3 (enceph	TM,7tm_1	5.3

	447000	D13160 '	Je 83003	lothelin rece	TM,SS,7tm_1,zf-C3HC4	5.3	
				ne morphogene	SS,TGFb_propeptide,TGF-beta	5.2	
			Hs.1051 gra	nzyme B (gra	SS,trypsin	5.2 5.2	
_	451418	BE387790		oothetical pr	TM MCM,FAT,FATC,PI3_PI4_kinase		
5				otein kinase, emokine (C-X3	TM.7tm_1	5.2	
				generative sp	TM	5.2	
	417696		Hs.82401 CI	069 antigen (p	TM,lectin_c	5.2 5.2	
	442991			pothetical pr	TM TM	5.1	
10	420567			nilar to prol p junction pr	TM.connexin	5.1	
	412676 423430			AD54, S. cerev	TM,SNF2_N,helicase_C	5.1 5.1	
	421633	AF121860	Hs.106260 sc	rting nexin 1	TM,PX	5.1	
1.5	436943			ispase 10, apo iemann-Pick di	TM,ICE_p10,ICE_p20,DED TM,SS,Patched	5.1	
15	414696 446312	AF002020 BE087853		:QV1-8T0681-2	TM	5.0	
	420397		Hs.97437 C	entrosomal pro	TM	5.0 5.0	
	410274	AA381807	Hs.61762 h	/poxia-inducib	SS	5.5	
20	TABLE 36	<b>3</b> *					
20	Pkey:	o Uniqu	e Eos probeset i	dentifier number			
	CAT numb	er: Gene	cluster number				
	Accession	: Genb	ank accession nu	imbers			
25	Pkey	CAT number	Accession				
23	446312	671114_1	BE087853 AI2	36184			
		_					
	TABLE 36	C: Unio	ie number corres	ponding to an Eos prot	eset		ontitled "The DNA
30	Pkey: Ref:	Com	anna course Th	e 7 digit numbers in this	s column are Gendank identile (Gi) ild	imbers. "Dunham, et al." refers to the publication	engueu me oran
20		SAGU	ence of human c	hromosome 22° Dunnai	m, et al. (1999) Mattie 402.405-455.		
	Strand:		ates UNA strand stes ductentide f	from which exons were ositions of predicted ex	ons.		
	Nt_positio	ne muc	ates indeceded b	Control of promotor and			
35	Pkey	Ref		Nt_position			
	401539	8072433		62028-62508 53526-53628,55755-55	920.57530-57757		
	402474 403549	7547175 8081591		137150-137362			•
	405257	7329310	Plus	73121-73273			
40	405475	1931025	Plus	1548-1702			
	TABLE 3	7A: ABOUT 280	GENES DOWN	REGULATED IN KIDN	EY CANCER ideay cancer compared to normal kidne	y These were selected as for Table 35A, except	that the numerator and
45	Table 37	A lists about 280	) genes significat	iby down-regulated in K	uney career compared to normal resure	,	
43	genomin Pkey:	ator were switch Uni	nue Fos probese	t identifier number			
	ExAcon:	Exe	emplar Accession	number, Genbank acco	ession number		
	Unigene		gene number gene gene title				
50	Unigene R1:		gene gene the jo of normal to th	rnor tissue			
30	1711					R1	
	Pkey	ExAccn	UnigenelD	UnigeneTitle phenylalanine hydroxy	dose	50.20	
	425260 445635	L47726 A1769774	Hs.1870 Hs.209831	ESTs. Weakly similar	to ALU1_HUMAN ALU S	48.14	
55	440243		Hs.226422	ESTs		42.54 40.14	
-	431657	AI345227	Hs.105448	ESTs, Weakly similar	to 834087 hypotheti	34.56	
	441120		Hs.164492 Hs.216640	ESTs ESTs		33.16	
	432488 416854		Hs.80296	Purtinia coff amtein A		32.06 29.54	
60	438452	Al220911	Hs.288959	Homo sapiens cONA	FLJ20920 fis, clone A	28.26	
	414523		Hs.76353 9 Hs.283021	serine (or cysteine) p chloride intracellular	rotemase timbles	28.16	
	430250 446795		Hs.156471	ESTs		27.23	
	451949		Hs.463	potassium inwardly-r	ectifying channel, s	26.98 26.54	
65	43212		Hs.117037	ESTs ESTs		25.42	
	448170 43663		Hs.170789 Hs.111	fibroblast growth fact	or 9 (glia-activat	23.99	
	42677		Hs.150178	ESTs		23.78 23.04	
	42883	9 Al767756	Hs.82302	ESTs	2 related transcriptio	22.38	
70			Hs.59506 Hs.75297	fibroblast growth fac	3 related transcriptio tor 1 (acidic)	22.28	
	41333 43757			FSTe		22.14	
	45106		Hs.25910		A; cDNA DKFZp564C1416 (f	22.12 20.40	
75	44735					20.30	
75	42592 44629					19.48	
	42507		Hs.1852	acid phosphatase, p	prostate	19.10 18.74	
	41831	18 U47732	Hs.84072	transmembrane 4 s	uperfamily member 3 VA; cDNA DKFZp761G02121 (	18.56	
80	43013 44156		l Hs.234074 Hs.7888	Homo saciens cion	e 23736 mRNA sequence	17.40	
00	4348i		Hs.101	cytochrome P450, s	subfamily IVF, polypept	17.30 17.06	
	4066	67 M12523	Hs.75442		NA; cDNA DKFZp564B1264 (I	16.54	
	4146	02 AW6300	38 Hs.76550	momo sapiens mru	407		

	418021	M15881	Hs.1137	uromodulin (uromucoid, Tamm-Horsfall gly	16.11
	410681	AW246890	Hs.65425	calbindin 1, (28kD)	15.84
	443324	R44013	Hs.164225 Hs.1363	ESTs cytochrome P450, subfamily XVII (steroid	15.68 15.46
5	421285 436637	NM_000102 AI783629	Hs.26766	ESTs	15.18
•	448406	AW772298	Hs.21103	Homo sapiens mRNA; cONA DKFZp564B076 (fr	14.52
	434874	N62448	Hs.135906	ESTs	14.46
	407744 45 <b>3</b> 685	A8020629 AL110309	Hs.38095	ATP-binding cassette, sub-family A (ABC1 gb:DKFZp564L0278_r1 564 (synonym: hfbr2)	13.84 13.48
10	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	13.24
	436624	T64297	Hs.5241	fatty acid binding protein 1, liver	13.05
	428931	AA994979	Hs.98967	ATPase, H(+)-transporting, lysosomal, no	12.97 12.66
	424823 431713	NM_006226 AK000388	Hs.153322 Hs.267997	phospholipase C, epsilon EHM2 gene	12.66
15	436679	Al127483	Hs.120451	ESTs, Weakly similar to unnamed protein	12.36
	413859	AW992356	Hs.8364	pyruvate dehydrogenase kinase, isoenzyme	12.32
	425707 440504	AF115402 AI948966	Hs.11713 Hs.130017	E74-like factor 5 (ets domain transcript ESTs, Wealdy similar to VATX_HUMAN VACUO	11.92 11.66
	417275	X63578	Hs.81849	parvalbumin	11.48
20	410929	H47233	Hs.30643	ESTs	11.40
	427167	A1239607	Hs.99196	ESTs	11.34 11.30
	445591 443622	AI471866 AI911527	Hs.149095 Hs.11805	ESTs ESTs	11.23
	438935	H40665	Hs.31564	ESTs	11.16
25	438461	AW075485	Hs.286049	phosphoserine arminotransferase	11.00
	415539 438081	AI733881 H49546	Hs.72472 Hs.298964	ESTS ESTS	10.84 9.76
	421688	AK000307	Hs.106825	hypothetical protein FLJ20300	9.74
••	407280	AJ241296	Hs.145609	ESTs	9.71
30	427969	NM_001963	Hs.2230	epidermal growth factor (beta-urogastron	9.61 9.52
	442448 442308	A1733144 AA989402	Hs.129611 Hs.45194	ESTs ESTs	9.51
	410467	AF102546	Hs.63931	dachshund (Orosophila) homolog	9.35
25	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	9.32
35	418068 459247	AW971155 N46243	Hs.293902 Hs.110373	ESTs, Weakly similar to prolyl 4-hydroxy ESTs	9.31 9.20
	423629	AW021173	Hs.18612	Homo sapiens cDNA: FLJ21909 fis, clone H	9.16
	410247	AF181721	Hs.61345	RU2S	9.10
40	430573	AA744550	Hs.136345	ESTs EST-	9.08 8.99
40	457411 443790	AW085961 NM_003500	Hs.130093 Hs.9795	ESTs acyt-Coenzyme A oxidase 2, branched chai	8.92
	435024	AI863518	Hs.127743	ESTs, Wealdy similar to V-ATPase G-subun	8.76
	435056	AW023337	Hs.5422	glycoprotein M6B	8.74
45	426451 450648	AI908165 AI703366	Hs.169946 Hs.26766	GATA-binding protein 3 ESTs	8.50 8.38
73	426255	BE262530	Hs.2006	glutathione S-transferase M3 (brain)	8.31
	431820	AW410408	Hs.271167	L-pipecotic acid oxidase	8.28
	451027	AW519204	Hs.40808 Hs.16355	ESTs ESTs	8.10 8.06
50	435823 429269	R07856 AA449013	Hs.99203	ESTS	8.02
	438199	AW016531	Hs.122147	ESTs	7.94
	442176	AA983764	Hs.128910	ESTs ESTs	7.94 7.86
	450164 445627	AI239923 AW818475	Hs.30098 Hs.7363	ESTs	7.85
55	445779	AI253104	Hs.189267		7.82
	407178	AA195651	Hs.104106		7.68 7.68
	426966 445659	AI493134 AW300508	Hs.159125 Hs.149229		7.50
	403204	A11000000	141110440	20.0	7.46
60	448037	AW195634	Hs.170401	ESTs	7.30 7.26
	413589 446063	AW452631 AI720140	Hs.258811 Hs.151079	coatomer protein complex, subunit gamma ESTs	7.26 7.26
	424626	AA344308	Hs.128427		7.25
	403381				7.16
65	414807	AI738616	Hs.77348 Hs.130730	hydroxyprostaglandin dehydrogenase 15-(N ESTs	7.12 7.12
	432102 442315	AW015506 AA173992	Hs.7956	ESTs	7.10
	453698	AA037615	Hs.42746	ESTs	7.02
70	415003	M11437	Hs.77741	kininggen	6.95 6.92
70	426418 452883	M90464 X80031	Hs.169825 Hs.150318		6.88
	408621	Al970672	Hs.46638	chromosome 11 open reading frame 8	6.76
	410781	AI375672	Hs.165028		6.74 6.66
75	424596 441031	AB020639 AI110684	Hs.151017 Hs.7645	estrogen-related receptor gamma fibrinogen, 8 beta polypeptide	6.66
, ,	451099	R52795	Hs.25954	interleukin 13 receptor, atpha 2	6.64
	437553	AI829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	6.63 6.64
	445286	U03886 AW194270	Hs.264 Hs.177236	GS2 gene 6 ESTs	6.54 6.52
80	408427 410442		Hs.63788	propionyl Coenzyme A carboxylase, beta p	6.46
	457001	J03258	Hs.2062	vitamin D (1,25- dihydroxyvitamin D3) re	6.46 6.43
	420205		Hs.88156 Hs.12683	ESTs ESTs	6.42 6.36
	441364	ODPUCPTIA	ms. 12003	, 20.4	5.00

	425649	บ30930	Hs.158540	UDP glycosyttransferase 8 (UDP-galactose	6.34 6.32
	405373 431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo	6.32
_	440094	AI651558	Hs.270372	ESTs	6.27 6.21
5	442764 424433	A1762254 H04607	Hs.131122 Hs.9218	ESTs ESTs	6.20
	415025	AW207091	Hs.72307	ESTs	6.16 6.16
	428927	AA441837 H67346	Hs.90250 Hs.269187	ESTs ESTs	6.06
10	439145 424683	N87519	Hs.27196	ESTs	6.04 5.94
	415314	N88802	Hs.5422	glycoprotein M6B ESTs	5.90
	424025 445911	AI701852 AI985987	Hs.301296 Hs.145645	ESTs. Moderately similar to ALU1_HUMAN A	5.89
	417332	AW972717	Hs.288462	Homo sapiens cDNA: FLJ21511 fis, clone C	5.86 5.84
15	440102 429609	A1672443 AF002246	Hs.131190 Hs.210863	ESTs cell adhesion molecule with homology to	5.82
	411666	AF106564	Hs.71346	neurofilament 3 (150kD medium)	5.82 5.74
	446224	AW450551 A1928242	Hs.13308 Hs.293438	ESTs ESTs, Highly similar to AF198488 1 trans	5.72
20	422305 436802	N34486	Hs.170504	FSTs	5.72 5.70
	412452	AA215731	Hs.283446	ESTs, Wealthy similar to ALAT_HUMAN ALANI ESTs	5.66
	445611 440038	AW418497 AA861627	Hs.145583 Hs.243989	ESTS	5.66
	424028	AF055084	Hs.153692	KIAA0686 protein ESTs, Highly similar to VAB1_HUMAN VACUO	5.61 5.60
25	410530	M25809 AA365752	Hs.64173 Hs.155965	ESTs Figury Simular to 4761-110/04/14 47/000	5.60
	425907 428523	AW974540	Hs.98626	ESTs	. 5.58 5.58
	429918	AW873986	Hs.119383 Hs.182575	ESTs solute carrier family 15 (H+/peptide tra	5.56
30	408369 446163	R38438 AA026880	Hs.25252	Homo sapiens cDNA FLJ13603 fis, clone PL	5.56 5.53
50	427398	AW390020	Hs.20415	chromosome 21 open reading frame 11 Homo sapiens mRNA; cDNA DKFZp564D1462 (f	5.52 5.51
	418504 440666	BE159718 AA902650	Hs.85335 Hs.192742		5.50
	432286	AW327432	Hs.255843	ESTs	5.48 5.46
35	451236	A1767406	Hs.207026 Hs.119651	ESTs, Weakly similar to B56205 transcrip glypican 3	5.43
	422746 416426	NM_004484 AA180256	Hs.210473		5.37 5.36
	414449	AA557660	Hs.76152	decorin Homo sapiens clone 24468 mRNA sequence	5.34
40	445898 451835	AF070623 T63643	Hs.13423 Hs.209715	ESTs, Weakly similar to ALU7_HUMAN ALU S	5.32
40	424566	M16801	Hs.1790	nuclear receptor subfamily 3, group C, m	5.22 5.18
	408604	D51408 AA287443	Hs.21925	ESTs gb:zs52c10.r1 NCI_CGAP_GCB1 Homo sapiens	5.18
	456576 433212	BE218049	Hs.121820		5.16 5.14
45	452114	N22687	Hs.8236	ESTs Homo sapiens cDNA: FLJ22785 fis, clone K	5.14
	458072 443005	AI890347 AI027184	Hs.271923 Hs.20091		5.14
	408554	AA836381	Hs.7323	ESTs	5.12 5.10
50	438609 429343		Hs.29199 Hs.19948		5.10
50	452223		Hs.8035	ESTs	5.10 5.09
	446925				5.08
	407664 414664			Homo saniens HSPC311 mRNA, partial cds	5.06 5.04
55	407978	AW385129	Hs.41717		5.04
	435343 419150		2 Hs.19902 Hs.89640		5.04
	442317	A1915599	Hs.12927	S ESTs	5.02 5.02
60	404319 433637		4 Hs.1354	DS ESTs	4.92
UU	440205		Hs.1884	65 ESTs	4.84 4.83
	432029		Hs.2899 4 Hs.1154	4-hydroxyphenylpyruvate dioxygenase 97 Homo sapiens cDNA: FLJ22655 fis, clone H	4.80
	453129 40778			1 S100 calcium-binding protein A2	4.78 4.75
65	43975	0 AL359053			4.74
	44363 44905				4.69
	42223	7 M13149	Hs.1498	histidine-rich glycoprotein	4.67 4.64
70	44247			gb:AF069475 Homo sapiens astrocytoma lib epididymis-specific, whey-acidic protein	4.58
70	43113 44062				4.58 4.51
	40304	6	LL 200	2 507-	4.48
	45083 45588		Hs.2869 '3	i3 ESTs gb:PM1-HT0340-201299-004-f12 HT0340 Homo	4.47
75	45350	O A147842			4.40 4.37
	40570 4266		865 Hs.171	731 solute carrier family 14 (urea transport	4.37
	4200: 4510:	32 W03692	Hs.258	32 Homo sapiens mRNA; cDNA DKFZp564P116 (fr	4.37 4.35
0/1	42620	00 AA37187			4.34
80	4188 4477			533 Homo sapiens cDNA FLJ14142 fis, clone MA	4.32
	4382	09 AL1206		1 KIAA0307 gene product	4.23 4.22
	4045	22			

	413272	AA127923	Hs.293256	ESTs	4.21
	423068	M25629		katlikrein 1, renal/pancreas/salivary	4.19
	416982	J05401		creatine kinase, mitochondrial 2 (sarcom	4.18
_	445512	AI241246		EST	4.17 4.16
5	445177 448475	AJ215070 BE613134	Hs.16135 Hs.247474	ESTs Homo sapiens cDNA: FLJ21032 fs, clone C	4.14
	402072	DE013134	113.241414	HORID SERVICES CONTROL I CAR TONE INC. ORDING C	4.09
	439285	AL133916	Hs.298998	ESTs	4.02
••	429621	AI823386	Hs.130874	Homo sapiens cDNA FLJ14181 fis, clone NT	3.99
10	450273	AW296454	Hs.24743	hypothetical protein FLJ20171	3.97 3.94
	453511 452620	AL031224 AA436504	Hs.33102 Hs.119286	transcription factor AP-2 beta (activati ESTs	3.92
	425642	X91220	Hs.158462	solute carrier family 12 (sodium/chlorid	3.91
	435884	AA701443	Hs.192868	ESTs	3.90
15	416889	AW250318	Hs.80395	mal, T-cell differentiation protein	3.89 3.88
	419677 431958	N77342 X63629	Hs.21851 Hs.2877	Homo sapiens cDNA FLJ12900 fis, clone NT cadherin 3, type 1, P-cadherin (placenta	3.84
	456844	AJ264155	Hs.152981	COP-diacylglycerol synthase (phosphatida	3.82
	442306	AJ820660	Hs.129205	ESTs	3.82
20	438453	D17056	Hs.288959	Homo sapiens cDNA: FLJ20920 fis, clone A	3.81
	407198	H91679	Un 2704	gb:yv04a07.s1 Soares fetal liver spleen sodium channel, nonvoltage-gated 1 atpha	3.80 3.79
	431441 413841	U81961 M34276	Hs.2794 Hs.75576	plasminogen	3.77
	431161	AA493591	13.700.0	gb:nh01a12.s1 NCI_CGAP_Thy1 Homo sapiens	3.76
25	428544	AA430034	Hs.191611	ESTs	3.74
	453903	AW299606	Hs.232777	ESTs	3.74 3.73
	434061 444805	AW024973 AB007899	Hs.283675 Hs.12017	NPD009 protein KIAA0439 protein; hornolog of yeast ubiqu	3.73
	440080	AW051597	Hs.143707	ESTs	3.71
30	440230	A1732970	Hs.126246	ESTs	3.70
	428735	AJ279246	Hs.192657	NPHS2 gene (podocin)	3.68 3.66
	421832	NM_016098	Hs.108725 Hs.234234	HSPC040 protein addotase B, fructose-bisphosphate	3.65
	430135 453055	NM_000035 AW291436	Hs.31917	ESTs	3.65
35	450696	AI654223	Hs.16026	Homo sapiens cDNA: FLJ23191 fis, clone L	3.59
	440232	AJ766925	Hs.112554	ESTs	3.57
	432099	U20760	Hs.272429	calcium-sensing receptor (hypocalciuric	3.57 3.56
	445924 411356	AI264671 H45377	Hs.164166	ESTs gb:yn99h03.r1 Soares adult brain N2bSHB5	3.56
40	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	3.55
	413752	8E161807		gb:MR3-HT0446-300300-203-h01 HT0446 Homo	3.53
	416298	NM_003891	Hs.1011	protein Z, vitamin K-dependent plasma gl	3.53 3.53
	423603 436610	AB007880 AW611912	Hs.129883 Hs.120414	KIAA0420 gene product ESTs	3.50
45	425905	AB032959	Hs.161700	KIAA1133 protein	3.48
	403625				3.47
	425210	AA054679	Hs.155150	ribonuclease P (14kD) ESTs, Highly similar to AF128113 1 promi	3.45 3.42
	430168 448877	AW968343 AI583696	Hs.300896 Hs.253313		3.40
50	456686	AI554303	Hs.35982	Homo sapiens cDNA FLJ12776 fis, clone NT	3.38
	414725	AA769791	Hs.120355	Homo sapiens cDNA FLJ13148 fis, clone NT	3.37
	453574	AI767947	Hs.50841	ESTs, Weakly similar to tuftelin [M.musc	3.32 3.31
	438535 414040	L09078 N58513	Hs.32171	gb:Homo sapiens mRNA fragment ESTs	3.30
55	451416	AW631469	Hs.203213		3.30
	444564	AI167877	Hs.143716		3.29
	408001	AA046458	Hs.95296	ESTs	3.27 3.24
	406666 421750	V00495 AK000768	Hs.75442 Hs.107872	afbumin hypothetical protein FLJ20761	3.24
60	445337	NM_013280		fibronectin leucine rich transmembrane p	3.23
•	423968	AF098277	Hs.136529		3.21
	427209	H06509	Hs.92423	KIAA1566 protein	3.20 3.20
	403442	AVAIDCODES	Un 02281	nudix (nucleoside diphosphate linked moi	3.19
65	419713 425548	AW968058 AA890023	Hs.92381 Hs.1906	protectin receptor	3.17
05	414502	AL133721	Hs.224680		3.16
	427811	M81057	Hs.180884		3.14
	436330	NM_004413		dipeptidase 1 (renal)	3.11 3.11
70	433942	AW272166 AL040127	Hs.123465 Hs.34074	i ESTs dipeptidylpeptidase VI	3.10
, 0	408692 448819	AL040127 AI589190	Hs.188372		3.10
	423041	BE170842	Hs.123123	Chloride channel Ka	3.10
	454554	AW847505	11- 00-170	gb:RC0-CT0210-280999-021-c10 CT0210 Homo	3.10 3.10
75	406664	L34041 AW206292	Hs.25478 Hs.199751		3.08
13	449850 427450		Hs.178121		3.08
	454788			gb:RC5-ST0300-300100-012-H06 ST0300 Homo	3.06
	444895	AI674383	Hs.301192	2 ESTs	3.06 3.05
80	457782 429023		2 Hs.2351	gb:yv40g05.s1 Soares fetal liver spleen protein C (inactivator of coagulation fa	3.05
80	429023 427041		Hs.97557	ESTs	3.01
	434788	AF154121	Hs.10286	7 sodium-dependent high-affinity dicarboxy	3.01
	419003	T78640	Hs.26859	5 ESTs	3.01

PCT/US02/29560 WO 03/025138

_	TABLE 37B: Pkey: CAT number	Unique l r: Gene d	Eos probeset ide uster number									
5	Accession:	Genban	k accession nun	nbers								
10	411356 413752 431161 431322 438535 442476	1240273_1 1 1386338_1 1 328713_1 3 331543_1 4 45946_1 5 543547_1	Accession H45377 H21137 AW838640 BE161807 BE161584 BE161700 BE161748 AA493591 AA829120 AA533792 AW970622 AA503009 AA502998 AA502989 AA502805 T92188 L09078 L03145 L09094 L09098 L03165 L09102 AF069475 AF069477 AF069476									
15	453685 454554	1223842_1	AW847505 AW8 AW806991 AWI	AL110309 AW088119 HZ2881 AW847505 AW811792 BE061442 BE061433 AW847506 AW806999 AW806996 BE061436 BE061430 BE142460 BE146499 AW806994 AW809156 AW806991 AW814082 AW806992 BE061669 AW807002 BE146659 AW806995 AW807000 AW845743 AW845747 AW847504 BE142458 BE061431 BE061435 AW847507 BE146650 BE142470 AW814096 AW807012 BE061438 AW807011 AW806993 BE142459 BE142459 BE142452 AW854330 BE061435 AW847507 BE146650 BE142470 AW814096 AW807012 BE061438 AW807011 AW806993 BE142465 BE142499 BE142469 AW806997 AW806998 BE061435 BE061433 BE061731 BE142464 AW847501 AW807001 BE142463 AW811800 BE061437 AW811802 BE061440 AW806997 AW806998								
20	454788 455887 456576 457782	12346941 1380836_1 201378_1 405265_1	AW820691 BE154173 BE1	54098 B£154096 19385 B£084078 Al478347								
25	407198		H31073									
23	TABLE 379 Pkey: Ref:	Unique refere	nce gi 1D	dentifier number								
20	Strand:		identification	de nocition								
30	Nt_position	n: chron	osomal nucleoti	de position								
35	Pkey 402072 403046 403204	Ref 8117363 3540153 7622392	Plus Minus	#_position 1983-72128 15707-55859,56369-56511 16214-16439								
	403381 403442 403625 404319	9438267 7210003 8569879 9211467	Plus Plus	26009-26178 174560-175270 5551-7111 54436-54608								
40	404559 405373 405701	8748893 2076718 4263751	Minus Plus	73499-73651,89575-89739 21294-21575 93243-93364								
45	Table 38. array suc	A lists about 860 th that the ratio o	genes up-regula i "average" kidni	ey cancer to "average normal adult ussues was great	RMAL ADULT TISSUES  s. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip er than or equal to 3.0. The "average" kidney cancer level was set to the 90th the 70th percentile amongst various non-malignant tissues. In order to remove generus non-malignant tissues was subtracted from both the numerator and the							
50	denomin Pkey: ExAccn: Unigene	ator before the ra Unic Exe ID: Unic	itio was evaluate jue Eos probese mplar Accession jene number	nyproizeoun, the 15th percentale value anongst value did.  It dentifier number number, Genbank accession number								
55	Unigene R1:		jene gene title n of tumor to no	mal adult tissues								
55	INT;	1/200			RI							
60	Pkey 435013 447768 445178		UnigenelO Hs.110024 Hs.19520 Hs.129614	Unigene Title  Hs.19520:FXYO domain-containing ion tran Hs.129614:kidney-specific membrane prote	15.71 14.07 12.56							
00	432542 443595 41 <b>37</b> 19	AW083920 AF169312 BE439580	Hs.16098 Hs.9613 Hs.75498	Hs.16098:claudin 2 NM_016109:Homo sapiens angiopoietin-like NM_004591:Homo sapiens small inducible c	12.41 11.77 10.39 10.18							
65	436878 440304 407065 413049	BE159984 Y10141	Hs.47448 Hs.125395 Hs.823	Hs.47448:ESTs Hs.126395:ESTs NIM_002151:Homo sapiens hepsin (transmemb	9.95 9.58 9.51							
70	425983 423161 430569 416768 422357	AL049227 AF241254 AA363733 AF016272	Hs.165619 Hs.124776 Hs.178098 Hs.1032 Hs.115418	Hs. 165619: mucin and cadherin-like Hs. 124776: Horno sapiens mR; cD DKFZp564N1 Hs. 178098: angiotens in 1 converting enzym NM_002909: Horno sapiens regenerating isle NM_004062: Horno sapiens cadherin 16, KSP-	8.88 8.77 8.45 7.94 7.78							
75	42073 40974 41393 42668 40685	5 AA077391 5 AF113676 2 AV660038	Hs.99899 Hs.297681 Hs.2056 Hs.352392	NM_001252:Homo sapiens tumor necrosis fa AA077391:7814E12 Chromosome 7 Fetal Brai NM_000295:Homo sapiens serine (or cystei Hs_2055:UDP glycosyltransferase 1 tamily Hs_352392:major histocompatibility compl	7.74 7.32 7.20 7.03							
80	41950 42895	8 AW997938 3 AA306610 5 AF037335 2 NM_00576	Hs.90786 Hs.348183 Hs.5338	Hs.90786:ATP-binding cassette, sub-famil NM_003823:Horno sapiens tumor necrosis fa NM_001218:Horno sapiens carbonic anhydras NM_005764:Horno sapiens epithelial protei NM_005764:Horno tapiens ep	6.57 6.36 6.31 6.20 6.20							
	42380				6.19							

	434779	AF153815	Hs.50151	Hs.50151:potassium inwardly-rectifying c	6.11 6.08
	435767 422664	H73505 AA315933	Hs.117874 Hs.120879	Hs.117874:ESTs Hs.120879:Homo saplens, clone MGC:32871	6.02
_	425280	U31519	Hs.1872	Hs.1872:phosphoenolpyruvate carboxykise	5.81
5	426559	AB001914	Hs.170414	NM_002570:Homo sapiens paired basic amin	5.73
	451564 418526	AU076698 BE019020	Hs.132760 Hs.85838	NM_001467;Homo sapiens glucose-6-phospha NM_004207;Homo sapiens solute carrier fa	5.69 5.68
	444151	AW972917	Hs.128749	Hs. 128749: alpha-methylacyl-CoA racemase	5.66
• •	426471	M22440	Hs.170009	NM_003236:Homo sapiens transforming grow	5.48
10	432579	AF043244	Hs.278439	NM_003946:Homo sapiens nucleolar protein	5.45 5.42
	448733 446650	NM_005629 AB016625	Hs.187958 Hs.15813	NM_005629:Homo sapiens solute carrier fa NM_003060:Homo sapiens solute carrier fa	5.36
	417089	H52280	Hs.18612	Hs.18512:Homo sapiens cD: FLJ21909 fis,	5.35
	437848	AI906419	Hs.284380	Hs.284380:gamma-glutamyttransferase 1	5.32
15	423081	AF262992	Hs.123159	Hs. 123159:sperm associated antigen 4	5.30 5.23
	421893 435886	NM_001078 BE265839	Hs.109225 Hs.12126	NM_001078:Homo sapiens vascular cell adh Hs.12126:hepatocellular carcinoma-associ	5.20
	410276	AI554545	Hs.359201	Hs.359201:ESTs	5.20
20	429451	BE409861	Hs.202833	NM_002133:Homo sapiens heme oxygese (dec	5.14
20	446404	AA019961	Hs.26216 Hs.128749	Hs.26216:Homo sapiens c0: FLJ22811 fis, NM_014324:Homo sapiens alpha-methylacyl-	5.13 5.09
	423445 449444	NM_014324 AW818436	Hs.351306	NM_004696:Homo sapiens solute carrier fa	5.05
	438106	BE245551	Hs.6079	NM_014863:Homo sapiens B cell RAG associ	5.02
25	400419	AF084545		AF084545:Homo sapiens versican Vint isof	5.01 4.99
25	453920 447881	A1133148 BE620886	Hs.36602 Hs.355279	NM_000204:Homo sapiens I factor (complem Hs.355279:Homo sapiens cD FLJ23711 fis.	4,97
	422253	W81526	Hs.113882	NM_000815:Homo sapiens gamma-aminobutyri	4.93
	439024	R96696	Hs.35598	Hs.35598.ESTs	4.88
20	414799	A1752416	Hs.77326	NM_000598:Homo sapiens insulin-like grow	4.80 4.77
30	426530 410055	U24578 AJ250839	Hs.278625 Hs.58241	NM_000592:Homo sapiens complement compon Hs.58241:gene for serine/threonine prote	4.72
	404240	7220000	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,		4,71
	414617	Al339520	Hs.288817	Hs.288817:hypothetical protein FLJ22761	4.68
35	448249	AW855331	Hs.337124	Hs.337124:ESTs Hs.21906:Homo sapiens clone 24670 mR seq	4.67 4.66
33	447818 449057	W79940 AB037784	Hs.21906 Hs.22941	Hs.22941:KIAA1363 protein	4.66
	422424	AI186431	Hs.296638	NM_004864:Homo sapiens prostate differen	4.62
	417336	R70429	Hs.81988	NM_001343:Homo sapiens disabled homolog	4.62 4.58
40	425873	NM_013390 NM_003645	Hs.160417 Hs.11729	NM_013390:Homo sapiens transmembrane pro NM_003645:Homo sapiens fatty-acid-Coenzy	4.58 4.58
40	444700 414998	NM_003643	Hs.77729	NM_002543:Homo sapiens oxidised low dens	4.56
	414763	U97276	Hs.77266	NM_002826:Homo sapiens quiescin Q6 (QSCN	4.48
	443358	H65417	Hs.17757	Hs. 17757:pleckstrin homology domain-cont	4.45 4.43
45	440091 447131	A1767388 NM_004585	Hs.37890 Hs.17466	Hs.37890:Homo sapiens, clone IMAGE:48275 NM_004585:Homo sapiens retinoic acid rec	4.43
77	406973	M34996	Hs.198253	Hs. 198253:major histocompatibility compl	4.42
	427740	BE242604	Hs.180616	NM_005505:Homo sapiens CD36 antigen (col	4.40
	436258	AW867491	Hs.107125	Hs.107125:plasmatemma vesicle associated	4.38 4.37
50	452884 444006	C05964 BE395085	Hs.31841 Hs.10086	Hs.31841:ESTs NM_016639:Homo sapiens type I transmembr	4.36
50	422627	BE336857	Hs.118787	NM_000358:Homo sapiens transforming grow	4.35
	418054	NM_002318	Hs.83354	NM_002318:Homo sapiens lysyl oxidase-lik	4.34
	419011	H56244	Hs.89552	NM_000846:Homo sapiens glutathione S-tra	4.34 4.33
55	404277 435563	AF210317	Hs.95497	Hs.95497:solute carrier family 2 (facili	4.30
-	431779	AW971178	Hs.268571	NM_001645:Homo sapiens apolipoprotein C-	4.29
	406645	M57466	Hs.814	Hs.814:major histocompatibility complex,	4.28 4.26
	421485 426812	AA243499 AF105365	Hs.104800 Hs.172613		4.25
60	407910	AA650274	Hs.41296	NM_013281:Homo sapiens fibronectin leuci	4.22
	438030	X98427	Hs.122634		4.22
	430661	AC005551	Hs.130714 Hs.283713		4.21 4.20
	444381 438203	BE387335 BE540090	Hs.7345	Hs.7345:MAD1 mitotic errest deficient-li	4.16
65	411358	R47479	Hs.94761	Hs.94761:KIAA1691 protein	.A.15
	418323	NM_002118		NM_002118:Homo sapiens major histocompat	4,12 4,11
	449853 415198	AF005823 AW009480	Hs.24040 Hs.943	NM_002246:Homo sapiens potassium channel NM_004221:Homo sapiens tural killer cell	4.11
	418751	BE389014	Hs.372548	T	4.09
70	414166	AW888941	Hs.75789	NM_006096:Homo sapiens N-myc downstream	4.07
	424125	M31669	Hs.1735	Hs. 1735:inhibin, beta B (activin AB beta	4.00 3.92
	416926 419175	H03109 AW270037	Hs.263395 Hs.362996		3.92
	419175 424218	AF031824	Hs.143212		3.91
75	412870	N22788	Hs.82407	Hs.82407:chemokine (C-X-C motif) ligand	3.88
	452203	X57522	Hs.352018		3.87 3.87
	446872 449961	X97058 AW265634	Hs.16362 Hs.133100		3.87
	424517	AI539443	Hs.13744	7 Hs.137447:Homo sapiens cD FLJ12169 fis,	3.86
80	425262	D87119	Hs.155411	3 Hs.155418:GS3955 protein	3.83
	443639		Hs.9661 Hs.73769	NM_002801:Homo sapiens proteasome (proso NM_000802:Homo sapiens folate receptor 1	3.82 3.81
	448133 418030		Hs.83321	Hs.83321:neuromedin B	3.81
			_		

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-	412939		Hs.75069 N	IM_005412.Homo sepiens serine hydroxymet	3.80 3.79
				IM_002555:Homo sapiens solute carrier fa	3.78
			He 200216	ls.180428:KIAA1181 protein ls.290216:ESTs	3.77
5	412006 430413		Hs.241392 P	(M_002985:Homo sapiens small inducible c	3.76
_	422282		Hs.114309	ts.114309:apolipoprotein L, 1	3.76 3.76
	420747	BE294407	Hs.99910	ls 99910 phosphofructokise, platelet	3.75
	414875	,	Hs.77522	NM_006120:Homo sapiens major histocompat Hs.88474:prostaglandin-endoperoxide synt	3.74
10	418793 446291	AW382987 BE397753	He 14623	NM, 006332:Homo saciens interferon, gamma	3.71
10	417289	D86962	Me 81875	He R1875 growth factor receptor-bound pr	3.69
	422672	X12784	He 119129	NM 001845:Homo sapiens collagen, type IV	3.68 3.68
	448569	BE382657	Hs.21486	NM_007315:Horno sapiens sigi transducer a	3.67
1.5	437270	R18087	Hs.323769	Hs.323769:cisplatin resistance related p Hs.192455:ESTs, Moderately similar to hy	3.67
15	408452 443986	AA054683 AI381750	He 283437	Hs 283437:HTGN29 protein	3.66
	418869	AW516565		AWS16565:x001d05.x1 Soares_NHCeC_cervica	3.65
	425998	AU076629		NM_002011:Homo sapiens fibroblast growth	3.62 3.62
••	428699	AW578252	Hs.190161	NM_014020:Homo sapiens LRB protein (LR8) NM_000211:Homo sapiens integrin, beta 2	3.61
20	418299	AA279530	Hs.83968 Hs.51483	Hs.51483:Homo sapiens, Similar to RIKEN	3.59
	432593 415765	AW301003 NM_005424	Hs.78824	NM 005424:Horno sapiens tyrosine kise wit	3.58
	445985	BE621800	Hs.29444	Hs.29444: putative small membrane protein	3.57
	424893	AW295112	Hs.153648	Hs.153648:protein tyrosine phosphatase,	3.57 3.57
25	426046	AA833655	Hs.206868	Hs.206868:Homo sapiens cD FLJ14056 fis, NM_001975:Homo sapiens enolase 2, (gamma	3.57
	424415	NM_001975	Hs.146580 Hs.74131	NM_00047:Homo sapiens arylsulfatase E (	3.56
	412612 443834	NM_000047 AI741510	Hs.173548	Hs.173548:ESTs	3.54
	431630	NM_002204	Hs.265829	NM_002204:Homo sapiens integrin, alpha 3	3.53 3.52
30	418371	M13560	Hs.84298	Hs.84298:CD74 antigen (invariant polypep	3.52 3.52
	444838	AV651680	Hs.208558	Hs.208558:ESTs Hs.59892:ESTs, Wealdy similar to alpha 5	3.52
	449378	AW664026	Hs.59892 Hs.69771	NM_001710:Homo sapiens B-factor, properd	3.50
	411393 414311	AW797437 AI693547	Hs.71746	Hs 71746:aminopeotidase-like 1	3.50
35	415149	X12451	Hs.78056	NM_001912:Homo sapiens cathepsin L (CTSL	3.50 3.49
	424321	W74048	Hs.1765	Hs. 1765:lymphocyte-specific protein tyro	3.48
	414825	X06370	Hs.77432	NM_005228:Homo sapiens epidermal growth Hs.191797:ESTs	3.48
	408194	AA601038 AW575742	Hs.191797 Hs.351676	Hs.351676:ESTs, Weakly similar to T02670	3.47
40	410600 416899	BE262645	Hs.80420	NM 002996:Homo saciens small inducible c	3.47
40	436856	A1469355	Hs.127310	Hs 127310:hypothetical protein BC014917	3.47 3.47
	419660	BE280337	Hs.194693	NM_003982:Homo sapiens solute carrier fa	3.47
	413566	AW604451	Hs.285814	Hs.285814:growth factor receptor-bound p Hs.240951:ked cuticle homolog 2 (Drosoph	3.46
45	412104 444488	AW205197 AW192879	Hs.240951 Hs.355660	Hs.355660:peptide-histidine transporter	3.46
43	449475	AI348027	Hs.108557	Hs.108557:hypothetical protein PP1057	3.46
	412276	BE262621	Hs.73798	NM 002415:Homo sapiens macrophage migrat	3.45 3.44
	449338	H73444	Hs.394	NM_001124:Homo sapiens adrenomedullin (A Hs.238927:Homo sapiens mR; cD DKFZp434H1	3.43
50	430304	AL122071	Hs.238927 Hs.78409	(locuslink)NM_030582:Homo sapiens collag	3.43
50	415388 432210	AF018081 AI567421	Hs.273330	Hs.273330:agrin	3.43
	418177	N44967	Hs.351554	Hs 351554:Homo sapiens cD FLJ32092 ffs,	3.42
	414888	AL039185	Hs.77558	Hs.77558:thyroid hormone receptor intera	3.42 3.41
<i>E E</i>	452445	AB002438	Hs.29596	Hs.29596:Homo sapiens mR from chromosome Hs.914:major histocompatibility complex,	3.41
55	414803 419201	X03100 M22324	Hs.914 Hs.1239	NM_001150:Homo sapiens alanyl (membrane)	3.41
	445139		Hs.12365	Hs.12365:syptotagmin XIII	3.41
	435021		Hs.73962	Hs.73962:EphA7	3.41 3.40
۲۵	417259			Hs.81800:chondroitin sulfate proteoglyca Hs.41271:Homo sapiens mR full length ins	3.39
60	439737		Hs.41271 Hs.172870		3.39
	410636 431590		Hs.26339	Hs. 263395:sema domain, transmembrane dom	3.38
	415000			2 Hs.239812:serologically defined breast C	3.36
	416700			NM_001909:Homo sapiens cathepsin D (lyso	3.36 3.35
65	440516		Hs.161	NM_001792:Horno sapiens cadherin 2, type Hs.23388:hypothetical protein DKFZp434F0	3.32
	423720 42190			BE392717:601307571F1 NIH_MGC_44 Homo sap	3.32
	40922			Hs.51233:tumor necrosis factor receptor	3.32
	42150			9 NM 006424:Homo sapiens solute carrier la	3.32
70	41672	9 146165	Hs.1027	NM_004165:Homo sapiens Ras-related assoc	3.30 3.30
	43030				3.29
	44508		Hs.25084 Hs.84298		3.29
	40682 44627			NM 005335:Homo sapiens hematopoietic cel	3.28
75	43714	5 AF007216	6 Hs.5462	NM_003759:Homo sapiens solute carrier ta	3.27 3.27
	44407	1 Al627808		24 Hs.110524:ESTs	3.27 3.27
	41466				3.26
	43657 42467			11 NM 005512:Homo sagiens glycoprotein A re	3.25
80	4246			70 Hs 146170:hypothetical protein FLJ22969	3.25
-	44970	3 H61001	Hs.1718	no Hs 171802:Homo sapiens, clone IMAGE:3956	3.25 3.25
	4147		Hs.7731		3.24
	4142	49 AI797 <b>9</b> 94	Hs.2799		
				413	5

					2 22
	430396 424456	D49742 AA341017	Hs.241363 Hs.25549	NM_004132:Homo sapiens hyaturon binding Hs. 25549:hypothetical protein FLJ 20898	3.23 3.23
	452303	R27257	Hs.57734	Hs.57734:G protein-coupled receptor kise	3.22
_	425390	AI092634	Hs.156114	NM_004648:Homo sapiens protein tyrosine	3.21
5	416033	NM_012201	Hs.78979	NM_012201:Homo sapiens golgi apparatus p	3.19 3.19
	450931 428065	N25156 A1634046	Hs.25648 Hs.157313	Hs.25648:tumor necrosis factor receptor Hs.157313:ESTs	3.18
	422616	BE300330	Hs.118725	NM_012248:Homo sapiens selenophosphate s	3.18
10	439318	AW837046	Hs.6527	Hs.6527:G protein-coupled receptor 56	3.17
10	427640	AF058293	Hs.180015 Hs.57655	NM_001355:Homo sapiens D-dopactrome taut Hs.57655:dudufin 2	3.17 3.16
	409936 436001	AK001691 AW903849	Hs.173840	Hs. 173840:similar to endothelial cell-se	3.16
	451154	AA015879	Hs.33536	Hs.33536:ESTs	3.16
1.5	420256	U84722	Hs.76206	NM_001795:Homo sapiens cadherin 5, type	3.16 3.15
15	407584 428593	W25945 AW207440	Hs.8173 Hs.185973	Hs.8173:hypothetical protein FLJ10803 NM_003676:Homo sapiens degenerative sper	3.15
	410026	AI912061	Hs.55016	Hs.55016:EPS8-related protein 2	3.15
	445333	BE537641	Hs.44278	Hs.44278:RAB17, member RAS oncogene fami	3.14
20	448143	AF039704	Hs.20478	NM_000391:Homo sepiens ceroid-lipofuscin	3.14 3.14
20	423007 416511	AA320134 NM_006762	Hs.196029 Hs.79356	Hs.196029:Homo sapiens mR for KIAA1657 p NM_006762:Homo sapiens Lysosomal-associa	3.14
	439237	AW408158	Hs.318893	Hs.318893:ESTs, Weakly similar to Z195_H	3.13
	446899	NM_005397	Hs.16426	NM_005397:Homo sapiens podocalyxin-like	3.13
25	413916	N49813	Hs.75615 Hs.3838	NM_000483:Homo sapiens apolipoprotain C- NM_006622:Homo sapiens serum-inducible k	3.13 3.12
25	434398 441283	AA121098 AA927670	Hs.131704	Hs.131704:ESTs	3.12
	418945	BE246762	Hs.89499	NM_000698:Homo sapiens arachidote 5-lipo	3.12
	418458	AA332941	Hs.85226	NM_000235:Horno sapiens lipase A, lysosom	3.12 3.11
30	408989	AW361666 H95990	Hs.49500 Hs.181244	Hs.49500:KIAA0746 protein Hs.181244:major histocompatibility compl	3.11
20	436906 411089	AA456454	Hs.355702	Hs.355702:ESTs, Weakly similar to AC0048	3.11
	432990	AL036071	Hs.279899	NM_003820:Homo sapiens tumor necrosis fa	3.11
	425009	X58288	Hs.154151	NM_002845:Homo sapiens protein tyrosine	3.10 3.10
35	443601 430603	AI078554 AA148164	Hs.42658 Hs.247280	Hs.42658:Homo sapiens cD FLJ30167 fis, c Hs.247280:chromosome 20 open reading fra	3.10
33	413672	BE156536	Hs.353632	Hs.3S3632:ESTs, Moderately similar to hy	3.09
	407786	AA687538	Hs.38972	NM_005727:Homo sapiens tetraspan 1 (TSPA	3.09
	414586	AA306160	Hs.16488	NM_002298:Homo sapiens lymphocyte cytoso Hs.81988:disabled homolog 2, mitogen-res	3.08 3.08
40	423712 438552	W46802 AJ245820	Hs.81988 Hs.6314	NM_012410:Homo sapiens type I transmembr	3.06
40	448364	T08958	Hs.297214	Hs.297214:HSPC141 protein	3.06
	426437	BE076537	Hs.169895	NM_004223:Homo sapiens ubiquitin-conjuga	3.06 3.06
	437679	NM_014214	Hs.5753 Hs.113987	NM_014214:Homo sapiens inositol(myo)-1(o NM_006498:Homo sapiens lectin, galactosi	3.06
45	422262 410480	AL022315 R97457	Hs.63984	NM_001257:Homo sapiens cadherin 13, H-ca	3.05
	435818	AA700553	Hs.368614	Hs.368614:ESTs	3.05
	418883	BE387036	Hs.1211	NM_001611:Homo sapiens acid phosphatase	3.05 3.05
	453613 408051	F06838 AI623351	Hs.374476 Hs.172148	Hs.374476:ESTs Hs.172148:ESTs	3.05
50	432278	AL137506	Hs.274256	Hs.274256:hypothetical protein FLJ23563	3.04
	407949	W21874	Hs.247057	Hs.247057:ESTs, Weakly similar to 210926	3.04
	418090	U57059	Hs.83429	NM_003810:Homo sapiens tumor necrosis fa Hs:292437:ESTs	3.04 3.03
	433165 425809	AA578904 AA370362	Hs.292437 Hs.57958	Hs.57958:EGF-TM7-latrophilin-related pro	3.03
55	443884	N20617	Hs.194397	Hs.194397:ESTs, Moderately similar to 22	3.03
	447831	Al433293	Hs.164115	Hs.164115:ESTs	3.02 3.01
	413278 418870	8E563085 AF147204	Hs.833 Hs.89414	NM_005101:Homo sapiens interferon-stimul Hs.89414:chemokine (C-X-C motif), recept	3.00
	456376	AA663904	Hs.89862	Hs.89862:TNFRSF1A-associated via death d	3.00
60	439738	BE246502	Hs.9598	Hs.9598:sema domain, immunoglobulin doma	3.00
	444416	AW288085	Hs.11156	NM_016494:Homo sapiens hypothetical prot Hs.89643:transketolase (Wemicke-Korsako	3.00 3.00
	406656 406826	M16714 AW516005	Hs.89643 Hs.84298	Hs.84298:CD74 antigen (invariant polypep	2.99
	418707	U97502	Hs.87497	Hs.87497:butyrophilin, subfamily 3, memb	2.99
65	421742	AW970004	Hs.107528		2.99 2.99
	406824 435605	AW515961 AF151815	Hs.84298 Hs.4973	Hs.84298:CD74 antigen (invariant polypep NM_015680:Homo sapiens hypothetical prot	2.98
	410491	AA465131	Hs.64001	Hs.64001:Homo sapiens clone 25218 mR seq	2.98
	427648	Al376722	Hs.180062	NM_004159:Homo sapiens proteasome (proso	2.98
70	411125	AA151647	Hs.68877	NM_000101:Homo sapiens cytochrome b-245, Hs.324507:hypothetical protein FLJ20986	2.98 2.98
	435550 429373	AI224456 NM_014694	Hs.324507 Hs.200594		2.98
	445701	AF055581	Hs.13131	NM_005475:Homo sapiens lymphocyte adapto	2.97
76	414649	AI672727	Hs.76753	NM_000118:Homo sapiens endoglin (Oster-R	2.97 2.97
75	444207	A1565004	Hs.374415 Hs.125359		2.97
	423225 407792	AA852604 AI077715	Hs.39384	NM_014344:Homo sapiens four jointed box	2.97
	445707	AI248720	Hs.114390	Hs.114390:ESTs	2.96
٥٨	452888				2.96 2.95
80	418478 411441	U38945 AL042355	Hs.1174 Hs.70202	Hs. 1174:cyclin-dependent kise inhibitor Hs. 70202:WD repeat domain 10	2.95
	443426		Hs.9329	Hs.9329:chromosome 20 open reading frame	2.94
	450876		Hs.28597	6 Hs.285976:LAG1 longevity assurance homol	2.94

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	426359			ts.10862:Homo sapiens cD: FLJ23313 fis, NM_001120:Homo sapiens tetracycline tran	2.94 2.93
	425421 449879		Hs.157145   Hs.287830	Hs.287830:Homo sapiens mR; cD DKFZp434E1	2.93
_	454075		Hs.16313	Hs.16313:Kruppel-like zinc finger protei	2.93
5	421595			Hs.301685:KIAA0620 protein Hs.334814:hypothetical protein FLJ14868	2.93 2.92
	457949 443987	W69171 AW163123	Hs.334814 Hs.10071	NM_016551:Homo sapiens seven transmembra	2.92
	430259	BE550182	Hs.375142	Hs.375142:RalGEF-like protein 3, mouse h	2.92
10	415906	AI751357	Hs.288741	Hs.288741:Homo sapiens cD: FLJ22256 fis, NM_006913:Homo sapiens ring finger prote	2.91 2.91
10	429762 451527	AI346255 AF022813	Hs.216354 : Hs.26518	NM_003271:Homo sapiens transmembrane 4 s	2.91
	425356	BE244879	Hs 155939	NM 005541:Homo sapiens inositol polyphos	2.91
	427080	AW068287	Hs.301175	NM_002872:Homo sapiens ras-related C3 bo	2.91 2.90
15	426432	AF001601 BE612705	Hs.169857 Hs.256697	NM_000305:Homo sapiens paraoxose 2 (PON2 Hs.256697:histidine triad nucleotide bin	2.89
13	431476 406659	AA663985	Hs.277477	Hs.277477:major histocompatibility compl	2.89
	451144	AW956103	Hs.61712	Hs.61712:Homo sapiens cD FLJ31548 fis, c	2.89 2.88
	456362	AW973003	Hs.179909 Hs.169902	Hs.179909:nuclear receptor coactivator 6 NM_006516:Homo sapiens solute carrier fa	2.88
20	426440 456974	BE382756 M12529	Hs.169401	NM_000041:Homo sapiens apolipoprotein E	2.88
20	418174	L20688	Hs.83656	Hs.83656:Rho GDP dissociation inhibitor	2.88 2.88
	446055	AI815981	Hs.12909	Hs.12909:mucolipin 1 NM_004428:Homo sapiens ephrin-A1 (EF1).	2.87
	423184 427700	NM_004428 AA262294	Hs.1624 Hs.180383	NM_004426:Homo sapiens dual specificity	2.87
25	410668	BE379794	Hs.159651	NM_016629:Homo sapiens hypothetical prot	2.87
	444143	AW747996	Hs.160999	Hs. 160999: ESTs, Weakly similar to 178885	2.87 2.86
	407151	H25836 A1825386	Hs.301527 Hs.352579	Hs.301527:ESTs, Moderately similar to un Hs.352579:Homo sapiens, chromosome 20 op	2.86
	449349 436997	AA741151	Hs.137323	Hs.137323:ESTs	2.86
30	446143	BE245342	Hs.306079	NM_013336:Homo sapiens protein transport	2.86 2.86
	417355	D13168	Hs.82002 Hs.267659	Hs.82002:endothelin receptor type B NM_006113:Homo sapiens vav 3 oncogene (V	2.86
	431685 408877	AW296135 AA479033	Hs.130315	Hs.130315:ESTs	2.85
	429615	AF258627	Hs.211562	NM_005502:Homo sapiens ATP-binding casse	2.85 2.84
35	412014	AI620650	Hs.43761	Hs.43761:gap junction protein, alpha 7, NM_006149:Homo sapiens lectin, galactosi	2.84
•	436749 419625	AA584890 U91616	Hs.5302 Hs.182885	NM_004556:Homo sapiens nuclear factor of	2.84
	439941	Al392640	Hs.18272	Hs. 18272:solute carrier family 38, membe	2.84
40	436496	AA281959	Hs.5210	NM_004877:Homo sapiens glia maturation f	2.84 2.83
40	422100	A1096988 AF035292	Hs.111554 Hs.6654	NM_005737:Horno sapiens ADP-ribosylation Hs.6654:KIAA0657 protein	2.83
	439730 447217	BE465754	Hs.17778	NM 003872:Homo sapiens neuropilin 2 (NRP	2.83
	428343	AL043021	Hs.12705	Hs. 12705: similar to HYPOTHETICAL 43.1 KD	2.82 2.82
45	440524	R71264	Hs.16798	Hs.16798:Homo sapiens mR; cD DKFZp564O24 NM_003119:Homo sapiens spastic paraplegi	2.81
45	415523 439668	AL042003 Al091277	Hs.296847 Hs.302634	Hs.302634:frizzled homolog 8 (Drosophila	2.81
	414570	Y00285	Hs.76473	NM_000876:Homo sapiens insufin-like grow	2.80 2.80
	426535	AU077012	Hs.288582	NM_006287:Homo saplens tissue factor pat Hs.55505:hypothetical protein FLJ20442	2.80
50	409649 406655	AA159216 M21533	Hs.55505 Hs.277477		2.79
50	415323	BE269352	Hs.949	NM_000433:Homo sapiens neutrophil cytoso	2.79 2.78
	443195	BE148235	Hs.193063		2.78
	451356 450708	AA748418 AA376654	Hs.164577 Hs.350065		2.78
55	433681	AI004377	Hs.200360	Hs 200360: Homo sapiens cD FLJ 13027 fis.	2.77 2.76
	442599	AF078037	Hs.324051	NM_006663:Homo sapiens RelA-associated i NM_001780:Homo sapiens CD63 antigen (mel	2.76
	414509 431394		Hs.76294 Hs.252351		2.76
	417331			Hs.81972:SHC (Src homology 2 domain cont	2.76
60	415995	NM_00457			2.75 2.75
	414911 425976		7 Hs.77602 Hs.334514	NM_000107:Homo sapiens damage-specific U 4 Hs.334514:chromosome 6 open reading fram	2.75
	407893		Hs.43621	Hs.43621:hypothetical protein MBC3205	2.75
	407903	AJ287341	Hs.15402		2.75 2.75
65	416062 428494		Hs.33479 Hs.18463		2.75
	421506			7 NM 003258:Homo saciens thymidine kise 1.	2.74
	42758	NM_01478	8 Hs.17970	3 NM_014788:Homo sapiens tripartite motif-	2.74 2.74
70	42452				2.74
70	439578 42518			1 Hs.155071:chromosome 20 open reading fra	2.74
	42801	3 AF151020	Hs.18144	MM 016456:Homo sapiens hypothetical prot	2.73 2.73
	43933				2.73
75	45093 42153			70 Hs. 146170:hypothetical protein FLJ22969	2.73
, ,	44050	2 AI824113	Hs.78281	Hs.78281:regulator of G-protein sighting	2.73
	44498	1 AW85539			2.72 2.72
	43921 41684		Hs.4132 Hs.8026		2.72
80	43317		5 Hs.1624	59 Hs.162459:ESTs	2.72
= =	42452	8 AW07397			2.71 2.70
	41121 43301			- ATV4 And deat	2.70
	4330		15.2733		

	425345	AU077297		NM_002827:Homo sapiens protein tyrosine	2.69 2.69
	428923 427923	BE047698 AW274357	Hs.188785 Hs.301406	Hs. 188785:ESTs Hs. 301406:hypothetical protein PP3501	2.69
	446644	NM_003272	Hs.15791	NM_003272:Homo sapiens transmembrane 7 s	2.69
5	421743	T35958	Hs.107614	Hs.107614:DKFZP564I1171 protein	2.68
	416207	NM_014745	Hs.79077	NM_014745:Horno sapiens KIAA0233 gene pro	2.68 2.68
	420372 420542	AW960049 NM_000505	Hs.293660 Hs.1321	Hs.293660:gene overexpressed in astrocyt NM_000505:Homo sapiens coagutation facto	2.67
	425069	AA687465	Hs.298184	Hs. 298184: potassium voltage-gated channe	2.67
10	418558	AW082266	Hs.86131	NM_003824:Homo sapiens Fas (TNFRSF6)-ass	2.67
	426251	M24283	Hs.168383	NM_000201:Homo sapiens intercellular adh	2.66 2.66
	406701	AA780613 AK000378	Hs.62964 Hs.267566	Hs.62954:ferritin, heavy polypeptide 1 Hs.267566:hypothetical protein FLJ20371	2.66
	431681 412833	AW960547	Hs.298262	Hs.298262:ribosomal protein S19	2.66
15	433101	AW572317	Hs.12082	Hs.12082:TIGA1	2.66
	414774	X02419	Hs.77274	NM_002658:Homo sapiens plasminogen activ	2.66
	427868	AI360119	Hs.181013 Hs.75617	NM_002629:Homo sapiens phosphoglycerate Hs.75617:collagen, type IV, alpha 2	2.66 2.66
	413929 424762	BE501689 AL119442	Hs.183684	Hs.183684:eukaryotic translation initiat	2.66
20	422048	NM_012445	Hs.288126	NM_012445:Homo sepiens spondin 2, extrac	2.65
	431350	Al192528	Hs.164537	Hs.164537:ESTs	2.65
	450184	W31096	Hs.237617 Hs.89868	Hs.237617:dipeptidylpeptidase 9 Hs.89868:KIAA0062 protein	2.65 2.65
	419285 414217	D31887 Al309298	Hs.279898	Hs.279898:Homo sapiens cO: FLJ23165 fis,	2.64
25	451253	H48299	Hs.26126	NM_006984:Homo sapiens claudin 10 (CLDN1	2.64
	435905	AW997484	Hs.5003	Hs.5003:SUT-ROBO Rho GTPase-activating	2.64
	432581	AU076465	Hs.278441	NM_014634:Homo sapiens KIAA0015 gena pro	2.63 2.63
	415782 430223	AA169345 NM_002514	Hs.123177 Hs.235935	Hs.123177:hypothetical protein BC011406 NM_002514:Homo sapiens nephroblastoma ov	2.63
30	417526	AA568906	Hs.82240	NM_004177:Homo sapiens syntaxin 3A (STX3	2.63
	409956	AW103364	Hs.727	NM_002192:Homo sapiens inhibin, beta A (	2.63
	449843	R85337	Hs.24030	NM_001860:Homo sapiens solute carrier fa	2.62 2.62
	417389	BE260964	Hs.82045 Hs.171802	NM_002391:Homo sapiens midkine (neurite Hs.171802:Homo sapiens, clone IMAGE:3956	2.62
35	446312 435099	BE087853 AC004770	Hs.4756	Hs.4756:flap structure-specific endonucl	2.62
33	417920	S47833	Hs.82927	NM_004037:Homo sapiens adenosine monopho	2.62
	435702	AI033647	Hs.121001	Hs.121001:Homo sapiens, clone MGC:45521	2.62
	422959	AV647015	Hs.349256	Hs.349256:paired immunoglobulin-like rec	2.62 2.62
40	419938 450954	AU076772 A1904740	Hs.1279 Hs.25691	NM_001733:Homo sapiens complement compon NM_005856:Homo sapiens receptor (calcito	2.61
40	421753	BE314828	Hs.107911	Hs.107911:ATP-binding cassette, sub-fami	2.61
	443577	AI078033	Hs.177170	Hs.177170:ESTs, Weakly similar to ALU8_H	2.61
	453886	R66282	Hs.20247	Hs.20247:ESTs	2.61 2.60
45	421883	X55079	Hs.1437	NM_000152:Homo sapiens glucosidase, alph Hs.21321:granute cell differentiation pr	2.60 2.60
4)	440457 410295	BE387593 AA741357	Hs.21321 Hs.356624	Hs.356624:ESTs	2.59
	420679	X57152	Hs.99853	NM_001436:Homo sapiens fibrillarin (FBL)	2.59
	451558	NM_001089	Hs.26630	NM_001089:Homo sapiens ATP-binding casse	2.59
50	444672	Z95636	Hs.11669	Hs.11669:laminin, alpha 5	2.59 2.59
30	408669 426194	AI493591 T50872	Hs.78146 Hs.2001	Hs.78146:ptatelet/endothelial cell adhes Hs.2001:thromboxane A synthase 1 (ptatel	2.59
	421814	L12350	Hs.108623	NM_003247:Homo sapiens thrombospondin 2	2.59
	456371	S76825	Hs.89695	Hs.89695:insulin receptor	2.59
55	429098	AF030249	Hs.196176	NM_001398:Homo sapiens enoyl Coenzyme A	2.59 2.59
55	414443 428484	AU077268 AF104032	Hs.76144 Hs.184601	NM_002609:Homo sapiens platelet-derived NM_003486:Homo sapiens solute carrier fa	2.59
	453309	AI791809	Hs.32949	NM 005218:Homo sapiens defensin, beta 1	2.59
	412867	AU076861	Hs.74637	NM_003217:Homo sapiens testis enhanced g	2.58
<b>(</b> 0	432827	Z68128	Hs.3109	Hs.3109:Rho GTPase activating protein 4	2.58
60	412669	AW880841 AK001763	Hs.96908 Hs.73239	NM_006034:Horno sapiens p53-induced prote Hs.73239:hypothetical protein FLJ10901	2.58 2.58
	412115 452866	R26969	Hs.268016		2.58
	435129	Al381659	Hs.267086	Hs.267086:ESTs	2.57
	424482	BE268621	Hs.149155	NM_003374:Homo sapiens voltage-dependent	2.57 2.56
65	410494	M36564	Hs.64016	NM_000313:Homo sapiens protein S (alpha)	2.56 2.56
	433895 442566	Al287912 R37337	Hs.3628 Hs.12111	NM_004834:Homo sapiens mitogen-activated Hs.12111:ESTs	2.56
	417640	D30857	Hs.82353	NM_006404:Homo sapiens protein C recepto	2.56
	442622	NM_000435		NM_000435:Homo sapiens Notch homolog 3 (	2.56
70	430346	AK000331	Hs.297641		2.55 2.55
	419344	U94905	Hs.277445 Hs.170156		2.55
	426500 408048	NM_014638 NM_007203		NM_007203:Homo sapiens A kise (PRKA) and	2.55
	450700	AW732799	Hs.25348	NM_005860:Homo sapiens follistatin-like	2.54
75	417018	M16038	Hs.80887	NM_002350:Homo sapiens v-yes-1 Yamaguchi	2.54
	419378		Hs.90078	Hs.90078:nucleotide-sugar transporter si	2.54 2.53
	422451 435906	AA310753 Al686379	Hs.42491 Hs.110796	Hs.42491:ESTs, Moderately similar to hyp Hs.110796:SAR1 protein	2.53
	433900	MUUU013		- Indicated and a second	2.53
80	417849		Hs.82733	NM_007361:Homo sapiens nidogen 2 (NID2),	2.53
	427380				2.52 2.52
	428385		Hs.184063	2 Hs.184062:chromosome 20 open reading fra Hs.5985:non-kise Cdc42 effector protein	2.52
	438000	A1825880	Hs.5985	120000 morrow was diona brazili	

					osoina far metaina) protaisa i	2.52
				Hs.21	858:serine (or cysteine) proteise i 07:L-fucose kise	2.52
		W21872 AA564248	Um 251202	He 35	1292:Homo sapiens cD FLJ32605 fis.	2.51
	430590	AW383947	Hs.246381	NM C	01251:Homo sapiens CD68 antigen (CD6	2.51 2.51
5	447026	BE313144	Hs.324844	Hs.32	4844:hypothetical protein IMAGE3455	2.50
	439223	AW238299		Hs.25	0618:UL16 binding protein 2 788:nicastrin	2.50
	435151	AA348482 AB002292	Hs.4788 Hs.20695	NM 1	06.19629:Homo sapiens Rho guanine nucle	2.50
	448202 449943	AF104266	Hs.24212	He 2	1212:latrophilin	2.50 2.50
10	425743	BE396495	Hs.159428	Hs.1	59428:BCL2-associated X protein	2.50 2.50
	444681	AJ243937	Hs.288316	Hs.2	38316:chromosome 6 open reading fram 007126:Homo sapiens valosin-containin	2.50
	421643	BE281170	Hs.106357 Hs.172813	NM	nnagge-Homo sapiens Rho quanine nucle	2.50
	426865 432306	D63476 Y18207	Hs.303090	MM	noczgr.Homo sagiens protein phosphata	2.49
15	421846	AA017707	Hs.1432	NM	002743:Homo sapiens protein kise C su	2.49 2.49
	421905	A1660247	Hs.32699	Hs.3	2699:Homo sapiens, Similar to RIKEN 002815:Homo sapiens proteasome (proso	2.49
	419493	AF001212	Hs.90744	NM_	004335:Homo sapiens bone marrow strom	2.48
	422530	AW972300 BE391929	Hs.118110 Hs.8752	NM	014255:Homo saoiens transmembrane pro	2.48
20	442821 416919	T97839	Hs.80464	NM	006402: Homo sapiens hepatitis 8 virus	2.48 2.48
20	.443105	X96753	Hs.9004	NM	001897:Homo sapiens chondroitin sulfa	2.48
	430040	AW503115	Hs.227823	NM	014287:Homo sapiens pMS protein (PMS)	2.47
	428028	U52112	Hs.182018	NM	001569:Homo sapiens interleukin-1 rec 356377:Homo sapiens, clone IMAGE:3633	2.46
25	424307	AW293399 R28982	Hs.356377 Hs.18106	Hs.	18106:ESTs, Wealdy similar to T06291	2.46
23	434511 454390	AB020713	Hs.56966	Hs	56966:KIAA0906 protein	2.46 2.46
	417785	X59812	Hs.82568	NM	_000784:Homo sapiens cytochrome P450,	2.46
	424673	AA345051	Hs.294092	Hs.	294092:Homo sapiens mR full length in 296326:ESTs, Wealdy similar to A33533	2.46
••	422003	AA361760	Hs.296326	HS.	37196:putative G protein coupled rece	2.46
30	432126	AA865239	Hs.37196 Hs.321231	NA	1 003779:Homo sapiens UDP-GaltbelaGcc	2.46
	445937 409354	A1452943 N68188	Hs.159472		159472:Homo sapiens cD: FLJ22224 fis,	2.46 2.46
	401179	1100100	1.0			2.45
	418151	AA864238	Hs.83583	NA	/_005731:Homo sapiens actin related pro	2.45
35	422648	D86983	Hs.118893	Hs	.118893:Melanoma associated gene /_005041:Homo sapiens perforin 1 (prefo	2.45
	427759	BE245578	Hs.2200 Hs.273790	1 N7	/ 007155:Homo sapiens zo pellucida glyc	2.45
	431222 411529	X56777 AA430348	Hs.317596	: 14	217596 Homo saniens cD FLJ1292/ fts.	2.45
	426825	AL133415	Hs.297753	a Ni	u 003380 Homo saciens vimentin (VIM), m	2.45 2.45
40	422242	AJ251760	Hs.273385		M_016592:Homo sapiens GS complex locus	2.44
	408105	AW152207	Hs.270977		s.270977:ESTs s.305890:BCL2-like 1	2.44
	426410	BE298446 Al245432	Hs.305890 Hs.101383	2 N	M 006291-Homo sapiens tumor necrosis fa	2.44
	421064 428157		Hs.19842	7 M	u 000180-Homo saniens bexokisė 2 (HKZ).	2.44
45	424398		Hs.14639	R N	M 014685:Homo sapiens homocysteine-inou	2.44 2.44
	424825	AF207069	Hs.15335	7 N	M_001084:Homo sapiens procollagen-lysin	2.43
	426031		Hs.16606	76 F	ls. 166066:cisplatin resistance associate ls. 56607:Williams-Beuren syndrome chromo	2.43
	409817		Hs.56607 Hs.2399		IM 004995 Homo saciens matrix metallopro	2.43
50	429359 426761		Hs.17208	20. 1	te 172089 pro-ancasis receptor inducing	2.43 2.43
50	429333	AF030403		53 f	M_013233:Homo sapiens serine threonine	2.43
	42592	3 NM_0050		08 1	NM_005026:Homo sapiens phosphoinositide- ls.273333:hypothetical protein FLJ10986	2.43
	43221			33 I	ds.8036;RAB3D, member RAS oncogene famil	2.42
55	43333 42053				Hs. 44004:AD031 protein	2.42
55	41324			57	Hs.193657:ESTs	2.42 2.42
	43502	9 AF167700		0	Hs.19280:cysteine-rich motor neuron 1 Hs.1519:protein kise, cAMP-dependent, re	2.42
	42237			ן ויי	NM_004148:Homo sapiens ninjurin 1 (NINU)1	2.42
60	44450 41491		·	161	Hs 194461:ESTs	2.42
00	41935			31	NM_006667:Homo sapiens progesterone rece	2.42 2.42
	43604	12 AF28442	2 Hs.1191		Hs.119178:cation-chloride cotransporter-	2.42
	41824				Hs.83883:transmembrane, prostate androge Hs.10669:development and differentiation	2.41
45	4442		'5 Hs.1066 Hs.468		NM_016614:Homo sapiens TRAF and TNF rece	2.41
65	40864 4237				He 143022-FSTs	2.41
	4417				Hs.7961:Homo sapiens clone 25012 mR sequ	2.41 2.41
	4280	72 BE25860			NM_016292:Homo sapiens heat shock protei	2.40
	4345				Hs.3989:plexin B2 Hs.8261:SPRY domain-containing SOCS box	2.40
70					Hs 41143:ohospholipase C, beta 1 (phosph	2.40
	4078 4534				Hs.32981:sema domain, immunoglobulin dom	2.40 2.40
	4086		2 Hs.152	2925	Hs.152925:KIAA1268 protein	2.40
	4224	48 AW372	322 Hs.116		Hs.116774:integrin, alpha 1	2.39
75	4162				Hs.161671:ESTs Hs.63883:transmembrane, prostate androge	2.38
	4526				NM 002733:Homo sapiens protein filse, AMP	2.38
	4325 419				Hs.285681:Williams Beuren syndrome chrom	2.38
	422		36 Hs.11	1779	Hs. 111779:secreted protein, acidic, cyst	2.38 2.38
80	() 413	092 AA126			Hs.118665:ESTs Hs.271786:ESTs, Wealdy similar to PC4395	2.37
	433				He 117855 solute carrier family 17 (anio	2.37
	451 447	267 A10338 526 AL0487			NM_002982:Homo sapiens small inducible c	2.37
	441				_	

	441623	AA315805		Hs.348710:Homo sapiens, clone IMAGE:4242	2.37 2.37
	420255 409274	NM_007289 NM_003930	Hs.1298 Hs.52644	NM_007289:Homo sapiens membrane metallo- NM_003930:Homo sapiens src tamily associ	2.36
	422801	AF125672	Hs.287994	Hs.287994:nuclear receptor co-repressor	2.36
5	407887	AA579668	Hs.41072	Hs.41072:serine (or cysteine) proteise i	2.36
	408212 430478	AA297567	Hs.43728	NM_015696:Homo sapiens wealthy similar to NM_014349:Homo sapiens apolipoprotein L,	2.36 2.36
	405102	NM_014349	Hs.241535	(MM_014043.) Retto deposio apospoposioni E.	2.35
	423583	AL122055	Hs.129836	Hs.129836:KIAA1028 protein	2.35
10	426125	X87241	Hs.166994	NM_005245:Homo sapiens FAT tumor suppres	2.35 2.35
	425204 420676	NM_002436 A1434780	Hs.1861 Hs.4248	NM_002436:Homo sapiens membrane protein, Hs.4248:Homo sapiens PP3781 mR, complete	2.35
	421079	AW404994	Hs.101695	Hs. 101695:NCK adaptor protein 2	2.35
	410039	AF207989	Hs.58014	Hs.58014:G protein-coupled receptor, fam	2.34
15	412958	BE391579	Hs.75087	NM_006712:Homo sapiens FAST kise (FASTK)	2.34 2.34
	430363 425397	M28713 J04088	Hs.274464 Hs.156346	NM_000398:Homo sapiens diaphorase (DH) ( NM_001067:Homo sapiens topoisomerase (D)	2.34
	451035	AU076785	Hs.430	NM_002670:Homo sepiens plastin 1 (I isof	2.34
00	449027	AJ271216	Hs.22880	Hs.22880:dipeptidylpeptidase III	2.34
20	429457	BE243065	Hs.202955 Hs.82426	Hs.202955:hypothetical protein FLJ20507 NM_014734:Homo sapiens KIAA0247 gene pro	2.34 2.34
	41 <i>77</i> 09 412805	D87434 AW954569	Hs.278675	Hs.278675:bromodomain-containing 4	2.34
	427647	W19744	Hs.180059	Hs.180059:Homo sapiens cO FLJ31360 fis,	2.34
25	430702	U56979	Hs.278568	NM_000186:Homo sapiens H factor 1 (compl	233 233
25	456804 453648	AI421645 W21493	Hs.139851 Hs.28329	NM_001233:Homo sapiens caveolin 2 (CAV2) Hs.28329:protein phosphatase 1, regulato	233
	450812	AB002360	Hs.25515	Hs.25515:MCF.2 cell line derived transfo	2.33
	402575	,			2.33
20	424670	W61215	Hs.116651	NM_005797:Homo sapiens epithelial V-like	2.32 2.32
30	452960 442968	AK001335 AK000606	Hs.31137 Hs.8868	NM_006504:Homo sapiens protein tyrosine NM_004871:Homo sapiens goligi SP receptor	2.32
	410639	BE269047	Hs.65234	Hs.65234:DEAD/H (Asp-Glu-Ala-Asp/His) bo	2.32
	415169	W42913	Hs.78089	NM_004231:Homo sapiens ATPase, H+ transp	2.32
26	450160	BE048099	Hs.183738	Hs. 183738:FERM, RhoGEF (ARHGEF) and plec	2.32 2.32
35	407223 426780	H96850 BE242284	Hs.172199	H96850;yw03b12.s1 Soares melanocyte 2NbH NM 001114;Homo sapiens adenylate cyclase	2.32
	434987	AW975114	Hs.371677	Hs.371677:ESTs	2.32
	416354	NM_000633	Hs.79241	NM_000633:Homo sapiens B-cell CLL/lympho	2.31
40	453107	NM_016113	Hs.279746	NM_016113:Homo sapiens transient recepto	2.31 2.31
40	422963 433618	M79141 AA602539	Hs.13234 Hs.345494	Hs.13234:ESTs, Weakly similar to hypothe Hs.345494:ESTs, Moderately similar to ZN	2.31
	438584	AA811347	115.575737	AA811347:ob81h06.s1 NCI_CGAP_GCB1 Homo s	2.31
	446126	AW085909	Hs.356618	Hs.356618:ESTs, Wealthy similar to PC4259	2.31
45	408716	Ai567839	Hs.151714	Hs.151714:peroxisomal proliferator-activ	2.30 2.30
45	433230 410168	AW136134 AW834050	Hs.220277 Hs.351432	Hs.220277:ESTs, Weakly similar to expres Hs.351432:tensin	2.30
	446342	BE298665	Hs.14846	Hs.14846:Homo sapiens mR; cD DKFZp564D01	2.30
	418452	BE379749	Hs.85201	NM_005127:Homo sapiens C-type (catcium d	2.30
50	453175	NM_006834	Hs.32217	NM_006834:Homo sapiens RAB32, member RAS	2.29 2.29
50	409012 452848	AL117435 AJ417193	Hs.49725 Hs.288912	Hs.49725:DKFZP434l216 protein Hs.288912:BBP-like protein 2	2.29
	418838	AW385224	Hs.35198	Hs.35198:ectonucleotide pyrophosphatase/	2.29
	422562	AI962060	Hs.11B397	NM_001129:Homo saplens AE binding protei	2.28 2.28
55	432828	AB042326	Hs.287402 Hs.334851	Hs.287402:chondroitin 4-sulfotransferase NM_006148:Homo sapiens LIM and SH3 prote	2.28
23	412948 426068	BE243313 AF029778	Hs.166154	NM_002226:Homo sapiens jagged 2 (JAG2).	2.28
	456919	NM_003900	Hs.182248	NM_003900:Homo sapiens sequestosome 1 (S	2.28
	452806	AW014549	Hs.58373	Hs.58373:ESTs	2.28 2.28
60	453983 407736	H94997 N41744	Hs.16450 Hs.349326	Hs.16450:ESTs Hs.349326:Homo sapiens cD FLJ30677 fis,	2.28
00	413211	AW967107	Hs.109274		2.28
	422051	AW327546	Hs.111024	Hs.111024:solute carrier family 25 (mito	2.27
	438438	AA257992	Hs.50651	Hs.50651:Janus kise 1 (a protein tyrosin	2.27 2.27
65	436278 454080	BE396290 Al199711	Hs.5097 Hs.576	NM_004710:Homo sapiens syptogyrin 2 (SYN NM_000147;Homo sapiens fucosidase, alpha	2.27
03	426542	AF190746	Hs.170310	NM_017424:Homo sapiens cat eye syndrome	2.27
	417115	AW952792	Hs.334612	NM_003094:Homo sapiens small nuclear rib	2.27 2.26
	402901	********	Un 74560	NM_006634:Homo sapiens vesicle-associate	2.26
70	412898 413020	Al129903 R98736	Hs.74669	R98736:yr31h09.r1 Soares fetal fiver spl	2.26
, ,	413939	AL047051	Hs.199961	Hs.199961:ESTs, Wealdy similar to hypoth	2.26
	408681	AW953853	Hs.281462	Hs.281462:hypothetical protein FLJ14251	2.25 2.25
	412330	NM_005100 R50192	Hs.788 Hs.165062	NM_005100:Homo sapiens A kise (PRKA) and Hs.165062:ESTs	2.25 2.25
75	442083 418271	NM_000919		NM_000919:Homo sapiens peptidylglycina a	2.25
	433376	AI249361	Hs.74122	NM_001225:Homo sapiens caspase 4, apopto	2.25
	438562	A1566826	Hs.25890	Hs. 25890:ESTs, Wealthy similar to transdu	2.25 2.25
	443883		Hs.9930 Hs.80680	NM_001235:Homo sapiens serine (or cystei Hs.80680:major vault protein	2.24
80	416976 416914		Hs.80426	Hs.80426:brain and reproductive organ-ex	2.24
• •	400288	X06256	Hs.14960	NM_002205:Homo sapiens integrin, alpha 5	2.24
	407904		Hs.10726		2.24 2.24
	429690	AW956329	Hs.23721	ns.23121.0310	

	443813	AA876372 I	Hs.93961 H	ls.93961:Homo sapiens mR; cD DKFZp667D09	2.24
		BE208364	H- 20283	ts 29283:ESTs, Weakly similar to LKHU pr	2.24 2.24
			Hs.50640	NM_003745:Homo sapiens JAK binding prote	2.23
5	407192			Hs.366318:ESTs NM_001885:Homo sapiens crystallin, alpha	2.23
,	425751 456437		Hs.115185	Hs.115185:ESTs	2.23
	413019	BE281604	Hs.75140	NM_002337:Homo sapiens low density lipop	2.23 2.23
	418862			Hs.89399:ATP synthase, H+ transporting, Hs.96849:Homo sapiens cD FLJ11492 fis, c	2.23
10	435284		He 211573	NM 005529:Homo sapiens heparan sulfate p	2.23
10	429630 427609	M85289 AK000436	Hs.179791	Hs.179791:RAB20, member RAS oncogene fam	2.23
	421917	AB028943	Hs.109445	Hs.109445:hypermethylated in cancer 2	2.23 2.23
	446616	R65964	Hs.334873	Hs.334873:carboxypeptidase M X04526:Human liver mR for beta-subunit s	2.23
1.5	407232	X04526	Hs.132904	Hs.132904:solute carrier family 4, sodiu	2.23
15	423798 446755	AF047033 AW451473	Hs.16134	NM 005990:Homo sapiens serine/threonine	2.22
	452865	AI924046	Hs.119567	Hs.119567:ESTs, Weakly similar to ALU1_H	2.22 2.22
	431393	AW971493	Hs.134269	Hs.134269:ESTs, Weakly similar to 200439 NM_002203:Homo sapiens integrin, alpha 2	2.22
20	431890	X17033	Hs.271986 Hs.193400	NM_000565:Homo sapiens interleukin 6 rec	2.22
20	428782 446006	X12830 NM_004403	Hs.13530	NM_004403:Homo sapiens deafness, autosom	2.22
	436418	AJ245874	Hs.4245	Hs 4245:chromosome 11 hypothetical prote	2.22 2.21
	423869	BE409301	Hs.134012	NM_006688:Homo sapiens C1q-related facto	2.21
25	437730	AW071087	Hs.239176	Hs. 239176:insufin-like growth factor 1 r Hs. 35052:ESTs	2.21
25	444020 413882	R92962 AA132973	Hs.35052 Hs.184492	Hs.184492:Homo sapiens mR; cD DKFZp66780	2.21
	412654	A1093480	Hs.374319	Hs.374319:ESTs	2.21
	448988	Y09763	Hs.22785	NM_004961:Homo sapiens gamma-aminobutyri	2.21 2.21
	426841	AI052358	Hs.131741	Hs.131741:ESTs NM_006943:Homo sapiens SRY (sex determin	2.21
30	408196	AL034548 AK000461	Hs.43627 Hs.26890	Hs.26890:cat eye syndrome chromosome reg	2.20
	451711 414325	AA251929	Hs.355341	Hs.355341;Homo sapiens, clone IMAGE:3536	2.20
	424512	X53002	Hs.149846	NM_002213:Homo sapiens integrin, beta 5	2.20 2.20
	448883	BE614989	Hs.7503	Hs.7503:hypothetical protein FLJ14153	2.20
35	411296	BE207307	Hs.10114	Hs.10114:growth suppressor 1 NM_003512:Homo sapiens H2A histone famil	2.20
	452268 416810	NM_003512 AF035606	Hs.28777 Hs.80019	NM_013232:Homo sapiens programmed cell d	2.20
	441415	H21497	Hs.7471	Hs 7471:BBP-like protein 1	2.20 2.19
	444212	AW503976	Hs.10649	NM_004848:Homo sapiens basement membrane	2.19
40	428044	AA093322	Hs.301404	NM_006743:Homo sapiens R binding motif p NM_002832:Homo sapiens protein tyrosine	2.19
	430017	AA263172 AJ278016	Hs.35 Hs.55565	Hs.55565:ankyrin repeat domain 3	2.19
	424490 431193	AW749505	Hs.296770	Hs.296770:KIAA1719 protein	2.19
	453686	AL110326	Hs.304679	Hs.304679:ESTs, Weakly similar to Z195_H	2.19 2.19
45	448262	AW880830	Hs.186273	Hs.186273:ESTs NM_002592:Homo sapiens proliferating cel	2.19
	416065	BE267931 C05768	Hs.78996 Hs.8078	Hs.8078:Homo sapiens clone FBD3 Cri-du-c	2.19
	442045 423804	AW403448	Hs.1706	NM_006084:Homo sapiens interferon-stimul	2.19
	428024	Z29067	Hs.2236	Hs.2236:NIMA (never in mitosis gene a)-r	2.19 2.19
50	424503	NM_002205		NM_002205:Homo sapiens integrin, alpha 5 Hs.5790:hypothetical protein dJ37E16.5	2.18
	437696	Z83844	Hs.5790	MS.3730.hypotheacar protein addit c 10.0	2.18
	405204 426158	NM_001982	2 Hs.19906	NM_001982:Homo sapiens v-erb-b2 erythrob	2.18
	417418		3 Hs.82116	NM 002468:Homo sapiens myeloid different	2.18 2.18
55	412773		Hs.74573	NM_012268:Homo sapiens similar to vaccin NM_000100:Homo sapiens cystatin B (stefi	2.18
	409402		Hs.695 Hs.14334		2.18
	443791 435049		Hs.4746	Hs.4746:hypothetical protein FLJ21324	2.18
	418389		Hs.29384	9 Hs.293849:ESTs	2.18 2.18
60	450712		Hs.27049		2.18
	422007		Hs.39168 Hs.28603		2.18
	453676 415718		Hs.20023	7 Hs.200237:ESTs	2.18
	452688		Hs.49930	Hs.49930:ESTs, Weakly similar to B34087	2.18 2.18
65					2.17
	40945		Hs.95612 Hs.8222		2.17
	41751 42720			rs NM 000628:Homo sapiens interleukin 10 re	2.17
	44098		Hs.7594	NR MGG31:Homo saciens solute carrier ta	2.17 2.17
70			Hs.7900		2.17
	42964		Hs.2115 1 Hs.3483	89 Hs 348389:hypothetical protein FLJ12875	2.17
	42721 43776			NM 003254:Homo sapiens tissue inhibitor	217
	45400		) Hs.5672	Hs.5672:golgi membrane protein SB140	2.17 2.16
75	42424	17 X14008	Hs.2347		2.16
	40385		Λ LL 2777	77 Hs.277477:major histocompatibility compl	2.16
	40664 40029		0 Hs.2774		2.16
	4423		13 Hs.8265	NM_004613:Homo sapiens transglutamise 2	2.16 2.16
80	) 4418	92 AB02898	1 Hs.802	Hs.8021:KIAA1058 protein	2.16
	4174				2.16
	4183 4140			TAC TAC	2.16
	7140				

		AMMESETE	11- 040430	the 240470 house the bland contain MCC2724	216
	440906 447660	AW161556 AW160386	Hs.240170 Hs.163667	Hs.240170:hypothetical protein MGC2731 Hs.163667:ESTs, Weakly similar to CA1H_H	2.16 2.16
	408279	AF216965	Hs.44095	Hs.44095:cyclin M3	2.16
_	426152	BE299190	Hs.167246	Hs.167246:P450 (cytochrome) oxidoreducta	2.16
5	437952	D63209	Hs.5944	NM_014585:Homo sapiens solute carrier fa	2.16 2.15
	415661 425302	AF057307 U79115	Hs.78575 Hs.155566	Hs.78575:prosaposin (variant Gaucher dis NM_003805:Homo sapiens CASP2 and RIPK1 d	2.15
	425996	W67330	Hs.374451	Hs.374451:ESTs	2.15
••	413745	AW247252	Hs.75514	NM_000270:Homo sapiens nucleoside phosph	2.15
10	422070	AF149785	Hs.111126 Hs.31924	Hs.111126:pituitary tumor-transforming 1 Hs.31924:ESTs	2.15 2.15
	448424 430035	AW009892 NM_003463	Hs.227777	NM_003463:Homo sapiens protein tyrosine	2.15
	438407	AI457122	Hs.129673	Hs.129673:eukaryotic translation initiat	2.15
16	435551	AF212365	Hs.5470	Hs.5470:interleutin 17B receptor	2.15
15	437741	BE561610	Hs.5809	Hs.5809:putative transmembrane protein;	2.15 2.15
	441192 435750	AA526626 AB029012	Hs.7736 Hs.4990	NM_016504:Homo sapiens mitochondrial rib Hs.4990:KIAA1089 protein	2.15
	411165	NM_000169	Hs.69089	NM_000169:Homo sapiens galactosidase, al	2.14
20	425252	AW391162	Hs.349306	Hs.349306:hypothetical protein FLJ31951	2.14
20	427600	AW630918	Hs.179774	NM_002818:Homo sapiens proteasome (proso	2.14 2.14
	426818 442110	AAS54827 AF113008	Hs.292996 Hs.8102	Hs.292996:postmeiotic segregation increa NM_001023:Homo sapiens ribosomal protein	2.14
	407797	AK000524	Hs.39850	Hs.39850:urldine kise-like 1	2.14
26	443044	N28522	Hs.8935	NM_014298:Homo sapiens quinotite phospho	2.14
25	437103	AW139408	Hs.152940 Hs.297007	Hs.152940:ESTs	2.14 2.14
	442069 424954	AW664144 NM 000546	Hs.1846	Hs.297007:Homo sapiens cD FLJ32174 fis, NM_000546:Homo sapiens turnor protein p53	2.14
	458097	AW341135	Hs.58104	Hs.58104:Homo sapiens, clone IMAGE:47309	2.14
~~	411925	AW014588	Hs.72925	NM_003475:Homo sapiens chromosome 11 ope	2.14
30	449644	AW960707	Hs.148324	Hs.148324:ESTs	2.14 2.14
	422675 428586	BE018517 M36712	Hs.119140 Hs.2299	NM_001970:Homo sapiens eukaryotic transl Hs.2299:CD8 antigen, beta polypeptide 1	214
	429379	NM_014840	Hs.200598	NM_014840:Homo sapiens KIAA0537 gene pro	2.13
	410290	AA402307	Hs.322844	Hs.322844:hypothetical protein DKFZp564A	2.13
35	443895	AW979048	Hs.292566	Hs.292566:YEA4 protein	2.13
	428145	BE243327	Hs.182626	NM_012264:Homo sapiens chromosome 22 ope	2.13 2.13
	453518 456534	AW503205 X91195	Hs.27268 Hs.100623	Hs.27268:Homo sapiens cD: FLJ21933 fis, Hs.100623:protein phosphatase 1, regulat	2.13
	419972	AL041465	Hs.182982	Hs.182982:golgin-67	2.13
40	424950	AA602917	Hs.156974	Hs.156974:ESTs	2.13
	427557	NM_002659	Hs.179657	NM_002659.Homo sapiens plasminogen activ	2.13
	431449	M55994	Hs.256278 Hs.172012	NM_001066:Homo sapiens tumor necrosis fa Hs.172012:hypothetical protein DKFZp434J	2.13 2.13
	418758 434202	AW959311 BE382411	Hs.3764	NM_000858;Homo sapiens guanylate kise 1	213
45	433233	AB040927	Hs.301804	Hs.301804:KIAA1494 protein	2.12
-	452700	AI859390	Hs.288940	Hs.288940:transmembrane protein 8 (five	2.12
	438033	T26483	Hs.6059	NM_016938:Homo sapiens EGF-containing fi	2.12 2.12
	400847 447547	NM_007229	Hs.18842	NM_007229:Homo sapiens protein kise C an	2.12
50	417052	NM_000712	Hs.81029	NM_000712:Homo sapiens biliverdin reduct	2.12
	413284	AU077055	Hs.289107	NM_001166:Homo sapiens baculoviral IAP r	2.11
	434558	AW264102	Hs.39168	Hs.39168:ESTs, Wealdy similar to T17340	2.11 2.11
	404030 410801	BE275469	Hs.66493	Hs.66493:Down syndrome critical region g	211
55	418613	AA744529	Hs.86575	Hs.86575:mitogen-activated protein kise	2.11
-	447087	AW403870	Hs.301872	Hs.301872:hypothetical protein MGC4840	2.11
	433026	AW160616	Hs.279921	NM_016127:Homo sapiens hypothetical prot	2.11
	426433	L38969	Hs.169875	NM_007112:Homo sapiens thrombospondin 3 NM_002752:Homo sapiens mitogen-activated	2.11 2.11
60	442439 437379	U09759 AL359575	Hs.246857 Hs.23765	Hs.23765:membrane metallo-endopeptidase-	211
00	400208	74555575	1.0.20700		2.11
	455705	AW161061	Hs.356580	Hs.356580:ESTs, Wealdy similar to zinc f	211
	417599	AA204688	Hs.62954	Hs.62954:ferritin, heavy polypeptide 1	2.10 2.10
65	416728 439920	AB024597 H05430	Hs.79658 Hs.288433	NM_001894:Homo sapiens casein kise 1, ep Hs.288433:neurotrimin	2.10
05	422309	U79745	Hs.114924		2.10
	436114	AA778232	Hs.19515	Hs.19515:ESTs, Highly similar to NRG3_HU	2.10
	405517			11 0000 4 10 ID 12 - C ID 10 M 4 -	2.10
70	421872 437712	AA359753 X04588	Hs.22824 Hs.85844	Hs.22824:MYB binding protein (P160) 1a Hs.85844:neurotrophic tyrosine kise, rec	2.10 2.10
70	431214	AA294921	Hs.348024		2.10
	412856	BE386745	Hs.74631	NM_001728:Homo sapiens basigin (BSG), mR	2.10
	442064	AI422867	Hs.88594	Hs.88594:Homo sapiens, clone IMAGE:43329	2.10
75	434845	BE267057	Hs.325321		2.10 2.10
75	426728 419596	NM_007118 BE379320	Hs.367689 Hs.91448	NM_007118:Homo sapiens triple functiol d NM_007026:Homo sapiens dual specificity	2.09
	448913	AA194422	Hs.22564	NM_004999:Horno sapiens myosin VI (MYO6),	2.09
	414721	X90392	Hs.77091	NM_006730:Homo sapiens deoxyribonuclease	2.09
οΛ	424658	NM_002406			2.09
80	432805 447032		Hs.3107 Hs.17138	Hs.3107:CD97 antigen Hs.17138:hypothetical protein FLJ20303	2.09 2.09
	447484		Hs.29256		2.09
	440188		Hs.7036	Hs.7036:N-acetytglucosamine kise	2.09
				4	

## 180259   AN 1971752   Ha.83341   ANJ respicir hyrotine kise   2.09   ## 1808  ## 18020422   AN 1971752   Ha.83341   ANJ respicir hyrotine kise   2.09   ## 200363   AN 1971752   Ha.83341   ANJ respicir hyrotine kise   2.09   ## 200363   AN 1971752   Ha.83341   ANJ respicir hyrotine kise   2.09   ## 200364   AN 297391   Ha.29776   Ha.29776/milegyin, gapless leftin, galactical   2.08   ## 200364   AN 1971752   Ha.29776   Ha.29776/milegyin, gapless leftin, galactical   2.08   ## 200365   AN 1971750   Ha.102541   Ha.10		445584	AF217518	Hs.8360 F	ts.8360:PTD012 protein	2.09
4 48943 AV195637 Hs. 15.557 Av195637 Av195637 Hs. 15.557 Av195637 Av195637 Hs. 15.557 Av195637 Av195637 Av195637 Av195637 Hs. 15.557 Av195637 Av195637 Av195637 Hs. 15.557 Av195637 Av195637 Av195637 Hs. 15.557 Av195637 Av195637 Av195637 Av195637 Hs. 15.557 Av195637 Av195637 Av195637 Hs. 15.557 Av195637 Av195637 Hs. 15.557 Av195637 Av195637 Hs. 15.557 Av195637 Av195637 Hs. 15.557 Av195637 Av195637 Av195637 Hs. 15.557 Av195637 Av195637 Av195637 Hs. 15.557 Av195637 Hs. 15.557 Av195637 Hs. 15.557 Av195637 Av195637 Hs. 15.557 Av195637 H						2.09 2.09
\$\frac{43910}{42972} \times Auggressed   \$\frac{4273}{42973} \times Auggressed   \$\frac{4273}{42972} \times Auggressed   \$\f					ks.83341:AXL receptor tyrosine kise	
422773 AV929385 Hs.299178 Hs.29917 Av92918 hs.29918 Hs.299178 Hs.299178 hs.29918 hs.	5			Hs.261587 1	Hs.261587:GCN2 elF2alpha kise	
16446   1037   14779	,		AW297985	He 205726	Hs.295726:integrin, atpha V (vitronectin	
11093					NM_005567:Homo sapiens lecum, galactusi NM_001515:Homo sapiens general transcrip	2.08
August				He 740	Hs 740:PTK2 protein tyrosine kise 2	
1179   AA299811   Hs 10294   Hs	10		AI559444	Hs.104679	Hs.104679:Homo sapiens, clone MGC:18216	
15					HS.102541:netini 4 NM 003551:Homo sapiens non-metastatic ce	2.08
13318					Hs 292882:ESTs	
Heart   Hear		413518	8E149455		NM_004048:Homo sapiens beta-2-microglobu	
## 4331	15					
41769 A4779393 Hs. 16277 403966 49915 A32833 A47749855 Hs. 16273 41940 MM, 002951 41940 MM, 002951 41940 MM, 002951 41980 MM, 002471 41980 MM, 002471 41980 MM, 002471 42699 U33035 Hs. 2499 42899 U33035 Hs. 2499 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402424 402425 402424 402426 402424 402426 402424 402426 402424 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 402426 4					Hs.337772:hypothetical protein BC009331	
August   A		412760			Hs.41324:ESTs	
49915 AJ23335	20		AI494299	HS. 10297		
419803 AV749865 Hs.17507 hs.17607 Js. milling local control of IRP A11907 Ms. milling local control of IRP A11907 Ms. milling local control of IRP A11907 Ms. milling local control of IRP A11907 Js. milling local control of IRP A11907 Ms. milling	20		AI223335		NM_002227:Homo sapiens Janus kise 1 (a p	
25 43914 M. 0013 3 te 551 M. 002437 ten sapiens MyO17 strasgene, M. 00183 ten sapiens MyO17 strasgene, M. 00183 ten sapiens MyO17 strasgene, M. 00183 ten sapiens instretien regula 2.06 M. 001572 ten sapiens protein kise C-I 2.08 M. 001572 ten sapiens protein kise C-I 2.06 M. 001572 ten sapiens sapiens protein 2.05 M. 001572 ten sapiens sapiens protein 2.05 M. 001572 ten sapiens sapiens sapiens protein 2.05 M. 001572 ten sapiens sapiens sapiens resistance 2.05 M. 00263 ten sapiens sapi		436823			Hs. 117077:zinc finger protein 254	
August					NM 002437:Homo sapiens MpV17 transgene,	
### 1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,000   1,	25			Hs.6551	NM 001183:Homo sapiens ATPase, H+ transp	
A072424   A06626   XDAS26   Hs. 215595   Hs. 215595   Hs. 215595   Ls. 215695 (quanine nucleoide binding pro   2.06   A073131   Hs. 24322   A1726066   T39307   Hs. 188572   A1726066   T39307   Hs. 188572   A1726066   T39307   Hs. 18274   Hs. 24324   A272437   A172439   Hs. 188572   Hs. 24324   A272437   A272437   Hs. 25435   Hs. 24324   A272437   A272437   Hs. 25435   Hs. 24324   A272437   A		426059			NM_001572:Homo sapiens interieron regula	
A			U33053	HS.2499	NM_002741.numb sapiens process nace of a	
ASS911			XQ4526	Hs.215595	Hs.215595:guanine nucleotide binding pro	
419728 U50330 Hs 1374 M 0061294-home sapients bone morphogenetil 2.05 42214 A126437 Hs 55405	30	458911				
1.5244					NM 006129:Homo sapiens bone morphogeneti	
44,2498					He 55405:hypothetical protein MGC16212	
413420   AW410235   Hs.75348   MM_00626334non sapiens proteasome (proso 409430   R21945   Hs.45785   A46735   Hs.57600   Hs.57600   Hs.57600   Hs.57600   Hs.57600   Hs.37148   A3948   BE255304   Hs.37148   Hs.17996   Mm_00264   A20015   Mm_004736   Hs.17996   Mm_0038034non sapiens flotillin 1 (FLOT 204   A204075   A440975	2.5	442498			NM_002612:Homo sapiens pyruvate denydrog	
109430   R21945   Rs.346735	35				NM 006263:Homo sapiens proteasome (proso	
409932 AJ376750 Hs.57600 adaptor-related protein complex 43848 BE256304 Hs.374424 43852 AV958181 Hs.374424 447637 AK000816 Hs.17986 Hs.27656 40064 430016 NM_004736 Hs.27656 NM_005803:Homo sapiens flotillin 1 (FLOT 2.04 NM 005803:Homo sapiens spendrypic and po 45 40075 AV499914 Hs.58927 Hs.58927:nuclear VCP-like 2.04 NM 005804 AJ304861 Hs.75799 NM_003135:Homo sapiens spendryprohyl is 408504 AJ304961 Hs.6599 NM_000342:Homo sapiens spendryprohyl is 412146 Mg2444 Hs.73722 NM_00142:Homo sapiens APEX nuclease (mu 2.04 NM 005803:Homo sapiens pepidyprohyl is 412146 Mg2444 Hs.73722 NM_00042:Homo sapiens APEX nuclease (mu 2.04 NM 005803:Homo sapiens Spire spir					Hs 346735: Homo sapiens, clone IMAGE: 3881	
40 433852 AV961818 Hs.374424 Hs.374424 ESTS 204 427837 AK000816 Hs.179986 NM_005803140mo sapiens flotillin 1 (FLOT 2.04 430016 NM_004736 Hs.227656 NM_004736:Homo sapiens xenotropic and po 2.04 40975 AV499914 Hs.58927 hls.58927:hucker VCP-like 2.04 40975 AV499914 Hs.7579 Hs.58927:hucker VCP-like 2.04 409504 A3,04961 Hs.58927 hls.589937:hucker VCP-like 2.04 409504 A3,04961 Hs.58997 hls.589937:hucker VCP-like 2.04 409504 A3,04961 Hs.58997 hls.599937:hucker VCP-like 2.04 409504 A3,04961 Hs.58997 hls.599937:hucker VCP-like 2.04 4096504 A3,04961 Hs.58997 hls.599937:hucker VCP-like 2.04 4096504 A3,04961 Hs.59991 hls.599937:hucker VCP-like 2.04 4096164 Hs.5991 hls.59957:hucker VCP-like 2.04 4096164 Hs.5991 hls.59957:hucker VCP-like 2.04 4096164 Hs.5991 hls.59957:hucker VCP-like 2.04 4096164 Hs.5991 hls.59958 hls.195891:hucker policies protein Protein Policies protein Protein Septems Protei		409932	A1376750		Hs.57600:adaptor-related protein complex	
ARCO00316	40				Hs 374424:ESTs	
400164 430016 NM_004736 Hs. 227656 410134 U68140 Hs. 58927 Hs. 58927:nuclear VCP-like 2.04 440975 AW499914 Hs. 7573 409504 AA304961 Hs. 699 NM_003135:Homo sapiens sigl recognition 412146 M9244 Hs. 73722 NM_003135:Homo sapiens peptidylprobl is 2.04 412146 M9244 Hs. 73722 NM_003135:Homo sapiens peptidylprobl is 2.04 412146 M9244 Hs. 73722 NM_003135:Homo sapiens peptidylprobl is 2.04 412746 AA316476 Hs. 73823 NM_003135:Homo sapiens peptidylprobl is 2.04 41086 AA126841 Hs. 183834 Hs. 71016 Hs. 7	40				NM_005803:Homo sapiens flotillin 1 (FLOT	
45 44975 AW499914 Hs. 58927 Hs. 58927:nuclear VCP-like 2.04 44975 AW499914 Hs. 7579:miprofin 9 2.04 AW39944 Hs. 7579:miprofin 9 2.04 AW39944 Hs. 7579:miprofin 9 2.04 AW39944 Hs. 73722 MM_00333-Homo sapiens sigl recognition 2.04 AW3940 Hs. 73722 MM_001641-Homo sapiens APEX nuclease (mu 2.04 Hs. 283558 Hs. 71811 AW3940 Hs. 283558 hypothetical protein PRO1855 2.04 Hs. 283558 hypothetical protein PRO1855 2.04 Hs. 283558 hypothetical protein PRO1855 2.04 Hs. 71811 AA0697112752011-31 Stratagene fibroblas 2.03 AA0697127752011-31 Stratagene fibroblas 2.03 AA0697127752011-31 Stratagene fibroblas 2.03 Hs. 7033 ESTS 2.03 Hs. 7033 ESTS 2.03 Hs. 74564 48393 AW015318 Hs. 23911 Hs. 39911 Homo sapiens Rus 13, member RAS 2.03 Hs. 39911 Homo sapiens Rus 13, member RAS 2.03 Hs. 39911 Homo sapiens Rus 13, member RAS 2.03 Hs. 39911 Homo sapiens Rus 13, member RAS 2.03 Hs. 39911 Homo sapiens Rus 13, member RAS 2.03 Hs. 39911 Homo sapiens Rus 13, member RAS 2.03 Hs. 39911 Homo sapiens Rus 13, member RAS 2.03 Hs. 39911 Homo sapiens Rus 13, member RAS 2.03 Hs. 39911 Homo sapiens Rus 13, member RAS 2.03 Hs. 39911 Homo sapiens Rus 13, member RAS 2.03 Hs. 39911 Homo sapiens Rus 13, member RAS 2.03 Hs. 39912 Hs. 399		400264	00.4700		ALLA ONATZE-Morno societis xentifonic and 00	
45					Hs.58927:nuclear VCP-like	
402504 A304961 Hs.599 NM_000342Horno sapiens peptidylprobyl is 2.04 NM_00342Horno sapiens speridylprobyl is 2.04 NM_00342Horno sapiens speridylprobyl is 2.04 NM_00342Horno sapiens APEX ruclease (mu 2.04 NM_00342Horno sapiens APEX ruclease (mu 2.04 NM_00379 A3069711 Hs.178111 A306 A316476 Nm_00393 Hs.7033 NM_001641:Horno sapiens APEX ruclease (mu 2.04 NM_007979 A3069711 Hs.178111 A3069 Nm_00393 Hs.7033 Nm_00394 Nm_00393 Hs.7033 Nm_00394 Hs.15136 Nm_003964 Nm_003991 Nm_0039	45			Hs.7579	Hs.7579:importin 9	
12146					NM_003135:Homo sapiens sigi recognition  NN_00042:Homo sapiens pentidylarolyl is	
Section   Sect					NM 001641:Homo sapiens APEX nuclease (mu	
A06729				Hs.283556	3 Hs.283558:hypothetical protein PRO1855	
## ## ## ## ## ## ## ## ## ## ## ## ##	50			Hs.17181	AAAGG711:7m52h11.s1 Stratagene fibroblas	2.04
424340 AA339036 Hs.7033 Hs.7033 Hs.7033 Hs.7033ESTs 424662 RM M.002870 Hs.151536 NM_002870 Homo sapiens RAB13, member RAS 415740 N80486 Hs.39911 Hs.74564 Hs.39911 Homo sapiens RAB13, member RAS 408393 AW015318 Hs.23165 Hs.23165 Hs.23165ESTs 421295 AW081061 Hs.103180 Hs.12680 Hs.12680 Hs.39818 Hs.23165ESTs 421295 AW081061 Hs.103180 Hs.23165 Hs.23165ESTs 421295 AW081061 Hs.103180 Hs.23165DC2 protein 44883 AA926960 Hs.348669 NM_001826Homo sapiens CD FLJ10196 fis, c 447289 BE617527 Hs.239818 Hs.239818:phosphoinosibide-3-kise, catal 422785 Al824114 Hs.28988 Hs.176065:ESTs 452666 AB26645 Hs.211534 Hs.28988 Hs.2176065:ESTs 452056 AW955065 Hs.101150 Hs.128410Homo sapiens CD FLJ31665 fis, 452056 AW955065 Hs.101150 Hs.128410Homo sapiens CD FLJ31665 fis, 423627 AV06965 Hs.105861 Hs.211534Homo sapiens FXVD domain-conta 423527 AV06965 Hs.105861 Hs.101860:Homo sapiens FXVD domain-conta 423527 AV06965 Hs.105861 Hs.105861:Hs.105861:engulfment and cell mobility 3 423644 Hs.289847 Hs.289371:growth arrest-specific 5 435309 T97205 Hs.289371:growth arrest-specific 5 435309 AA92847 Hs.225838 Hs.376602 427157 U51166 Hs.239318 Hs.225838 Hs.376602 427157 U51166 Hs.239311 Hs.39300 Hs.225838:ESTs 424833 NM_003894 Hs.153405 NM_003291 Hs.317824 Hs.225838:ESTs 440086 NM_005402 Hs.59360 NM_003402Homo sapiens period homolog 2 NM_003402Homo sapiens speriod homolog 2 NM_00402Homo sapiens speriod homolog 2 NM_00402Hom				Hs.18383		
Mail			AA339036	Hs.7033	Hs 7033 ESTs	
Hs. 39911   Hs.	55				S NM 002870 Homo sapiens RAB13, member KAS	
Algorithms   Alg	دد				Hs 39911: Homo sapiens mR for FLJ00089 pr	
Mail		412749	AA378417		NM_003145:Homo sapiens sigl sequence rec	
May					n He 103180:DC2 orolein	
May	60			Hs.12680	Hs.12680:Homo sapiens cD FLJ10196 fis, c	
459580 AA022888 Hs.176065: ESTs Ls.289988 Hs.289988 hs.2191564 hs.2191664 hs.299898 hs.2191664 hs.299898 hs.219164 hs.219162 h	•				35 (1111_00.1011111111111111111111111111111	
A					65 He 176065:ESTs	
452696		42278		Hs.2890	RR He 289088 heat shock 90kD protein 1, alp	
Assess	65				34 Hs.211534;Homo sapiens CD FLJ31003 its,	
A25527   A1206965   Hs. 105861   Hs. 105861 engultment and cell mobility 3   201					18 MM 014164 Homo sapiens FXYU domain-conta	
Age					61 Hs.105861:engulfment and cell motility 3	
Hs. 289721 growth arrest-specific 5   2.01	70	42954	5 AJ824164		30 Hs.356130:ESTs	
Hs. 28374	/(				21 No 289721:prowth arrest-specific 5	
Hs. 193400   Hs.				4 Hs.2837	741 Hs.283741:exosome component Rrp46	
407347 A829947 75 435370 A964074 Hs.225838 Hs.225838:ESTs 2.01 430657 AA62910 Hs.370602 ESTs, Weakly similar to hypoth 2.01 427157 U51166 Hs.173824 NM_003211:Homo sapiens thymine-D glycosy 2.01 424833 NM_003894 Hs.153405 NM_003934:Homo sapiens period homotog 2 2.01 40086 NM_005402 Hs.53405 NM_003934:Homo sapiens v-ral simian leuk 2.01 438543 AA810141 Hs.192182 Hs.92182:ESTs 2.01 41745 NM_002291 Hs.82124 NM_002291:Homo sapiens laminin, beta 1 ( 2.01 412790 NM_014767 Hs.74583 NM_014767:Homo sapiens KIAA0275 gene pro 2.01		4533	29 T97205		(00 Hs.193400:interleukin 6 receptor	
A30657	79	4073			R38 Hx 225R38:ESTs	2.01
427157	75			10 Hs.370	ROO He 370602 ESTs. Weakly similar to hypoth	
40086 NM_005402 Hs.6906 NM_005402:Horno sapiens v-ral simian leuk 201 80 438543 AA810141 Hs.192182 Hs.192182:ESTs 201 417426 NM_002291 Hs.82124 NM_002291:Horno sapiens laminin, beta 1 ( 2.01 412790 NM_014767 Hs.74583 NM_014767-ND sapiens KIAA0275 gene pro 2.01		4271	57 U51166			2.01
80 438543 AA810141 Hs.192182 Hs.192182:ESTs 2201 417426 NM_002291 Hs.82124 NM_002291:Homo sapiens laminin, beta 1 ( 2.01 412790 NM_014767 Hs.74583 NM_014767:Homo sapiens KIAA0275 gene pro 2.01					6 NM_005402:Horno sapiens v-ral simian leuk	
417426 NM_002291 Hs.82124 NM_002291 Hs.001291 Horno sapients Mariant, USE 27 412790 NM_014767 Hs.74583 NM_014767	80	0 4385	43 AA8101	41 Hs.192	192 Nr 102182:FSTs	
4VI		4174	26 NM_002		03 NM 014767:Homo sepiens KIAA0275 gene pro	2.01
						2.01

WO 03/025138

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TABLE 38B:
                                                 Unique Eos probeset identifier number
                Pkey:
                                                 Gene cluster number
                CAT number:
                                                 Genhank accession numbers
                 Accession:
                                    CAT Number
                                                            Accession
                                                            BI030997 AA921874 AW188822 BI027862 AI347618 AI361453 AI088754 AW207491 AA077391 BG012775 BG997382 AA286833 AA150722 BI007625 BI027864 BI009100 BI006275 BI006276 BI0031000 BI006277 BI006277 BI007627 BI006266 BI006991 BI006990 BI007763 BI007762 BG997377 AA150780 BI033518 BI027818 BG015789 BI033807 AA341445
                 409745
                                   MH1944 5
10
                                                            N64410 AA248866 AA248779 W02010
AL390180 AA359908 BE177778 BE177779 AW893733 BF756318
                 419671
                                    253275_1
                 437495
                                    65231_1
                                                             AA229762 AA230035
                 418869
                                     12789 14
                                     129028_1
                                                             AA677593 AA618150 AA557952
                  432648
                                                             BG171436 BE079601 BE079534 AA299964 BE392717 BE883402 BE079532 BE018148 BF889427 W00396
15
                  421902
                                     276321_1
                                                             BI030997 AA921874 AW188822 BI027862 AJ347618 AJ361453 A1088754 AW207491 AA077391 BG012775 BG997382 AA286833 AA150722 BI007625
BI027864 BI009100 BI006275 BI006270 BI031000 BI029864 BI006277 BI007627 BI006266 BI006991 BI006990 BI007763 BI007762 BG997377
                  414667
                                     MH1944 5
                                                             AA150780 BI033518 BI027818 BG015789 BI033807 AA341445
                                                             AW173494 AI804345 AA669490
AW837178 T77002 F13038
                  435185
                                     127115_1
20
                  411331
                                     1076355_1
                                                             T63141 AI821021 BF370092 BF370127 BF370060 T62998
                                     2328579 1
                  451876
                                                             BC006097 X03066 NM_002120 M26040 AW469119 AW469127 AI299772 AW518149 AI144456 AW628070 AI629032 AI358810 AI880433 AI440472 AI357070 AI865365 AW014799 AI767973 AW518041 AA908398 AW768606
                                     23110_1
                  400261
                                    21979_1
1066666_1
                                                              AF086037 H89360 H89546
                  439195
25
                                                             AW936378 AW936544 AW813513
                  454694
                                                              AW934714 AW749864 AW749902 BE162498 BE161005 BE162499 BE161006 AA190449 AW513465 BE162500 BE161007
                  416913
                                     924456_1
                                                              AW974073 T56957
                  459362
                                      1238130_1
                  TABLE 38C:
30
                                                   Unique number corresponding to an Eos probeset
                  Pkey:
Ref:
                                                   Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA
                                                    sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
                                                   Indicates DNA strand from which exons were predicted.
                   Strand:
                                                   Indicates nucleotide positions of predicted exons.
                   Nt_position:
35
                                                                                    Nt_position
92752-93015
                   Pkey
                                      Ref
                                                               Strand
                   403346
                                      8569726
                                                              Plus
                                                                                    193-608
                   401621
                                      8570184
                                                              Minus
                                                                                     70823-70990
                                      8569726
                                                               Plus
                   403344
 40
                                                                                     116132-116407,116653-116922
                    404240
                                      5002624
                                                               Minus
                                                                                     13510-13725,13847-14015
                    401964
                                      3126781
                                                               Minus
                    404277
                                       1834458
                                                               Minus
                                                                                    91665-91946
                                      8102330
                                                                                     35816-36004,36587-36684
                    405121
                                                               Minus
                                      9797670
                                                                                     205146-205240,205428-205542
                                                               Minus
                    402493
 45
                                       9188523
                                                                                      25692-25895
                    402121
                                                               Ptus
                     402474
                                       7547175
                                                               Minus
                                                                                     53526-53628,55755-55920,57530-57757
                                                                                      69533-69868
                    403887
                                       7710553
                                                               Minus
                                                                                      120428-120703
                                       8469086
                    403328
                                                                Minus
                     401241
                                       4827300
                                                                Minus
                                                                                      30503-30844,31056-31248
  50
                     401736
                                       3219338
                                                                                      1771-1894
                                                                                      37929-38224
                     405029
                                       7533975
                                                                Minus
                                                                                      173667-173783,176876-177055
                     404171
                                       9930793
                                                                Plus
                                                                                      6973-7118
                     401797
                                       6730720
                                                                Ptus
                                                                Plus
                                       9929642
                                                                                      120173-120337
                     401234
   55
                     404170
                                       9930793
                                                                Plus
                                                                                      168836-169248
                                                                                      30940-31386
                     406122
                                          9144087
                                                                Minus
                    TABLE 39A: 856 GENES UP REGULATED IN RENAL CANCER COMPARED TO NORMAL ADULT TISSUES AND TO NON-MAUGNANT RENAL TISSUES THAT ARE LIKELY TO ENCODE PROTEINS AMENABLE TO MODULATION BY SMALL MOLECULES, PEPTIDES, OR ANTIBODIES
                    Encourse reviews amenable to monocontrol of small monocontrol of the small small state and the small s
   60
                    the ratio of "everage" renal cancer to "average" normal adult tissues was greater than or equal to 20, the ratio of "average" renal cancer to "average" normal adult tissues was greater than or equal to 20, the ratio of "average" renal cancer to "average" normal adult tissues was greater than or equal to 2.0, the "average" renal cancer lavel was set to the 90th percentile value amongst various renal specimens, the "average" normal adult tissue level was set to the 70th percentile value amongst various non-matignant tissues, the "average" non-matignant renal tissues, the "average" renal cancer value was greater than or equal to 50 units, and the predicted protein contained a structural domain that is indicative of having an oncogenic
   65
                     function or of transducing an intracellular signal, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or
                      ion_transporter).
                      Pkey:
                                                      Unique Eos probeset identifier number
                                                      Exemplar Accession number. Genbank accession number
                      ExAccn:
    70
                     UnigenelD:
                                                      Unigene number
                      Unigene Title:
                                                       Unigene gene tide
                                                       Ratio of tumor to normal adult tissues
                                                                 UnigenelD
                                                                                      Unigene Title
                                                                                                                                                                                                    R1
                      Pkay
                                         ExAcon
                                                                                                                                                                                                     15.71
    75
                                         H91923
                                                                 Hs.110024
                      435013
                                                                                                                                                                                                     14.07
                                                                                       Hs.19520:FXYD domain-containing ion tran
                                         X86400
AI792241
                      447768
                                                                 Hs.19520
                                                                                                                                                                                                     12.56
                                                                                       Hs.129614:kidney-specific membrane prote
                                                                 Hs 129614
                      445178
                                                                                                                                                                                                     12.41
                                         AW083920
                                                                 Hs.16098
                                                                                        Hs.16098:claudin 2
                      432542
                                                                                                                                                                                                     11.77
                                         AF169312
                                                                  Hs.9613
                                                                                        NM_016109:Homo sapiens angiopoietin-like
                      443595
    80
                                                                 Hs.75498
Hs.47448
                                                                                                                                                                                                     10.39
                       413719
                                         BE439580
                                                                                        NM 004591:Homo sepiens small inducible c
                                                                                                                                                                                                     10.18
                                                                                        Hs.47448:ESTs
                                         RE465204
                       435878
                                         BE159984
                                                                 Hs.125395
                                                                                        Hs.125395:ESTs
                                                                                                                                                                                                     9.95
                      440304
```

9.58

407065

Y10141

					251
	413049	NM_002151		IM_002151:Homo sapiens hepsin (transmemb	9.51 8.88
		AK000226	Hs.165619 1 Hs.124776 I	ts.165619:mucin and cadherin-tike ts.124776:Homo sapiens mR; cD DKFZp564N1	8.77
		AL049227 AF241254	Hs.178098	ts.178098:angiotensin I converting enzym	8.45
5	416768	AA363733	Hs 1032	VM 002909:Homo sapiens regenerating isle	7.94 7.78
_	422357	AF016272	Hs.115418	NM_004062:Homo sapiens cadherin 16, KSP- NM_001252:Homo sapiens tumor necrosis fa	7.78
	420737	L08096 AA077391	Hs.99899	AA077391:7B14E12 Chromosome 7 Fetal Brai	7.74
	409745 413936	AF113676	Hs 297681	NM 000295:Homo sapiens serine (or cystei	7.32 7.20
10	426682	AV660038	Hs.2056	Hs 2056:UDP glycosyltransferase 1 family	7.03
	406851	AA609784	Hs.352392 Hs.90786	Hs.352392:major histocompatibility compl Hs.90786:ATP-binding cassette, sub-famil	6.57
	419508 428953	AW997938 AA306610	Hs.348183	NAL 003823:Homo sapiens tumor necrosis fa	6.36
	436895	AF037335	Hs.5338	NM 001218:Homo sapiens carbonic anhydras	6.31 6.20
15	431842	NM_005764	Hs.271473	NM_005764:Homo sapiens epithelial protei Hs.374303:hypothetical protein MGC20576	6.20
	430014 423803	H59354 NM_005709	Hs.374303 Hs.132945	NM 005709:Homo sapiens PDZ-73 protein (P	6.19
	434779	AF153815	Hs.50151	Hs.50151:potassium inwardly-rectifying c	6.11 6.08
••	435767	H73505	Hs.117874	Hs.117874:ESTs Hs.120879:Homo sapiens, clone MGC:32871	6.02
20	422664	AA315933 U31519	Hs.120879 Hs.1872	Hs 1872 phosphoenolovruvate carboxykise	5.81
	425280 426559	AB001914	Hs.170414	NM 002570:Homo sapiens paired basic amin	5.73 5.69
	451564	AU076698	Hs.132760	NIA 001467: Homo sapiens glucose-b-phospha	5.68
25	418526	BE019020	Hs.85838 Hs.128749	NM_004207:Homo sapiens solute carrier fa Hs.128749:alpha-methylacyl-CoA racemase	5.66
25	444151 426471	AW972917 M22440	Hs.170009	NM 003236:Homo sapiens transforming grow	5.48
	432579	AF043244	Hs.278439	NM 003946:Homo sapiens nucleolar protein	5.45 5.42
	448733	NM_005629	Hs.187958	NM_005629:Homo sapiens solute carrier fa NM_003060:Homo sapiens solute carrier fa	5.36
30	446650 417089	AB016625 H52280	Hs.15813 Hs.18612	Hs.18612:Homo sapiens cD: FLJ21909 fis.	5.35
20	437848	AI906419	Hs.284380	Hs. 284380:pamma-glutamyltransferase 1	5.32 5.30
	423081	AF262992	Hs.123159	Hs.123159:sperm associated antigen 4 NM_001078:Homo sapiens vascular cell adh	5.23
	421893	NM_001078	Hs.109225 Hs.12126	Hs.12126:hepatocellular carcinoma-associ	5.20
35	435886 410276	BE265839 AI554545	Hs.359201	Hs 359201:ESTs	5.20 5.14
33	429451	BE409861	Hs.202833	NM_002133:Homo sapiens heme oxygese (dec	5.13
	446404	AA019961	Hs.26216	Hs.26216:Homo sapiens cD: FLJ22811 fis, NM_014324:Homo sapiens alpha-methylacyl-	5.09
	423445 449444	NM_014324 AW818436	Hs.128749 Hs.351306	NM 004696:Homo sapiens solute carrier fa	5.05
40	438106	BE245551	Hs.6079	NM 014863:Homo sapiens B cell RAG associ	5.02 5.01
	400419	AF084545		AF084545:Homo sapiens versican Vint isof NM_000204:Homo sapiens I factor (complem	4.99
	453920	Al133148 BE620886	Hs.36602 Hs.355279	Hs 355279-Homo sagiens cD FLJ23711 fts.	4.97
	447881 422253	W81526	Hs.113882		4.93 4.88
45	439024	R96696	Hs.35598	Hs.35598:ESTs	4.80
	414799	A1752416	Hs.77326 Hs.278625	NM_000598:Homo sapiens insufin-like grow NM_000592:Homo sapiens complement compon	4,77
	426530 410055	U24578 AJ250839	Hs.58241	Hs.58241:gene for serine/threonine prote	4,72 4,71
	404240				4.68
50	414617		Hs.288817		4.67
	448249 447818		Hs.337124 Hs.21906	Hs.21906:Homo sapiens ctone 24670 mR seq	4.66
	449057			Hs 22941:KIAA1363 protein	4.66 4.62
	422424		Hs.29663		4.62
55	417338 425873		Hs.81988 90 Hs.16041		4.58
	444700			NM 003645; Homo sagiens fatty-acid-Coenzy	4.58 4.56
	414998	8 NM_0025			4.48
60	41476: 44335		Hs.77266 Hs.17757	He 17757-pleckstrin homology domain-cont	4.45
00	44009			Hs 37890:Homo sapiens, clone IMAGE:48275	4.43 4.43
	44713	1 NM_0045	85 Hs.17460		4.42
	40697		Hs.1982 4 Hs.1806		4.40
65	42774 43625				4.38 4.37
0.5	45288	4 C05964	Hs.3184	1 Hs.31841:ESTs	4.36
	44400				4.35
	42262 41805			4 NM 002318:Homo sapiens lysyl oxidase-lik	4.34
70			Hs.8955		4.34 4.33
	4042	77	- 11.0545	7 Hs.95497:solute carrier family 2 (facili	4.30
	43556			71 NM_001645:Homo sapiens apolipoprotein C-	4.29
	4317 4066		Hs.814	Hs.814:major histocompatibility complex,	4.28 4.26
75	3 4214	85 AA2434	99 Hs.104		4.25
	4268				4.22
	4079 4380			634 Hs.122634:ESTs	4.22
. ــــ	4306	61 AC0055	51 Hs.130	714 Hs. 130714:ESTs, Moderately similar to AF	4.21 4.20
86					4,16
	4382 4113			61 Hs.94761:KIAA1691 protein	4.15
	4183				4,13
				400	

	449853	AF006823		NM_002246:Homo sapiens potassium channel	4.11 4.11
	415198 418751	AW009480 BE389014		NM_004221:Horno sapiens tural killer cell Hs.372548:phosphoinositide-3-kise, regul	4.09
	414166	AW888941		NM_006096:Homo sapiens N-myc downstream	4.07
5	424125	M31669		Hs. 1735:inhibin, beta B (activin AB beta	4.00
	416926	H03109	Hs.263395 Hs.362996	Hs.263395:sema domain, transmembrane dom Hs.362996:KIAA0779 protein	3.92 3.92
	419175 424218	AW270037 AF031824	Hs.143212	NM_003650:Homo sapiens cystatin F (leuko	3.91
	412870	N22788	Hs.82407	Hs.82407:chemotine (C-X-C motif) tigand	3.88
10	452203	X57522	Hs.352018	NM_000593:Homo sapiens transporter 1, AT	3.87 3.87
	446872	X97058 AW265634	Hs.16362 Hs.133100	NM_004154:Homo sepiens pyrimidinergic re Hs.133100:ESTs	3.87
	449961 424517	A1539443	Hs.137447	Hs.137447:Homo sapiens cD FLJ12169 fis,	3.86
	425262	D87119	Hs.155418	Hs.155418:GS3955 protein	3.83
15	443639	BE269042	Hs.9661	NM_002801:Homo sapiens proteasome (proso	3.82 3.81
	448133 418030	AA723157 BE207573	Hs.73769 Hs.83321	NM_000802:Homo sapiens folate receptor 1 Hs.83321:neuromedin B	3.81
	412939	AW411491	Hs.75069	NM_005412:Homo sapiens serine hydroxymet	3.80
	409162	H25530	Hs.50868	NM_002555:Homo sapiens solute carrier fa	3.79
20	427715	BE245274	Hs.180428	Hs.180428:KIAA1181 protein	3.78 3.77
	412006 430413	AW451618 AW842182	Hs.290216 Hs.241392	Hs.290216:ESTs NM_002985:Homo sapiens small inducible c	3.76
	422282	AF019225	Hs.114309	Hs.114309:apolipoprotein L, 1	3.76
25	420747	BE294407	Hs.99910	Hs.99910:phosphofructokise, platelet	3.76 3.75
25	414875	H42679 AW382987	Hs.77522 Hs.88474	NM_006120:Homo saplens major histocompat Hs.88474:prostaglandin-endoperoxide synt	3.74
	418793 446291	BE397753	Hs.14623	NM_006332:Homo sapiens interferon, gamma	3.71
	417289	D86962	Hs.81875	Hs.81875:growth factor receptor-bound pr	3.69
20	422672	X12784	Hs.119129	NM_001845:Homo sapiens collagen, type IV	3.68 3.68
30	448569 437270	BE382657 R18087	Hs.21486 Hs.323769	NM_007315:Homo sapiens sigl transducer a Hs.323769:cisplatin resistance related p	3.67
	408452	AA054683	Hs.192455	Hs.192455:ESTs, Moderately similar to hy	3.67
	443986	AI381750	Hs.283437	Hs.283437:HTGN29 protein	3.66
25	418869	AW516565	U- 10000	AW516565:xq01d05.x1 Soares_NHCeC_cervica	3.65 3.62
35	425998 428699	AU076629 AW578252	Hs.165950 Hs.190161	NM_002011:Homo sapiens fibroblast growth NM_014020:Homo sapiens LR8 protein (LR8)	3.62
	418299	AA279530	Hs.83968	NM_000211:Homo sapiens integrin, beta 2	3.61
	432593	AW301003	Hs.51483	Hs.51483:Homo sapiens, Similar to RIKEN	3.59
40	415765	NM_005424	Hs.78824 Hs.29444	NM_005424:Homo sapiens tyrosine kise wit Hs.29444:putative small membrane protein	3.58 3.57
40	445985 424893	BE621800 AW295112	Hs.153648	Hs. 153648: protein tyrosine phosphatase,	3.57
	426046	AA833655	Hs.206868	Hs.206868:Homo sapiens cD FLJ14056 fis,	3.57
	424415	NM_001975	Hs.146580	NM_001975:Homo sapiens enolase 2, (gamma	3.57 3.56
45	412612 443834	NM_000047 AI741510	Hs.74131 Hs.173548	NM_000047:Homo sapiens arylsulfatase E ( Hs.173548:ESTs	3.54
40	431630	NM_002204	Hs.265829	NM_002204:Homo sapiens integrin, alpha 3	3.53
	418371	M13560	Hs.84298	Hs.84298:CD74 antigen (invariant polypep	3.52
	444838	AV651680	Hs.208558	Hs.208558:ESTs	3.52 3.52
50	449378 411393	AW664026 AW797437	Hs.59892 Hs.69771	Hs.59892:ESTs, Wealdy similar to alpha 5 NM_001710:Homo sapiens B-factor, properd	3.50
50	414311	AI693547	Hs.71746	Hs.71746:aminopeptidase-like 1	3.50
	415149	X12451	Hs.78056	NM_001912:Homo sapiens cathepsin L (CTSL	. 3.50 3.49
	424321	W74048	Hs.1765 Hs.77432	Hs. 1765:lymphocyte-specific protein tyro NM_005228:Homo sapiens epidermal growth	3.48
55	414825 408194	X06370 AA601038	Hs.191797	Hs. 191797:ESTs	3.48
	410600	AW575742	Hs.351676	Hs.351676:ESTs, Wealdy similar to T02670	3.47
	416899	BE262645	Hs.80420	NM_002996:Homo sapiens small inducible c	3.47 3.47
	436856 419660	AI469355 BE280337	Hs.127310 Hs.194693		3.47
60	413566	AW604451	Hs.285814		3.47
	412104	AW205197	Hs.240951	Hs.240951;ked cuticle homolog 2 (Drosoph	3.46
	444488	AW192879	Hs.355660		3.46 3.46
	449475 412276	AJ348027 BE262621	Hs.108557 Hs.73798	NM_002415:Homo sapiens macrophage migrat	3.45
65	449338	H73444	Hs.394	NM_001124:Homo sapiens adrenomedullin (A	3.44
	430304	AL122071	Hs.238927		3.43 3.43
	415388	AF018081	Hs.78409 Hs.273330	(locuslink)NM_030582:Homo sapiens collag Hs.273330:aprin	3.43
	432210 418177	AI567421 N44967	Hs.351554		3.42
70	414888	AL039185	Hs.77558	Hs.77558:thyroid hormone receptor intera	3.42
	452445	AB002438	Hs.29596	Hs.29596:Homo sapiens mR from chromosome	3.41 3.41
	414803 419201	X03100 M22324	Hs.914 Hs.1239	Hs.914:major histocompatibility comptex, NM_001150:Homo sapiens alanyl (membrane)	3.41
	445139	AB037848	Hs.12365	Hs. 12365:syptotagmin XIII	3.41
75	435021	AA922192	Hs.73962	Hs.73962:EphA7	3.41
	417259	AW903838	Hs.81800	Hs.81800:chondroitin sulfate proteoglyca Hs.41271:Homo sapiens mR full length ins	3.40 3.39
	439737 410636	AI751438 AA088177	Hs.41271 Hs.172870		3.39
	431590		Hs.263395	Hs.263395:sema domain, transmembrane dom	3.38
80	415000	AW025529			3.36 3.36
	416700 440516		Hs.34347! Hs.161	NM_001909:Homo sapiens cathepsin D (lyso NM_001792:Homo sapiens catherin 2, type	3.35
	423720		Hs.23388		3.32

					3.32
		BE392717	E	E392717:601307571F1 NIH_MGC_44 Homo sap Is.51233:tumor necrosis factor receptor	3.32
	409220		Hs.51233 h Hs.105039 h	IS.51233:tumor necrosis factor receptor IM_006424:Homo sapiens solute carrier fa	3.32
	421502 416729			IM_004165:Homo sapiens Ras-related assoc	3.30
5	430302		Hs.238679 I	ls.238679:Rag D protein	3.30
	445084	H38914		ls.250848:Homo sapiens cD FLJ14761 fis,	3.29 3.29
	406825			ls,84298:CD74 antigen (invariant polypep VM 005335:Homo sapiens hematopoietic cel	3.28
	446272 437145	BE268912 AF007216		NM_003759:Homo sapiens solute carrier fa	3.27
10	444071	AI627808		ts.110524:ESTs	3.27
	414662	AL036058	Hs.76807	ts.76807:major histocompatibility comple	3.27 3.26
	436576	A1458213		Hs.77542:ESTs, Weakly similar to \$26650	3.25
	424675	NM_005512		NM_005512:Homo sapiens glycoprotein A re Hs. 146170:hypothetical protein FLJ22969	3.25
15	437897 449703	AA770561 H61001	Hs.146170 Hs.171802	Hs.171802:Homo sapiens, clone IMAGE:3956	3.25
13	414788	X78342	Hs.77313	NM_003674:Homo sapiens cyclin-dependent	3.25
	414249	AI797994		Hs.279929:gp25L2 protein	3.24 3.23
	430396	D49742		NM_004132:Homo sapiens hyaluron binding	3.23
20	424456	AA341017 R27257	Hs.25549 Hs.57734	Hs. 25549:hypothetical protein FLJ20898 Hs. 57734:G protein-coupled receptor kise	3:22
20	452303 425390	AI092634	Hs.156114	NM_004648:Homo sapiens protein tyrosine	3.21
	416033	NM_012201	Hs.78979	NM_012201:Homo sapiens golgi apparatus p	3.19
	450931	N25156	Hs.25648	Hs.25648:tumor necrosis factor receptor	3.19 3.18
25	428065	A1534046	Hs.157313	Hs.157313:ESTs NM_012248:Homo sapiens selenophosphate s	3.18
25	422616 439318	BE300330 AW837046	Hs.118725 Hs.6527	Hs.6527:G protein-coupled receptor 56	3.17
	427640	AF058293	Hs.180015	NM_001355:Homo sapiens D-dopachrome taut	3.17
	409936	AK001691	Hs.57655	Hs.57655:dudulin 2	3.16 3.16
20	436001	AW903849	Hs.173840	Hs.173840:similar to endothelial cell-se	3.16
30	451154	AA015879	Hs.33536 Hs.76206	Hs.33536:ESTs NM_001795:Homo sapiens cadherin 5, type	3.16
	420256 407584	U84722 W25945	Hs.8173	Hs.8173:hypothetical protein FLJ10803	3.15
	428593	AW207440	Hs.185973	NM_003676:Homo sapiens degenerative sper	3.15
	410026	AI912061	Hs.55016	Hs.55016:EPS8-related protein 2	3.15 3.14
35	445333	BE537641	Hs.44278	Hs.44278:RAB17, member RAS oncogene fami NM_000391:Homo sapiens ceroid-lipofuscin	3.14
	448143 423007	AF039704 AA320134	Hs.20478 Hs.196029	Hs. 196029:Homo sapiens mR for KIAA1657 p	3.14
	416511	NM_006762	Hs.79356	NM_006762:Homo sapiens Lysosomal-associa	3.14
	439237	AW408158	Hs.318893	Hs.318893:ESTs, Weakly similar to Z195_H	3.13 3.13
40	446899	NM_005397	Hs.16426	NM_005397:Homo sapiens podocatyxin-like	3.13
	413916	N49813	Hs.75615 Hs.3838	NM_000483:Homo sapiens apolipoprotein C- NM_006622:Homo sapiens serum-inducible k	3.12
	434398 441283	AA121098 AA927670	Hs.131704	Hs.131704:ESTs	3.12
	418945	BE246762	Hs.89499	NM_000698:Homo sapiens arachidote 5-lipo	3.12 3.12
45	418458	AA332941	Hs.85226	NM_000235:Homo sapiens lipase A, lysosom	3.11
	408989	AW361666 H95990	Hs.49500 Hs.181244	Hs.49500:KIAA0746 protein Hs.181244:major histocompatibility compl	3.11
	436906 411089	AA456454	Hs.355702	Hs.355702:ESTs, Weakly similar to AC0048	3.11
	432990	AL036071	Hs.279899	NM_003820:Homo sapiens tumor necrosis fa	3.11 3.10
50	425009	X58288	Hs.154151	NM_002845:Homo sapiens protein tyrosine Hs.42658:Homo sapiens cD FLJ30167 fis, c	3.10
	443601	AI078554 AA148164	Hs.42658 Hs.247280		3.10
	430603 413672	BE156536	Hs.353632	Hs.353632:ESTs, Moderately similar to hy	3.09
	407786	AA687538	Hs.38972	NM_005727:Homo sapiens tetraspan 1 (TSPA	3.09 3.08
55	414586		Hs.16488	NM_002298:Homo sapiens lymphocyte cytoso	3.08
•	423712		Hs.81988 Hs.6314	Hs.81988:disabled homolog 2, mitogen-res NM_012410:Homo sapiens type I transmembr	3.06
	438552 448364		Hs.297214		3.06
	426437		Hs.169895	NM_004223:Homo sapiens ubiquitin-conjuga	3.06 3.06
60	437679			NM_014214:Homo sapiens inositol(myo)-1(o	3.06
	422262		Hs.113987 Hs.63984	NM_006498:Homo sapiens lectin, galactosi NM_001257:Homo sapiens cadherin 13, H-ca	3.05
	410480 435818			Hs.368614:ESTs	3.05
	418883			NM_001611:Homo sapiens acid phosphatase	3.05
65	453613	F06838	Hs.37447		3.05 3.05
	408051		Hs.17214 Hs.27425		3.04
	432278 407949		Hs.24705		3.04
	41809		Hs.83429		3.04
70	43316	5 AA578904			3.03 3.03
	42580				3.03
	44388 44783		Hs.19439 Hs.16411		3.02
	41327			NM_005101:Homo sapiens interferon-stimul	3.01
75	41887	0 AF147204			3.00 3.00
	45637			Hs. 89862:TNFRSF1A-associated via death d Hs. 9598:sema domain, immunoglobulin doma	3.00
	43973 44441				3.00
	40665		Hs.89643	Hs.89643:transketolase (Wernicke-Korsako	3.00
80	40682	6 AW51600	5 Hs.84290	Hs.84298:CD74 antigen (invariant polypep	2.99 2.99
	41870		Hs.8749		2.99
	42174 40682				2.99
	T0004				

	435605	AF151815	Hs.4973	NM_015680:Homo sapiens hypothetical prot	2.98
	410491			Hs.64001:Homo sapiens clone 25218 mR seq NM_004159:Homo sapiens proteasome (proso	2.98 2.98
	427648 411125		Hs.180062 Hs.68877	NM_000139.homo sapiens cytochroma b-245.	2.98
5	435550		Hs.324507	Hs.324507:hypothetical protein FLJ20986	2.98
	429373	NM_014694	Hs.200594	NM_014694:Homo sapiens KIAA0605 gene pro	2.98
	445701 414649	AF055581	Hs.13131 Hs.76753	NM_005475:Homo sepiens lymphocyte adapto NM_000118:Homo sepiens endoglin (Osler-R	2.97 2.97
	444207	A1572727 A1565004	Hs.374415	Hs.374415:ESTs	2.97
10	423225	AA852604	Hs.125359	NM_006288:Homo sapiens Thy-1 cell surfac	2.97
	407792	Al077715	Hs.39384	NM_014344:Homo sapiens four jointed box	2.97 2.96
	445707 452888	AI248720 AW955454	Hs.114390 Hs.30942	Hs.114390:ESTs NM_004093:Homo sapiens ephrin-B2 (EFNB2)	2.96
_	418478	U38945	Hs.1174	Hs.1174:cyclin-dependent kise inhibitor	2.95
15	411441	AL042355	Hs.70202	Hs.70202:WD repeat domain 10	2.95
	443426 450876	AF098158 AF189062	Hs.9329 Hs.285976	Hs.9329:chromosome 20 open reading frame Hs.285976:LAG1 longevity assurance homol	2.94 2.94
	426359	AA376409	Hs.10862	Hs.10862:Homo sapiens cD: FLJ23313 fis.	2.94
••	425421	L11669	Hs.157145	NM_001120:Homo sapiens tetracycline tran	2.93
20	449879	H03573	Hs.287830	Hs.287830:Homo sapiens mR; cD DKFZp434E1	2.93 2.93
	454075 421595	R43826 AB014520	Hs.16313 Hs.301685	Hs.16313:Kruppel-like zinc finger protei Hs.301685:KIAA0620 protein	2.93
	457949	W69171	Hs.334814	Hs.334814:hypothetical protein FLJ14868	2.92
25	443987	AW163123	Hs.10071	NM_016551:Homo sapiens seven transmembra	2.92
25	430259	8E550182	Hs.375142 Hs.288741	Hs.375142:RalGEF-like protein 3, mouse h Hs.288741:Homo sapiens c0: FLJ22256 fis,	2.92 2.91
	415906 429762	A1751357 A1346255	Hs.216354	NM_006913:Homo sapiens ring finger prote	2.91
	451527	AF022813	Hs.26518	NM_003271:Homo sapiens transmembrane 4 s	2.91
20	425356	BE244879	Hs.155939	NM_005541:Homo sapiens inositol polyphos	2.91 2.91
30	427080 426432	AW068287 AF001601	Hs.301175 Hs.169857	NM_002872:Homo sapiens ras-related C3 bo NM_000305:Homo sapiens paraoxose 2 (PON2	2.90
	431476	BE612705	Hs.256697	Hs.256697:histidine triad nucleotide bin	2.89
	406659	AA663985	Hs.277477	Hs.277477:major histocompatibility compl	2.89
35	451144	AW956103	Hs.61712	Hs.61712:Homo sapiens cD FLJ31548 fis, c Hs.179909:nuclear receptor coactivator 6	2.89 2.88
33	456362 426440	AW973003 BE382756	Hs.179909 Hs.169902	NM_006516:Homo sapiens solute carrier la	2.88
	456974	M12529	Hs. 169401	NM_000041:Homo sapiens apolipoprotein E	2.88
	418174	L20688	Hs.83656	Hs.83656:Rho GDP dissociation inhibitor	2.88 2.88
40	446055 423184	AI815981 NM_004428	Hs.12909 Hs.1624	Hs.12909:mucolipin 1 NM_004428:Homo sapiens ephrin-A1 (EF1),	2.87
40	427700	AA262294	Hs.180383	NM_001946:Homo sapiens dual specificity	2.87
	410668	BE379794	Hs.159651	NM_016629:Homo sapiens hypothetical prot	2.87
	444143	AW747996	Hs.160999	Hs. 160999:ESTs, Weakly similar to 178885	2.87 2.86
45	407151 449349	H25836 A1825386	Hs.301527 Hs.352579	Hs.301527:ESTs, Moderately similar to un Hs.352579:Homo sapiens, chromosome 20 op	2.86
7,5	436997	AA741151	Hs.137323	Hs.137323:ESTs	2.86
	446143	BE245342	Hs.306079	NM_013336:Homo sapiens protein transport	2.86 2.86
	417355 431685	D13168 AW296135	Hs.82002 Hs.267659	Hs.82002:endothelin receptor type B NM_006113:Homo sapiens vav 3 oncogene (V	2.86
50	408877	AA479033	Hs.130315	Hs. 130315:ESTs	2.85
	429615	AF258627	Hs.211562	NM_005502:Homo sapiens ATP-binding casse	2.85
	412014	A1620650	Hs.43761 Hs.5302	Hs.43761:gap junction protein, alpha 7, NM_006149:Homo sapiens lectin, galactosi	2.84 2.84
	436749 419625	AA584890 U91616	Hs.182885	NM_004556:Homo sapiens nuclear factor of	2.84
55	439941	Al392640	Hs.18272	Hs. 18272:solute carrier family 38, membe	2.84
	436496	AA281959	Hs.5210	NM_004877:Homo sapiens glia maturation f	2.84 2.83
	422100 439730	AI096988 AF035292	Hs.111554 Hs.6654	NM_005737:Homo sapiens ADP-ribosytation Hs.6654:KIAA0657 protein	2.83
	447217	BE465754	Hs.17778	NM_003872:Horno sapiens neuropilin 2 (NRP	2.83
60	428343	AL043021	Hs.12705	Hs.12705:similar to HYPOTHETICAL 43.1 KD	2.82 2.82
	440524 415523	R71264 AL042003	Hs.16798 Hs.296847	Hs.16798:Homo sapiens mR; cD DKFZp564O24 NM_003119:Homo sapiens spastic paraplegi	2.81
	439668	AL042003 Al091277	Hs.302634		2.81
	414570	Y00285	Hs.76473	NM_000876:Homo sapiens insulin-like grow	2.80
65	426535	AU077012 AA159216	Hs.288582 Hs.55505	NM_006287:Homo sapiens tissue factor pat Hs.55505:hypothetical protein FLJ20442	2.80 2.80
	409649 406655	M21533	Hs.277477		2.79
	415323	BE269352	Hs.949	NM_000433:Homo sapiens neutrophil cytoso	2.79
70	443195	BE148235	Hs.193063		2.78 2.78
70	451356 450708	AA748418 AA376654	Hs.164577 Hs.350065		2.78
	433681	AI004377	Hs.200360	Hs.200360:Homo sapiens cD FLJ13027 fis,	2.77
	442599	AF078037	Hs.324051		2.76 2.76
75	414509 431394	AW161311 AK000692	Hs.76294 Hs.252351	NM_001780:Homo sapiens CD63 antigen (mel Hs.252351:HERV-H LTR-associating 2	2.76
, ,	417331	AW411297	Hs.81972	Hs.81972:SHC (Src homology 2 domain cont	2.76
	415995	NM_004573	Hs.355888		2.75
	414911	NM_000107 C75094	Hs.77602 Hs.334514		2.75 2.75
80	425976 407893	BE408359	Hs.43621	Hs.43621:hypothetical protein MBC3205	2.75
-	407903	AI287341	Hs.154025	Hs.154029:bHLH factor Hes4	2.75
	416062	AA724811	Hs.33479		2.75 2.75
	428494	AA233439	Hs.18463	HS. 104034; hypothesis a hosery Les conco	دان

	421506	BE302796	Hs.105097 N	M_003258:Homo sapiens thymidine kise 1,	2.74
			Hs.179703 N	IM_014788:Homo sapiens tripartite motif-	2.74 2.74
	424527	AW138558		ls.334873:carboxypeptidase M	2.74
_				is:350547:nuclear receptor co-repressor/ is:155071:chromosome 20 open reading fra	2.74
5	425188	AK002052 AF151020	Hs.155071 H Hs.181444 N	IM_016456:Horno sapiens hypothetical prot	2.73 -
	428013 439333		Hs 132986 F	ls.132986;Homo sapiens cD FLJ31588 fis,	2.73
	450935	BE514743	He 355753	VM 005851:Homo sapiens tumor suppressor	2.73 2.73
	421532	AW138207	Hs.146170 I	s.146170:hypothetical protein FLJ22969	2.73
10	440502	AI824113		rls.78281:regulator of G-protein siglling	2.72
	444981	AW855398		Hs.41322:ESTs	2.72
	439219 416847	N33883 L43821	Hs.80261	NM_006403:Homo sapiens enhancer of filam	2.72
	433179	AW362945	Hs.162459	Hs.162459:ESTs	2.72 2.71
15	424528	AW073971	Hs.238954	Hs.238954:ESTs, Wealdy similar to putati	2.70
	411213	AA676939		NM_003873:Horno sapiens neuropilin 1 (NRP NM_004045:Horno sapiens ATX1 antioxidant	2.70
	433012 425345	NM_004045 AU077297	Hs.279910 Hs.155894	NM_002827:Homo sapiens protein tyrosine	2.69
	425345 428923	BE047698		Hs.188785:ESTs	2.69
20	427923	AW274357		Hs 301406:hypothetical protein PP3501	2.69 2.69
	446644	NM_003272	Hs.15791	NM_003272:Homo sapiens transmembrane 7 s	2.68
	421743	T35958	Hs.107614	Hs. 107614:DKFZP564I1171 protein NM_014745:Homo sapiens KIAA0233 gene pro	2.68
	416207	NM_014745 AW960049	Hs.79077 Hs.293660	Hs.293660:gene overexpressed in astrocyt	2.68
25	420372 420542	NM_000505	Hs.1321	NM 000505:Homo sapiens coagulation facto	2.67
23	425069	AA687465	Hs.298184	Hs.298184:potassium voltage-gated channe	2.67 2.67
	418558	AW082266	Hs.86131	NM_003824:Homo sapiens Fas (TNFRSF6)-ass	2.66
	426251	M24283	Hs.168383	NM_000201:Homo saplens intercellular adh	2.66
20	406701	AA780613	Hs.62954 Hs.267566	Hs.62954:ferritin, heavy polypeptide 1 Hs.267566:hypothetical protein FLJ20371	2.66
30	431681 412833	AK000378 AW960547	Hs.298262	Hs.298262:ribosomal protein S19	2.66
	433101	AW572317	Hs.12082	Hs.12082:TIGA1	2.66 2.66
	414774	X02419	Hs.77274	NM_002658:Homo sapiens plasminogen activ	2.66
	427868		npHs.181013	NM_002629:Homo sapiens phosphoglycerate	2.66
35	413929	BE501689	Hs.75617	Hs.75617:collagen, type IV, afpha 2 Hs.183684:eukaryotic translation initiat	2.66
•	424762 422048	AL119442 NM_012445	Hs.183684 Hs.288126	NM_012445:Homo sapiens spondin 2, extrac	2.65
	431350	A1192528	Hs.164537	Hs.164537:ESTs	2.65
	450184	W31096	Hs.237617	Hs.237617:dipeptidylpeptidase 9	2.65 2.65
40	419285	D31887	Hs.89868	Hs.89868:KIAA0062 protein Hs.279898:Homo sapiens cD: FLJ23165 fis,	2.64
	414217	AI309298	Hs.279898 Hs.26126	NM_006984:Homo sapiens claudin 10 (CLDN1	2.64
	451253 435905	H48299 AW997484	Hs.5003	Hs 5003:SUT-ROBO Rho GTPase-activating	2.64
	432581	AU076465	Hs.278441	NM 014634:Homo sapiens KIAA0015 gene pro	2.63
45	415782	AA169345	Hs.123177	Hs.123177:hypothetical protein BC011406	2.63 2.63
	430223	NM_002514		NM_002514:Homo sapiens nephroblastoma ov NM_004177:Homo sapiens syntaxin 3A (STX3	2.63
	417526	AA568906	Hs.82240	NM_002192:Homo sapiens syntaxin 34 (0176) NM_002192:Homo sapiens inhibin, beta A (	2.63
	409956 449843	AW103364 R85337	Hs.727 Hs.24030	NM_001860:Homo sapiens solute carrier fa	2.62
50	417389	BE260964	Hs.82045	NM 002391:Homo sapiens midkine (neunte	2.62
-	446312	BE087853	Hs.171802	Hs.171802:Homo sapiens, clone IMAGE:3956	2.62 2.62
	435099	AC004770	Hs.4756	Hs.4756:flap structure-specific endonucl NM_004037:Homo sapiens adenosine monopho	2.62
	417920		Hs.82927 Hs.121001		2.62
55	435702 422959		Hs.349256	Hs 349256; paired immunoglobulin-like rec	2.62
75	419938		Hs.1279	NM_001733:Homo sapiens complement compon	2.62 2.61
	450954	A1904740	Hs.25691	NM_005856:Homo sapiens receptor (calcilo	2.61
	421753	BE314828	Hs.107911		2.61
60	443577		Hs.177170 Hs.20247	Hs 20247:FSTs	2.61
UU	453886 421883		Hs.1437	NM 000152:Homo sapiens glucosidase, alph	2.60
	440457			Hs.21321:granule cell differentiation pr	2.60 2.59
	41029	5 AA741357		4 Hs.356624:ESTs	2.59
65	420679		Hs.99853		2.59
65	45155 44467		39 Hs.26630 Hs.11669		2.59
	40866		Hs.78146	Hs.78146:platelet/endothelial cell adhes	2.59
	42619		Hs.2001	Hs 2001 thromboxane A synthase 1 (platel	2.59 2.59
	42181		Hs.10862		2.59
70			Hs.89695		2.59
	42909 41444			NM 002609:Homo sapiens platelet-derived	2.59
	42848		2 Hs.18460	)1 NM_003486:Homo sapiens solute carrier ta	2.59
	45330		Hs.32949	NM 005218:Homo sapiens defensin, beta 1	2.59 2.58
75	41286	57 AU07686	1 Hs.7463	7 NM_003217:Homo sapiens testis enhanced g	2.58
	43282		Hs.3109		2.58
	41266 4121			9 Hs.73239;hypothetical protein FLJ10901	2.58
	4528		Hs.2680		2.58
80	4351	29 AI38165	Hs.2670	86 Hs.267085:ESTs	2.57 2.57
	4244	82 BE26862			2.56
	4104		Hs.6401 2 Hs.3628	in the same and th	2.56
	4338	95 Al28791	. ns020	1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -	

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					2.56
	442566 417640	R37337 D30857	Hs.12111 Hs.82353	Hs.12111:ESTs NM_006404:Homo sapiens protein C recepto	2.56 2.56
	442622	NM_000435	Hs.8546	NM_000435:Homo sapiens Notch homolog 3 (	2.56
-	430346	AK000331	Hs.297641	Hs.297641:retinoblastoma-associated fact	2.55 2.55
5	419344 426500	U94905 NM_014638	Hs.277445 Hs.170156	Hs.277445:diacytgtycerol kise, zeta (104 NM_014638:Homo saptens KIAA0450 gene pro	2.55
	408048	NM_007203	Hs.42322	NM_007203:Homo sapiens A kise (PRKA) and	2.55
	450700	AW732799	Hs.25348	NM_005860:Homo sapiens follistatin-like	2.54
10	417018	M16038 R24922	Hs.80887 Hs.90078	HM_002350:Homo sapiens v-yes-1 Yemaguchi Hs.90078:nucleotide-sugar transporter si	2.54 2.54
10	419378 422451	AA310753	Hs.42491	Hs.42491:ESTs, Moderately similar to hyp	2.53
	435906	AI686379	Hs.110796	Hs.110796:SAR1 protein	2.53
	400231	411004503	11- 007704	Aug portocal lama antique didence of (AROW)	2.53 2.53
15	417849 427380	AW291587 NM_005534	Hs.82733 Hs.177559	NM_007361:Homo sapiens nidogen 2 (NID2), NM_005534:Homo sapiens interferon gamma	2.52
13	428385	AF112213	Hs.184062	Hs.184062:chromosome 20 open reading fra	2.52
	438000	AI825880	Hs.5985	Hs.5985:non-kise Cdc42 effector protein	2.52
	448719	AA033627	Hs.21858 Hs.7907	Hs.21858:serine (or cysteine) proteise i Hs.7907:L-fucose kise	2.52 2.52
20	422396 420787	W21872 AA564248	Hs.351292	Hs.351292:Homo sapiens cD FLJ32605 fis,	2.51
20	430590	AW383947	Hs.246381	NM_001251:Homo sapiens CD68 antigen (CD6	2.51
	447026	BE313144	Hs.324844	Hs.324844:hypothetical protein IMAGE3455	2.51 2.50
	439223 435151	AW238299 AA348482	Hs.250618 Hs.4788	Hs.250618:UL16 binding protein 2 Hs.4788:nicestrin	2.50
25	448202	AB002292	Hs.20695	NM_014629:Homo sapiens Rho guanine nucle	2.50
	449943	AF104266	Hs.24212	Hs.24212:tatrophilin	2.50
	425743	BE396495	Hs.159428 Hs.288316	Hs.159428:BCL2-associated X protein Hs.288316:chromosome 6 open reading fram	2.50 2.50
	444681 421643	AJ243937 BE281170	Hs.106357	NM_007126:Homo sapiens valosin-containin	2.50
30	426865	D63476	Hs.172813	NM_003899:Homo sapiens Rho guanine nucle	2.50
	432306	Y18207	Hs.303090	NM_005398:Homo sapiens protein phosphata	2.49 2.49
	421846 421905	AA017707 A\$660247	Hs.1432 Hs.32699	NM_002743:Homo sapiens protein kise C su Hs.32699:Homo sapiens, Similar to RIKEN	2.49
	419493	AF001212	Hs.90744	NM_002815:Homo sapiens proteasome (proso	2.49
35	422530	AW972300	Hs.118110	NM_004335:Homo sapiens bone marrow strom	2.48
	442821	BE391929	Hs.8752 Hs.80464	NM_014255:Homo sapiens transmembrane pro	2.48 2.48
	416919 443105	T97839 X96753	Hs.9004	NM_006402:Homo sapiens hepatitis B virus NM_001897:Homo sapiens chondroitin sulfa	2.48
	430040	AW503115	Hs.227823	NM_014287:Homo sapiens pM5 protein (PM5)	2.48
40	428028	U52112	Hs.182018	NM_001569:Homo sapiens interleukin-1 rec	2.47 2.46
	424307	AW293399 R28982	Hs.356377 Hs.18106	Hs.356377:Homo sapiens, clone IMAGE:3633 Hs.18106:ESTs, Wealdy similar to T06291	2.46
	434511 454390	AB020713	Hs.56986	Hs.56966:KIAA0906 protein	2.46
4.5	417785	X59812	Hs.82568	NM_000784:Homo sapiens cytochrome P450,	2.46
45	424673	AA345051	Hs.294092	Hs. 294092: Homo sapiens mR full length in	2.46 2.46
	422003 432126	AA361760 AA865239	Hs.296326 Hs.37196	Hs.296326:ESTs, Weakly similar to A33533 Hs.37196:putative G protein coupled rece	2.46
	445937	AI452943	Hs.321231	NM_003779:Homo sapiens UDP-Gal:betaGlcc	2.46
60	409354	N68188	Hs.159472	Hs.159472:Homo sapiens cD: FLJ22224 fis,	2.46 2.46
50	401179 418151	AA964239 ~	omp Hs.83583	NM_005731:Homo sapiens actin related pro	2.45
	422648	D86983	Hs.118893	Hs.118893:Melanoma associated gene	2.45
	427759	BE245578	Hs.2200	NM_005041:Homo sapiens perforin 1 (prefo	2.45
55	431222	X56777	Hs.273790	NM_007155:Homo sapiens zo pellucida glyc Hs.317596:Homo sapiens cD FLJ12927 fis,	2.45 2.45
23	411529 426825	AA430348 AL133415	Hs.317596 Hs.297753		2.45
	422242	AJ251760	Hs.273385		2.45
	408105	AW152207	Hs.270977	Hs.270977:ESTs	2.44 2.44
60	426410 421064	BE298446 Al245432	Hs.305890 Hs.101382	Hs.305890:BCL2-like 1 NM_006291:Homo sapiens tumor necrosis fa	2.44
00	428157	AI738719	Hs.198427	NM_000189:Homo sapiens hexokise 2 (HK2),	2.44
	424398	BE397787	Hs.146393		2.44 2.44
	424825 426031	AF207069 AA295251	Hs.153357 Hs.166066		2.43
65	420031	BE295464	Hs.56607	Hs.56607:Williams-Beuren syndrome chromo	2.43
	429359	W00482	Hs.2399	NM_004995:Homo sapiens matrix metaflopro	2.43
	426761	AI015709	Hs.172089 Hs.199263		2.43 2.43
	429332 425923	AF030403 NM_005026			2.43
70	432211	BE274530	Hs.273333		2.43
	433339	AF019226	Hs.8036	Hs.8036:RAB3D, member RAS oncogene famil	2.42 2.42
	420539 413243	AA282735 AA769266	Hs.44004 Hs.193657	Hs.44004:AD031 protein ' Hs.193657:ESTs	2.42
	413243	AF167706	Hs.19280	Hs.19280:cysteine-rich motor neuron 1	2.42
75	422374	AW732869	Hs. 1519	Hs.1519:protein kise, cAMP-dependent, re	2.42
	444501	AW247624		NM_004148:Homo sapiens ninjurin 1 (NINJ1	2.42 2.42
	414919 419355	AW087337 AA428520	Hs.19446' Hs.90061	Hs.194461:ESTs NM_006667:Homo sapiens progesterone rece	2.42
	436042	AF284422	Hs.11917	Hs.119178:cation-chloride cotransporter-	2.42
80	418245		Hs.83883		2.42 2.41
	444215 408683		Hs.10669 Hs.46847		2.41
	423701		Hs.14302		2.41

			7004 1	ds.7961:Homo sapiens clone 25012 mR sequ	2.41
			Hs.7961   Hs.182366	NM_016292:Homo sapiens heat shock protei	2.41
	428072 434599		Hs.3989 1	Hs.3989;plexin B2	2.40
			He 9261	Hs 8261:SPRY domain-containing SOCS box	2.40 2.40
5	407894		Hs.41143	Hs.41143:phospholipase C, beta 1 (phosph	2.40
	453449	W16752		Hs.32981:sema domain, immunoglobulin dom Hs.152925:KIAA1268 protein	2.40
	408688	AI634522 AW372922		Hs.116774:integrin, alpha 1	2.39
	422448 416269	AA177138	Hs 161671	Hs.161671:ESTs	2.39
10	452679	Z42387	Nº 83883	Ne 83883 transmembrane, prostate androge	2.38 2.38
••	432981	NM_002733	Hs.3136	NM_002733:Homo sapiens protein kise, AMP	2.38
	419846	NM_015977		Hs.285681:Williams Beuren syndrome chrom Hs.111779:secreted protein, acidic, cyst	2.38
	422110 413092	Al376736 AA126856	Hs.111779 Hs.118665	Hs 118665:ESTs	2.38
15	433969	AW207279	Hs.271786	Hs. 271786:ESTs. Weakly similar to PC4395	2.37
1.5	451267	AI033894	Hs.117865	Hs 117865:solute carrier family 17 (anic	2.37 2.37
	447526	AL048753	Hs.303649	NM_002982:Homo sapiens small inducible c Hs.348710:Homo sapiens, clone IMAGE:4242	2.37
	441623	AA315805	Hs.348710 Hs.1298	NM_007289:Homo sapiens membrane metallo-	2.37
20	420255 409274	NM_007289 NM_003930	Hs.52644	NM_003930:Homo sapiens are family associ	2.36
20	422801	AF125672	Hs.287994	Hs 287994:nuclear receptor co-repressor	2.36
	407887	AA579668	Hs.41072	Hs.41072:serine (or cysteine) proteise i	2.36 2.36
	408212	AA297567	Hs.43728	NM_015696:Homo sapiens weakly similar to	2.36
25	430478	NM_014349	Hs.241535	NM_014349:Homo sapiens apolipoprotein L,	2.35
25	405102 423583	AL122055	Hs.129836	Hs.129836:KIAA1028 protein	2.35
	425365	X87241	Hs.166994	NM 005245:Homo sapiens FAT tumor suppres	2.35 2.35
	425204	NM_002436	Hs.1861	NM_002436:Homo sapiens membrane protein,	2.35 2.35
••	420676	AI434780	Hs.4248	Hs.4248:Homo sapiens PP3781 mR, complete Hs.101695:NCK adaptor protein 2	2.35
30	421079	AW404994	Hs.101695 Hs.58014	Hs.58014:G protein-coupled receptor, fam	2.34
	410039	AF207989 BE391579	Hs.75087	NM 006712:Homo sapiens FAST kise (FASTK)	2.34
	412958 430363	M28713	Hs.274464	NM 000398 Homo sapiens diaphorase (DH) (	2.34 2.34
	425397	J04088	Hs.156346	NM_001067:Homo sapiens topoisomerase (D)	2.34
35	451035	AU076785	Hs.430	NM_002670; Homo sapiens plastin 1 (I isof Hs.22880; dipeptidy/peptidase III	2.34
	449027	AJ271216	Hs.22880 Hs.202955	Hs.202955:hypothetical protein FLJ20507	2.34
	429457 417709	BE243065 D87434	Hs.82426	NM_014734:Homo sapiens KIAA0247 gene pro	2.34
	412805	AW954569	Hs.278675	Hs 278675:bromodomain-containing 4	2.34 2.34
40	427647	W19744	Hs.180059	Hs.180059:Homo sapiens cD FLJ31360 fis,	2.33
	430702	U56979	Hs.278568		2.33
	456804	AI421645	Hs.139851 Hs.28329	Hs.28329:protein phosphatase 1, regulato	2.33
	453648 450812	W21493 AB002360	Hs.25515	Hs.25515:MCF.2 cell line derived transfo	2.33
45 .	402575	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,			2.33 2.32
	424670	W61215	Hs.116651	NM_005797:Homo sapiens epitheliał V-like	2.32
	452960	AK001335	Hs.31137	NM_006504:Homo sapiens protein tyrosine NM_004871:Homo sapiens golgi SP receptor	2.32
	442968	AK000606 BE269047	Hs.8868 Hs.65234	Hs 65234:DEAD/H (Asp-Glu-Ala-Asp/His) bo	2.32
50	410639 415169	W42913	Hs.78089	NM 004231:Homo sapiens ATPase, H+ transp	2.32
50	450160		Hs.18373	Hs.183738:FERM, RhoGEF (ARHGEF) and plec	2.32 2.32
	407223			H96850:yw03b12.s1 Soares melanocyte 2NbH NM_001114:Homo sapiens adenylate cyclase	2.32
	426780		Hs.17219 Hs.37167		2.32
55	434987 416354			NM 000633 Homo sapiens B-cell CLL/lympho	2.31
33	453107			6 NM_016113:Homo sapiens transient recepto	2.31 2.31
	422963	M79141	Hs.13234	Hs. 13234:ESTs, Weakly similar to hypothe	2.31
	433618		Hs.34549	Hs.345494:ESTs, Moderately similar to ZN AA811347:ob81h06.s1 NCI_CGAP_GC81 Homo s	2.31
60	438584		Hs.35661	A He 356618:ESTs. Wealdy similar to PC4259	2.31
00	446126 408716		Hs.15171	4 Hs.151714:peroxisomal proliferator-activ	2.30
	433230		Hs.22027	7 Hs.220277:ESTs, Wealthy similar to expres	2.30 2.30
	41016	8 AW834050			2.30
65	44634				2.30
65	41845 45317			NM 006834:Homo saciens RAB32, member RAS	2.29
	40901			5 Hs.49725:DKFZP434I216 protein	2.29
	45284	8 Al417193	Hs.2889		2.29 2.29
70	41883				2.28
70				no Ne 287402 chondroitin 4-sulfotransferase	2.28
	43282 41294			51 NM 006148:Homo sapiens LIM and SH3 prote	2.28
	42606	8 AF02977	8 Hs.1661	54 NM_002226:Homo sapiens jagged 2 (JAG2),	2.28 2.28
	45691	9 NM_0039	000 Hs.1822		2.28
75					2.28
	45398 40773		Hs.1645 Hs.3493	126 Hs 349326:Homo sapiens cD FLJ30677 fis.	2.28
	4132			274 Hs. 109274:hypothetical protein MGC4365	2.28
	4220	51 AW3275	46 Hs.1110	124 Hs. 111024:solute carrier family 25 (mito	2.27 2.27
80					2.27
	4362 4540			NM 000147:Homo sapiens fucosidase, alpha	2.27
	4265				2.27
				420	

	417115	AW952792	Hs.334612	NM_003094:Homo sapiens small nuclear rib	2.27 2.26
	402901 412898	Al129903	Hs.74669	NM_006634:Homo sapiens vesicle-associate	2.26
_	413020	R98736		R98736:yr31h09.r1 Soares fetal liver spl	2.26
5	413939	AL047051	Hs.199961	Hs. 199961:ESTs, Wealdy similar to hypoth	2.26 2.25
	408681 412330	AW953853 NM_005100	Hs.281462 Hs.788	Hs.281462:hypothetical protein FLJ14251 NM_005100:Homo sapiens A kise (PRKA) and	2.25
	442083	R50192	Hs.165062	Hs.165062:EST8	2.25
	418271	NM_000919	Hs.83920	NM_000919:Homo sapiens peptidylglycine a	2.25
10	433376	AI249361	Hs.74122	NM_001225:Homo sapiens caspase 4, apopto	2.25
	438562 443883	AI566826 AA114212	Hs.25890 Hs.9930	Hs.25890:ESTs, Weakly similar to transdu NM_001235:Homo sapiens serine (or cystei	2.25 2.25
	416976	BE243985	Hs.80680	Hs. 60680:major vault protein	2.24
	416914	AA344481	Hs.80426	Hs.80426:brain and reproductive organ-ex	2.24
15	400288	X06256	Hs.149609	NM_002205:Homo sapiens integrin, alpha 5	2.24 2.24
	407904 429690	W44735 AW956329	Hs.107260 Hs.23721	Hs.107260:putative UDP-Galc:polypeptide Hs.23721:ESTs	2.24
	443813	AA876372	Hs.93961	Hs.93961:Homo sapiens mR; cD DKFZp667D09	2.24
•	427458	8E208364	Hs.29283	Hs.29283:ESTs, Weakly similar to LKHU pr	2.24
20	454294	AB000734	Hs.50640	NM_003745:Homo sapiens JAK binding prote	2.24 2.23
	407192 425751	AA609200 T19239	Hs.366318 Hs.1940	Hs.366318:ESTs NM_001885:Homo sapiens crystatīm, alpha	2.23
	456437	AI924228	Hs.115185	Hs.115185:ESTs	2.23
0.5	413019	BE281604	Hs.75140	NM_002337:Homo sapiens low density lipop	2.23
25	418862	BE550964	Hs.89399	Hs.89399:ATP synthase, H+ transporting,	2.23 2.23
	435284 429630	AA879470 M85289	Hs.96849 Hs.211573	Hs.96849:Homo sapiens cD FLJ11492 fis, c NM_005529:Homo sapiens heparan suffate p	2.23
	427609	AK000436	Hs.179791	Hs.179791:RAB20, member RAS oncogene fam	2.23
20	421917	AB028943	Hs.109445	Hs. 109445:hypermethylated in cancer 2	2.23
30	445616	R65964	Hs.334873	Hs.334873:carboxypeptidase M	2.23 2.23
	407232 423798	X04526 AF047033	Hs.132904	X04526:Human liver mR for beta-subunit s Hs. 132904:solute carrier family 4, sodiu	2.23
	446755	AW451473	Hs.16134	NM_005990:Homo sapiens serine/threonine	2.22
	452865	A1924046	Hs.119567	Hs.119567:ESTs, Wealtly similar to ALU1_H	2.22
35	431393	AW971493	Hs.134269	Hs.134269:ESTs, Weakly similar to 200439	2.22 2.22
	431890 428782	X17033 X12830	Hs.271986 Hs.193400	NM_002203:Homo sapiens integrin, atpha 2 NM_000565:Homo sapiens interteukin 6 rec	2.22
	446006	NM_004403	Hs.13530	NM_004403:Homo sapiens deafness, autosom	2.22
40	436418	AJ245874	Hs.4245	Hs.4245:chromosome 11 hypothetical prote	2.22
40	423869	BE409301	Hs.134012	NM_006688:Homo sapiens C1q-related facto	2.21 2.21
	437730 444020	AW071087 R92962	Hs.239176 Hs.35052	Hs.239176:insufin-like growth factor 1 r Hs.35052:ESTs	2.21
	413882	AA132973	Hs.184492	Hs.184492:Homo sapiens mR; cD DKFZp667B0	2.21
	412654	AI093480	Hs.374319	Hs.374319:ESTs	2.21
45	448988	Y09763	Hs.22785	NM_004961:Homo sapiens gamma-aminobutyri	2.21 2.21
	426841 408196	A1052358 AL034548	Hs.131741 Hs.43627	Hs.131741:ESTs NM_005943:Homo sapiens SRY (sex determin	2.21
	451711	AK000461	Hs.26890	Hs.26890:cat eye syndrome chromosome reg	2.20
	414325	AA251929	Hs.355341	Hs.355341:Homo sapiens, clone IMAGE:3536	2.20
50	424512	X53002	Hs.149846	NM_002213:Homo sapiens integrin, beta 5	2.20 2.20
	448883 411296	BE614989 BE207307	Hs.7503 Hs.10114	Hs.7503:hypothetical protein FLJ14153 Hs.10114:growth suppressor 1	2.20
	452268	NM_003512	Hs.28777	NM_003512:Horno sapiens H2A histone famil	2.20
	416810	AF035606	Hs.80019	NM_013232:Homo sapiens programmed cell d	2.20
55	441415	H21497	Hs.7471	Hs.7471:BBP-like protein 1	2.20 2.19
	444212 428044	AW503976 AA093322	Hs.10649 Hs.301404	NM_004848:Homo sapiens basement membrane NM_006743:Homo sapiens R binding motif p	2.19
	430017	AA263172	Hs.35	NM_002832:Homo sapiens protein tyrosine	2.19
<i>c</i> 0	424490	AJ278016	Hs.55565	Hs.55565:ankyrin repeat domain 3	2.19
60	431193	AW749505	Hs.296770		2.19 2.19
	453686 448262	AL110326 AW880830	Hs.304679 Hs.186273	Hs.304679:ESTs, Weakly similar to Z195_H Hs.186273:ESTs	2.19
	416065	BE267931	Hs.78996	NM_002592:Homo sapiens proliferating cel	2.19
	442045	C05768	Hs.8078	Hs.8078:Homo sapiens clone FBD3 Cri-du-c	2.19
65	423804	AW403448	Hs.1706	NM_006084:Homo sapiens interferon-stimul Hs,2236:NIMA (never in mitosis gene a)-r	2.19 2.19
	428024 424503	Z29067 NM_002205	Hs.2236 Hs.149609		2.19
	437696	Z83844	Hs.5790	Hs.5790:hypothetical protein dJ37E16.5	2.18
70	405204				2.18
70	426158	NM_001982			2.18 2.18
	417418 412773	NM_002468 H15785	Hs.82116 Hs.74573	NM_002468:Homo sapiens myeloid different NM_012268:Homo sapiens similar to vaccin	218
	409402	AF208234	Hs.695	NM_000100:Homo sapiens cystatin B (stefi	2.18
	443791	N64458	Hs.143345		2.18
75	435049	AL122067	Hs.4746	Hs.4746:hypothetical protein FLJ21324	2.18 2.18
	418389 450712	AA830613 AI732130	Hs.293849 Hs.270496	* * * * * * * * * * * * * * * * * * *	2.18
	422007	A1739435	Hs.39168	Hs.39168:ESTs, Wealdy similar to T17340	2.18
90	453676	AW853745	Hs.286035		2.18
80	415718 452688	F30631 AA721140	Hs.200237 Hs.49930		2.18 2.18
	415988		Hs.78943		2.18
	409453		Hs.95612		2.17

					earse us a series at recombin (tra	2.17
			Hs.82226	NM_0	02510:Homo sapiens glycoprotein (tra 00628:Homo sapiens interleukin 10 re	2.17
			Hs.173936	NM_U	06931:Homo sapiens solute carrier fa	2.17
	440983	,	Hs.7594 Hs.79006	NM C	12145:Homo saniens deoxythymidylate	2.17
5	416084 429642		Hs.211579	NM (	106500:Homo sapiens melanoma adhesion	2.17
,	427213		Hs.348389	Hs.34	8389:hypothetical protein FLJ12876	2.17 2.17
	437763		Hs.5831	NM (	03254:Homo sapiens tissue inhibitor	2.17
	454000	AA040620	Hs.5672	Hs.56	72:golgi membrane protein S8140	2.16
	424247	X14008	Hs.234734	NM_	000239:Homo sapiens lysozyme (ret army	2.16
10	403857		44 077477	140.3	77477:major histocompatibility compl	2.16
	406648	AA563730	Hs.277477	ns.z	1747 Fallague (Illauxonispossinis)	2.16
	400265	MI 004513	Hs.8265	NM	004613:Homo sapiens transglutamise 2	2.16
	442379	NM_004613 AB028981	Hs.8021	He R	N21-KIAA1058 omtein	2.16
15	441892 417446	AL118671	Hs.82163	NM_	000898:Homo sapiens monoamine oxidase	2.16 2.16
13	418386	AA361739	Hs.84549	NM	002494:Homo sapiens DH dehydrogese (U	2.16
	414053	BE391635	Hs.75725	NM_	003564:Homo sapiens transgelin 2 (TAG	2.16
	440906	AW161556	Hs.240170	Hs.2	40170:hypothetical protein MGC2731 63667:ESTs, Wealdy similar to CA1H_H	2.16
	447660	AW160386	Hs.163667			2.16
20	408279	AF216965	Hs.44095	Hs.	14095:cyclin M3 167246:P450 (cytochrome) oxidoreducta	2.16
	426152	BE299190	Hs.167246 Hs.5944	NM	014585 Homo sapiens solute camer ta	2.16
	437952	D63209 AF057307	Hs.78575	He '	78575-noncannsin (variant Gaucher dis	2.15
	415661 425302	U79115	Hs.155566	NM	_003805:Homo sapiens CASP2 and RIPK1 d	2.15
25	425996	W67330	Hs.374451	He	374451:FSTs	2.15 2.15
23	413745	AW247252	Hs.75514	NM	_000270:Homo sapiens nucleoside phosph	2.15
	422070	AF149785	Hs.111126	Hs.	111126:pituitary tumor-transforming 1	2.15
	448424	AW009892	Hs.31924	Hs.	31924:ESTs	2.15
	430035	NM_003463	Hs.227777	NM	L_003463:Homo sapiens protein tyrosine 129673:eukaryotic translation initial	2.15
30	438407	AI457122	Hs.129673	HS.	5470:interleukin 17B receptor	2.15
	435551	AF212365	Hs.5470 Hs.5809	FIS Lie	5809:putative transmembrane protein;	2.15
	437741	BE561610 AA526626	Hs.7736	NA NA	1_016504:Homo sapiens mitochondrial rib	2.15
	441192 435750	AB029012	Hs.4990	He	A990-KIAA1089 protein	2.15
35	433730	NM_000169		NA	A 000169:Homo sapiens galactosidase, al	2.14 2.14
33	425252	AW391162	Hs.349306	2 140	249306-bycothetical protein FLJ31951	2.14
	427600	AW630918	Hs.179774	t Ni	A_002818:Homo sapiens proteasome (proso	2.14
	426818	AA554827	Hs.292996	ō H≾	292996:postmeiotic segregation increa M_001023:Homo sapiens ribosomal protein	2.14
	442110	AF113008	Hs.8102		M_001023:Homo sapieris ribustimai protes- s.39850:uridine kise-like 1	2.14
40	407797	AK000524	Hs.39850	ITK N	M_014298:Homo sapiens quinolite phospho	2.14
	443044	N28522	Hs.8935 Hs.15294	nΗ	s 152940:ESTs	2.14
	437103	AW139408 AW664144	Hs.29700	7 H	e 297007-Homo saniens cD FLJ32174 fis,	2.14
	442069 424954		<b></b>	N	M. OOOSAS-Homo saciens turnor protein 053	2.14 2.14
45	458097			ı M	s 58104 Homo saniens, clone IMAGE:4/309	2.14 2.14
10	411925				M_003475:Homo sapiens chromosome 11 ope	2.14
	449644			24 H	ls.148324:ESTs	2.14
	422675		Hs.11914	to i	IM_001970:Homo sapiens eukaryotic transl ts.2299:CD8 antigen, beta polypeptide 1	2.14
	428586	M36712	Hs.2299	1 1 on	IM_014840:Homo sapiens KIAA0537 gene pro	2.13
50	429379		0 Hs.20059 Hs.3228	30 F 44 I	ts.322844:hypothetical protein DKFZp564A	2.13
	410290 443895			66 H	ts 292566:YEA4 protein	2.13
	42814			26 1	VM 012264:Homo sapiens chromosome 22 ope	2.13 2.13
	45351			a i	Hs. 27268: Homo sapiens cD: FLJ21933 fis,	2.13
55	45653		Hs.1006		Hs.100623:protein phosphatase 1, regulat	213
	41997				Hs.182982:golgin-67	2.13
	42495				Hs.156974:ESTs NM_002659:Homo sapiens plasminogen activ	2.13
	42755			137 170	NM_001066:Horno sapiens turnor necrosis fa	2.13
60	43144		Hs.2562 1 Hs.1720	112	He 172012 hypothetical protein DKFZP434J	2.13
UU	41875 43420	_		4	NM_000858:Homo sapiens guanylate kise 1	2.13
	43323			ROA.	He 301804-KIAA1494 protein	2.12 2.12
	45270			940	Hs.288940:transmembrane protein 8 (five	2.12
	43803		Hs.605	9	NM_016938:Homo sapiens EGF-containing fi	2.12
65	40084	47	<b></b>		NM_007229:Homo sapiens protein kise C an	2.12
	4475				NM_007229:Homo sapiens biliverdin reduct	2.12
	4170				NM 001166:Homo sapiens baculoviral IAP (	2.11
	4132				Hs.39168:ESTs, Weakly similar to T17340	2.11
70	4345 ) 4040		02 113.031	•		2.11
/(	4108		9 Hs.664	193	Hs.66493:Down syndrome critical region g	211 2.11
	4186		29 Hs.865	575	Hs.86575:mitogen-activated protein kise	2.11
	4470	187 AW4038	70 Hs.30		Hs.301872:hypothetical protein MGC4840	2.11
_	4330				NM_016127:Homo sapiens hypothetical prot NM_007112:Homo sapiens thrombospondin 3	2.11
7:			Hs.16		NM_002752:Homo sapiens mitogen-activated	2.11
	4424				Hs.23765:membrane metallo-endopeptidase-	211
	4373		/J N3.23	.03		2.11
	400 455		061 Hs.35	6580	Hs.356580:ESTs, Weakly similar to zinc f	2.11
8	0 417				He 63064 ferritin heavy polypeptide 1	2.10
0		728 AB0245	97 Hs.79	658	NM_001894:Homo sapiens casein kise 1, ep	2.10 2.10
		920 H05430	Hs.28	38433	Hs. 288433:neurotrimin	2.10
		309 U79745	Hs.11	14924	NM_004694:Homo sapiens solute carrier fa	
					Λ	21

	436114 405517	AA778232	Hs.19515	Hs.19515:ESTs, Highly similar to NRG3_HU	2.10 2.10
	421872	AA359753	Hs.22824	Hs.22824:MYB binding protein (P160) 1a	2.10
	437712	X04588	Hs.85844	Hs.85844:neurotrophic tyrosine kise, rec	2.10
5	431214	AA294921	Hs.348024	NM_002881:Homo sapiens v-ral simian leuk	2.10
	412856	BE386745	Hs.74631	NM_001728:Homo sapiens basigin (BSG), mR	2.10
	442064	AI422867	Hs.88594	Hs.88594:Horno sapiens, clone IMAGE:43329 Hs.325321:WD repeat domain 18	2.10 2.10
	434845 426728	BE267057 NM_007118	Hs.325321 Hs.367689	NM_007118:Homo sapiens tripte functiol d	2.10
10	419596	BE379320	Hs.91448	NM_007026:Homo sapiens dual specificity	2.09
	448913	AA194422	Hs.22564	NM_004999:Homo sapiens myosin VI (MYO6),	2.09
	414721	X90392	Hs.77091	NM_006730:Homo sapiens deoxyribonuclease	2.09
	424658	NM_002406	Hs.151513	NM_002406:Homo sapiens mannosyl (alpha-1	2.09 2.09
15	432805 447032	X94630 AK000310	Hs.3107 Hs.17138	Hs.3107:CD97 antigen Hs.17138:hypothetical protein FLJ20303	2.09
13	447484	AA464839	Hs.292566	Hs.292566:YEA4 protein	2.09
	440188	AK001812	Hs.7036	Hs.7036:N-acetylglucosamine kise	2.09
	445584	AF217518	Hs.8360	Hs.8360:PTD012 protein	2.09
20	402559		11- 00044	11- 02244-AVIte-America bina	2.09 2.09
20	418043 448888	AW377752 AW196663	Hs.83341 Hs.200242	Hs.83341:AXL receptor tyrosine kise Hs.200242:caspase recruitment domain fam	2.09
	436910	AA926944	Hs.261587	Hs.261587:GCN2 elF2alpha kise	2.09
	422573	AW297985	Hs.295726	Hs.295726:integrin, alpha V (vitronectin	2.08
	416448	L13210	Hs.79339	NM_005567:Homo sapiens lectin, galactosi	2.08
25	428727	AF078847	Hs.191356	NM_001515:Homo sapiens general transcrip	2.08 2.08
	410301	AW502935	Hs.740 Hs.104679	Hs.740:PTK2 protein tyrosine kise 2 Hs.104679:Homo sapiens, clone MGC:18216	2.08
	449538 421205	AI559444 AL137540	Hs.102541	Hs.102541:netrin 4	2.08
	411779	AA292811	Hs.72050	NM_003551:Homo sapiens non-metastatic ce	2.08
30	427704	AW971063	Hs.292882	Hs. 292882:EST8	2.07
	413518	BE149455	Hs.75415	NM_004048:Homo sapiens beta-2-microglobu	2.07
	447345	BE247767	Hs.18166	Hs.18166:KIAA0870 protein Hs.332329:EST	2.07 2.07
	407143 448431	C14076 BE613061	Hs.332329 Hs.337772	Hs.337772:hypothetical protein BC009331	2.07
35	412760	AW379030	Hs.41324	Hs.41324:ESTs	2.07
-	446859	AJ494299	Hs.16297	NM_005694:Homo sapiens COX17 homolog, cy	2.07
	403966				2.07
	409115	A1223335	Hs.50651	NM_002227:Homo sapiens Janus kise 1 (a p	2.07 2.07
40	436823 414045	AW749865 NM_002951	Hs.117077 Hs.75722	Hs.117077:zinc finger protein 264 NM_002951:Homo sapiens ribophorin II (RP	2.06
40	413980	NM 002437	Hs.75659	NM_002437:Homo sapiens MpV17 transgene,	2.06
	439414	NM_001183	Hs.6551	NM_001183:Homo sapiens ATPase, H+ transp	2.06
	426059	BE292842	Hs.166120	NM_001572:Homo sapiens interferon regula	2.06
45	429849	U33053	Hs.2499	NM_002741;Homo sapiens protein kise C-li	2.06 2.06
43	402424 406626	X04526	Hs.215595	Hs.215595:guanine nucleotide binding pro	2.06
	458911	AA373131	Hs.24322	Hs.24322:ATPase, H+ transporting, lysoso	2.05
	426086	T94907	Hs.188572	Hs.188572:ESTs	2.05
60	419726	U50330	Hs.1274	NM_006129:Homo sapiens bone morphogeneti	2.05 2.05
50	452344	A1264357	Hs.55405	Hs.55405:hypothetical protein MGC16212 NM_002612:Homo sapiens pyruvate dehydrog	2.05
	442498 422114	U54617 AW194851	Hs.8364 Hs.111801	NM_015908:Homo sapiens arseta resistance	2.05
	413420	AW410235	Hs.75348	NM_006263:Homo sapiens proteasome (proso	2.05
	409430	R21945	Hs.346735		2.05
55	409932	AI376750	Hs.57600	Hs.57600:adaptor-related protein complex	2.05 2.04
	434848	BE256304 AW961818	Hs.32148 Hs.374424	Hs.32148:AD-015 protein Hs.374424:ESTs	2.04
	453852 427637	AK000816	Hs.179986		2.04
	400264				2.04
60	430016	NM_004736		NM_004736:Homo sapiens xenotropic and po	2.04 2.04
	410134	U68140	Hs.58927	Hs.58927:nuclear VCP-like Hs.7579:importin 9	2.04
	440975 432280	AW499914 BE440142	Hs.7579 Hs.2943	NM_003135:Homo sapiens sigl recognition	2.04
	409504	AA304961	Hs.699	NM 000942-Homo sapiens peptidylprotyl is	2.04
65	412146	M92444	Hs.73722	NM_001641:Homo sapiens APEX nuclease (mu	2.04
	434203	BE262677	Hs.283558		2.04
	422754	AA316476	Hs.171811		2.04 2.04
	406729 413086	AA069711 AA126841	Hs. 183834	AA069711:zm52b11.s1 Stratagene fibroblas Hs.183834:ESTs	2.03
70	424340	AA339036	Hs.7033	Hs.7033:ESTs	2.03
. •	450440	AB024334	Hs.25001	NM_012479:Homo sapiens tyrosine 3-monoox	2.03
	424662	NM_002870			2.03
	415740	N80486	Hs.39911 Hs.74564	Hs.39911:Homo sapiens mR for FLJ00089 pr NM_003145:Homo sapiens sigl sequence rec	2.03 2.03
75	412749 408393	AA378417 AW015318	Hs.23165	Hs.23165:ESTs	203
, ,	421295	AW081061	Hs.103180	Hs.103180:DC2 protein	2.03
	445417	AK001058	Hs.12680	Hs.12680:Homo sapiens cD FLJ10196 fis, c	2.03
	414883	AA926960	Hs.348669		2.03 2.02
80	447298		Hs.239818 Hs.176069		2.02
30	459580 422785		Hs.28908		2.02
	452696	AJ826645	Hs.21153	4 Hs.211534:Homo sapiens cD FLJ31665 fis,	2.02
	452056	AW955065	Hs.10115	0 Hs.101150:KIAA1949 protein	2.02

PCT/US02/29560 WO 03/025138

	450690	AA296696	Hs.333418	NM_014164:Homo sapiens FXYD domain-conta	2.02
	423527	AI206965	Hs.105861	Hs. 105861:engulfment and cell motility 3	2.01 2.01
	429545	AI824164	Hs.356130	Hs.356130:ESTs Hs.199067:v-erb-b2 erythroblastic leukem	2.01
5	439180 437193	AI393742 BE259190	Hs.199067 Hs.289721	Hs 289721 growth arrest-specific 5	2.01
,	436014	AF281134	Hs.283741	Hs.283741:exosome component Rrp45	2.01 2.01
	453329	T97205	Hs.193400	Hs.193400:interleukin 6 receptor T23514:seq3329 1-NIB Homo sapiens cD clo	2.01
	407347	AA829847 AI964074	Hs.225838	Hs 225838:ESTs	2.01
10	435370 430657	AA482910	Hs.370602	Hs 370602-ESTs. Weakly similar to hypoth	2.01 2.01
••	427157	U51166	Hs.173824	NM_003211:Homo sapiens thymine-D glycosy NM_003894:Homo sapiens period homolog 2	2.01
	424833	NM_003894 NM_005402	Hs.153405 Hs.6906	NM_005402:Homo sapiens v-ral simian leuk	2.01
	440086 438543	AA810141	Hs.192182	Hs.192182:ESTs	201 201
15	417426	NM_002291	Hs.82124	NM_002291:Homo sapiens taminin, beta 1 ( NM_014767:Homo sapiens KIAA0275 gene pro	201
	412790	NM_014767 AV655500	Hs.74583 Hs.93961	Hs.93961:Homo sapiens mR; cD DKFZp667D09	2.01
	445892	WAGGGGAW	10.555		
	TABLE 39	B:	-	- 4 t a - 416 - a combon	
20	Pkey:	_ `	jue Eos probe e cluster num	set identifier number ner	
	CAT num! Accession		bank accessi		
	• • • • • • • • • • • • • • • • • • • •		A		
25	Pkey 409745	CAT Number MH1944_5	Accession RI030997	AA921874 AW188822 BI027862 AI347618 AI361453 AI	088754 AW207491 AA077391 BG012775 BG997382 AA286833 AA150722 BI007625 6277 BI007677 BI006266 BI006991 BI006990 BI007763 BI007762 BG997377
23	403743	MU11044_0	04037064	01000100 01006275 RKIIB//U BIUJ 1000 01743007 017	088754 AW207491 AA077391 BISS 12770 BISS 127
			AA150780	BI033518 BI05/818 BC015/65 Bi055601 WOLLD	
	418869	12789_14 276321_1	RG17143	AA230035 BE079601 BE079534 AA299964 BE392717 BE88340	2 BE079532 BE018148 BF889427 W00396.
30	421902 400231	MH494_5	RC01331	AF261085 BC004109 AY007133 BC009001 BC00100	1 TORSE DIRECTOR NAME AND ASSOCIATION ASSO
50		· -	RG92642	BG389312 BG4//333 AlU31/99 BI/03443 BIZOUNDE	20020000 E25525 BINSB182 E34574 F33506 BM471326 F34677
			AW27671	2 AA 187508 F 34866 AA 114243 AA322361 W23333 AA	PERSON DE 100070 DE 2004ES DE 706770 DE 745057 RG 755835 BE 266758
			R1094125	VY13841 RF883081 RC112110 DE123203 DE12101	
35			BE25934	2 BM450181 BG748174 BE299322 BM423307 BM460	379 BM459071 BM450106 BM467584 BM464548 BM465044 BM450176 BF569359
			BM45903	4 BM455329 BM471815 BI862301 BG331736 H04903	AA374894 BE902964
	438584	1241536_1	AW9779	19 AA81 1347 D797 15	
	413020	1485885_1	RE04811	3 R98736 Z42904	E222576 A1191715 A1423108 BF064068 BG057819 A1208589 A1890535 A1262890 1160385 A1335883 BF440017 BG231884 A1343699 A1280745 A1871338 A1123739
40	400265	1145_1	X58141	NM_001119 AI246766 BE643243 AI802409 BE301053 AI884624 /	E222576 A191715 A1423108 BF094080 B207375 13 A2378 A1123739 1160385 A135983 BF440017 BG231884 A1343699 A1280745 A1871338 A1123739 120663 AW571658 BF109839 AW273280 A1888380 A1571860 A1357126 AW194105
			AI87112	AW080375 A1350160 A1300855 A1616556 A10052007	THE DESCRIPTION AND AUGUST DESCRIPTION AND AUGUST A
			A113147	4 AW316548 AW128942 AW5/ 1002 AG00302 ATTO	100000 AA00004 AA000446 D16732 H47612 H45402 AA668719 AA722441
45			A175387	4 BF 593905 BEBS2630 AlGS7570 BE652907 Al083831 F	AI908017 AI378201 AA373410 K1073217676 AL527067 BF313768 AL042441 AL037806 H0630 NM_014190 BM469282 AL524786 AL527067 BF313768 AL042441 AL037806 AL527067 BF313768 AL642441 AL037806 AL527067 BF313768 AL642441 AL037806 AL527067 BF313768 AL642441 AL037806 AL6632431 BG958742 AL232151 AL332588 WKT987 H66049 R92289 H47699 AA380016 AL532433 BG958742 AL232151
43			R119501	3 BE219292 BF055534 195785 BE033037 MV0400327	200 HA2774 H22074 D00095 P75803 HA2172 RF770251 AL529310 F03180
			H26003	R62487 BG766512 BE815124 AW130122 H30101 No.	AND THE LOCAL AIRCE AND THE AND THE REST AND THE AND T
			R92185	58 AAA70463 AA618163 AA601963 W74212 AA02152	3369 AA617840 H14351 AI080422 AI31302 AA08449 AA076114 AA633470 AA581793 ) AA421274 AA903521 AA411402 AA08448 AA983449 AA076114 AA633470 AA581793 ) 3340 AA976536 AA360268 AA976223 T95786 AA527774 AI620298 AA180888
50			AA0190	60 AA814222 AA693469 N99931 N67840 R26834 BF3	) AA417274 AA9U3221 AA411402 A4646444444444444444444444444444444444
-			AA1492	18 AA565201 BI001597 BE076303 AVVIO3737 AVVIO	777
	40020	B 16640_1	X78817	NM 001666 050921 AW002308 AW575450 BF50751	AVADAGE AND
	40020	3 100-10_1	AI9130	55 AW083235 AI078474 AI323022 AV1304020 AV1 123	20 10003 AMPROSES AMPROSOT RESESTAS RG745612 BG979546 AW793245
55			AW769	893 AW407608 AW075982 AIZ48207 AI762309 AI6120	70 A249937 AW003361 AW00037 LI 19 BE714919 BF847786 BG684161 AV695278 BG491029 BE793244 BE830893
			BIU141	121 R09703 Bi013066	ALESSAGE REGISTRES DEGREE REGISTRES ALESSAGE ALESS
	40026	4 1145_1	X5814	NM_001119 AI246786 BE645243 AI685698 AI208590	BE222576 AI191715 AI423108 BF064068 BG057819 AI206589 AI880535 AI262890 AI160385 AI335983 BF440017 BG231884 AI343599 AI280745 AI871338 AI123739 AI306653 AW571658 BF109839 AW273280 AIB88380 AI571860 AI357126 AW194105
		_	A12462	41 BE33338 VISSS848 VIROS403 RE30 1023 VICCHOS.	75 155 155 155 155 155 155 155 155 155 1
60			A1171	74 AW316548 AW128942 AW57 1002 AI303302 ATT	07 T S S S S S S S S S S S S S S S S S S
			A1753	174 RF593905 BE832830 Alb37970 BE634103 DC 4040	21 27 27 27 27 27 27 27 27 27 27 27 27 27
			ΔΔ991	443 T51951 AW514058 AIZ///63 AA42190/ AIV6565	11-10-10 POSSES NATED A A 380016 AL 532433 BG958742 AL292151
65			H2600	13 R62487 BG766512 BE815124 AW 130122 H30101 N	35407 DIOTAGE ALCCCOAD ALCCCOAD ALCCCOAD AA 790797 AA 506995 AAR 27496 AA 534305
05			R921	15 H18680 R43192 AA401390 AA977941 AUG 1344 AA	33470 AA581/93
			AA84	3358 AA470463 AA618163 AA601963 W/4212 AA6213	20 AA4212/4 AA9035/1 AA911422 342340 AA976636 AA360268 AA976223 T95786 AA527774 A1620298 AA180888 342340 AA976572 A1092819 A1291438 AA459586 AA136373 R50213 BE622752 AA401414
70	)		AA18	0973 AA766800 W96432 BI550308 H52236 AM451025	BG420468 BG627542
	4067		AA06	9711 14 A1655785	
	4073	147 810943	_1 1233	, , , , , , , , , , , , , , , , , , ,	
	TAB	LE 39C:			
75	) Pke	r:		ber corresponding to an Eos probeset	Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA 402-489-495
	Ref:		economes a	human chromosome 22 Utilinarii, et al. (1999) <u>Ivature</u>	402:489-495.
	Stra		Indicates D	IA strand from which exons were predicted.	
0.4	Nt :	position:	Indicates no	deolide positions of predicted exons.	
80	<i>)</i> Pke	y Ref	Stra	nd Nt_position	
	404	240 50026	24 Minu	s 116132-116407,116653-116922	
	404	277 18344	58 Min		422
					433

```
113477-113893
                      9438647
          401179
                                     Plus
                                     Minus
                                                   120922-121296
                      8076881
          405102
          402575
                      9884830
                                     Minus
                                                   109742-109883
                                                   175426-175667
                      RR94222
          402901
                                     Minus
 5
                                                   126569-126754
                                     Plus
          405204
                      7230116
                                                   2524-3408
          403857
                      7708910
                                     Minus
          400847
                      9188605
                                                   44643-44835
                                     Plus
                                                   149362-151749
          404030
                      7671252
                                     Plus
                                                   114757-114877
          405517
                      9454624
                                     Phis
10
                      9864273
                                                   33539-33715
          402559
                                     Plus
          403966
                       8568881
                                      Plus
                                                   158193-158277,160116-160290
           402424
                       9796344
                                     Minus
                                                   64925-65073
15
          TABLE 40A: ABOUT 977 GENES UP-REGULATED IN STOMACH CANCER
          Table 40A fists about 977 genes up-regulated in stomach cancer compared to normal adult fissues. These were selected from $9680 probesets on the Affymetrix/Eos Hu03 Gene/Chip array such that the ratio of "average" stomach cancer to "average" normal adult fissues was greater than or equal to 2.0. The "average" stomach cancer level was set to
          the 90th percentile amongst various stomach cancers. The 'everage' normal adult tissue level was set to the 90th percentile amongst various non-malignant tissues. In order to
           remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst various non-malignant tissues was subtracted from both the numerator and
20
           the denominator before the ratio was evaluated.
                               Unique Eos probeset identifier number
           Pkey:
                               Exemplar Accession number, Genbank accession number
           ExAcon:
           UnigenelD:
                               Unigene number
           Unigene Title:
                               Unigene gene title
25
           R1:
                               Ratio of tumor to normal adult tissues
                                      UnigeneID
                                                   Unigene Title
           Pkey
                       ExAcon
           411243
                       AB039886
                                      Hs.69319
                                                   CA11
                                                                                                         30.66
                                                                                                         16.94
           418007
                       M13509
                                      Hs.83169
                                                    matrix metalloproteinase 1 (interstitial
30
                                                                                                         13.51
           444325
                       AW152618
                                      Hs.16757
                                                   ESTs
           445891
                                                                                                         11.92
                       AW391342
                                      Hs.199460
                                                   ESTs
                                      Hs.174759
                                                                                                         11 08
           448811
                       AI590371
                                                    Homo sapiens mRNA; cDNA DKFZp56482062 (1
                                                                                                         10.84
           431723
                       AW058350
                                      Hs.16762
                       NM_001898
                                                   cystatin SN
                                                                                                         10.38
           409757
                                      Hs.123114
35
                                                                                                         9.11
                                                   catheosin E
           421110
                       AJ250717
                                      Hs.1355
                                                    matrix metalloproteinase 3 (stromelysin
                                                                                                         8.66
                       BE440042
                                      Hs.83326
           428368
                                                    Homo sapiens mRNA; cDNA DKFZp564B2062 (f
                       N99013
                                      Hs.16762
                                                                                                         8.50
            446998
                                                                                                         7.11
            406687
                       M31126
                                      Hs.272620
                                                    pregnancy specific beta-1-glycoprotein 9
                                                                                                         6.86
                       AF196478
                                      Hs.188401
                                                    annexin A10
            428651
40
                                                    progastricsin (pepsinogen C)
                                                                                                          6.51
                       M18667
                                      Hs.1867
            425211
                                                    matrix metalloproteinase 12 (macrophage
                                                                                                          6.49
            423673
                       BE003054
                                      Hs.1695
                        U33317
                                      Hs.711
                                                    defensin, alpha 6, Paneth cell-specific
                                                                                                          6.39
            409683
                                                    ESTs, Weakly similar to LITB_HUMAN LITHO
                                                                                                          6.31
                                      Hs.105484
            422260
                       AA315993
                                                    similar to SALL1 (sal (Drosophila)-like
                                                                                                          6.25
                                      Hs.189095
            428664
                        AK001566
 45
                                                                                                          5.72
                        AB033025
                                      Hs.50081
                                                    KIAA1199 protein
            409041
                                      Hs.44532
                                                                                                          5.72
            408380
                        AF123050
                                                    DKFZP434C013 protein
                                                                                                          5.46
                        AA306610
                                       Hs.194676
            428953
            450685
                        L15533
                                       Hs 423
                                                    pancreatitis-associated protein
                        AF154830
                                       Hs.50966
                                                     carbamoyl-phosphate synthetase 1, mitoch
                                                                                                          5.34
            409187
 50
            434206
                        AW136973
                                       Hs.288516
                                                    ESTs, Weakly similar to $69890 mitogen i
                                                                                                          5.16
                        234277
                                       Hs.103707
                                                     apomucin
                                                                                                          5.14
            421346
                                                    collagen, type X, alpha 1 (Schmid metaph
                                                                                                          5.06
            427585
                        D31152
                                       Hs 179729
                                       Hs. 159177
            425679
                        X05997
                                                     lipase, gastric
                                                     trefoil factor 1 (breast cancer, estroge
                                                                                                          4.93
                        AI910275
                                       Hs.1406
            421582
 55
            434414
                        AI798376
BE545072
                                                    gb:tr34b07.x1 NCI_CGAP_Ov23 Homo sapiens hypothetical protein FLJ10461
                                                                                                          4.92
                                                                                                          4.89
                                       Hs.122579
            422956
                                                     ESTs, Weakly similar to TMS2_HUMAN TRANS
                                                                                                          4.84
                                       Hs.170675
            448105
                        AW591433
                                       Hs.163443
                                                     Homo sapiens cDNA FLJ11576 fis, clone HE
                                                                                                          4.72
                        C18863
            423575
                        M34455
                                       Hs.840
                                                     indolearnine-pyrrole 2,3 dioxygenase
                                                                                                          4.72
             413385
 60
                                       Hs.82772
                                                                                                          4.68
                        AW067903
AW004854
                                                     collagen, type XI, alpha 1
             417866
                                                     Homo sapiens cDNA; FLJ23537 fis, clone L
                                       Hs 228320
             448693
                                                                                                          4.51
                                       Hs.202656
                                                     ESTs
                        BE218239
             441377
                                       Hs.1247
                                                     apolipoprotein A-IV
                                                                                                          4.48
                        AU076799
            419278
```

cysteine knot superfamily 1, BMP antagon

cyclin-dependent kinase inhibitor 2A (me

Homo sapiens cDNA; FLJ22751 fis, clone K

ESTs, Weakly similar to AF172993 1 PLUNC

taminin, gamma 2 (nicein (100kD), katini

tissue specific transplantation antigen small inducible cytokine subfamily A (Cy

inhibin, beta A (activin A, activin AB a

tumor necrosis factor (ligand) superfami Homo sapiens cDNA: FLJ21245 fis, clone C

small inducible cytokine subfamily B (Cy

leukemia inhibitory factor (cholinergic

deleted in malignant brain tumors 1

hypothetical protein FLJ20556

AW190902

U38945

H55709

AJ243212

A1796330

AK000563

AW811606

AL581519

AW363590

N78223

Z15008

U58766

BF439580

AA464510

AW103364

U03398

AI572490

AA321649

407811

403422

403776

418478

428242

421341

451181

432168 454464

448844

428434

452461

409420

431611

413719

430044

409956

422420

420159

428227

65

70

75

80

Hs.40098

Hs.1174

Hs.2250

Hs.279611

Hs 207461

Hs.272805

Hs.271819

Hs.177164

Hs.65551

Hs.108106

Hs.54451

Hs 264428

Hs.75498

Hs.727

Hs.1524

Hs.2248

Hs.99785

Hs.152612

**ESTs** 

**ESTs** 

**ESTs** 

transcription factor

4.47

4.38

4.32

4.32

4.30 4.30

4.26

4.23

4.20

4.14

4,13

4.08

4.04

4.04

4.03

4.02

4.01

4.00 3.98

3.91

	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	3.87
	452304			ESTs, Weakly similar to S10590 cysteine RAB6 interacting, kinesin-like (rabkines	3.84 3.82
			Hs.73625 Hs.77367	monokine induced by gamma interferon	3.81
5	419833	AA251131	Hs.220697	ESTs ESTs	3.81 3.74
	446232 4 <b>323</b> 98		He 2070	trefeil factor 2 (spasmolytic protein 1)	3.70
	451105	AI761324		gb:wi60b11.x1 NCI_CGAP_Co16 Homo sapiens	3.67 3.66
10	413281 432867	AA861271 AW016936	Hs.34395 Hs.233364	ESTs ESTs	3.66
10	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	3.65 3.65
	457465	AW301344	Hs.195969 Hs.72222	ESTs Homo sapiens cDNA FLJ13459 fis, clone PL	3.61
	414918 418738	AJ219207 AW388633	Hs.6682	ESTs	3.60
15	427778	AA412323	Hs.105323 Hs.134013	ESTs ESTs, Moderately similar to NK homeobox	3.60 3.59
	454293 452194	H49739 A1694413	Hs.298262	ESTs, Weakly similar to dJ88J8.1 [H.sapi	3.57
	442577	AA292998	Hs.163900	ESTs	3.57 3.53
20	426174 452862	AA547959 AW378065	Hs.115838 Hs.8687	ESTs ESTs	3.51
20	418869	AW516565	Hs.258279	ESTs	3.48 3.48
	430178	AW449612 AI924533	Hs.152475 Hs.105607	ESTs ESTs	3.46
	430397 418054	NM_002318	Hs.83354	lysyl oxidase-like 2	3.45 3.44
25	442295	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE solute carrier lamily 6 (neurotransmitte	3.44
	425921 431764	NM_007231 AA515212	Hs.162211 Hs.271819	Homo sapiens cDNA: FLJ22751 fis, clone K	3.43
	421948	L42583	Hs.111758	keratin 5A ESTs, Weakly similar to CA54_HUMAN COLLA	3.43 3.41
30	444381	BE387335 R37725	Hs.283713 Hs.261108	ESTs	3.41
30	442896 452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	3.39 3.39
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	3.39
	408832 406685	AW085690 M18728	Hs.63428	ESTs gb:Human nonspecific crossreacting antig	3.37
35	437527	AJ241019	Hs.145644	ESTs	3.37 3.37
	433084	M18079 NM_007115	Hs.282265 Hs.29352	fatty acid binding protein 2, intestinal turnor necrosis factor, alpha-induced pro	3.36
	452401 441318	AI078234	Hs.176130		3.35
40	458897	U85642	Hs.138506		3.33 3.33
40	413808 411274	J00287 NM_002776	Hs.182183 Hs.69423	caldesmon 1 kaltikrein 10	3.32
	418406	X73501	Hs.84905	cytokeratin 20	3.32 3.32
	419559	Y07828	Hs.91096 Hs.1640	ring finger protein collagen, type VII, alpha 1 (epidermolys	3.31
45	423217 423271	NM_000094 W47225	Hs.126256	interleukin 1. beta	3.31 3.30
•-	411558	AA102670	Hs.70725		3.30
	427722 422310	AK000123 AA316622	Hs.180479 Hs.98370	cytochrome P540 family member predicted	3.30
50	430704	AW813091		gb:RC3-ST0186-240400-111-d07 ST0186 Homo	3.29 3.29
50	411263 443211		Hs.69360 Hs.14365		3.29
	443426		Hs.9329	chromosome 20 open reading frame 1	3.28 3.28
	441085				3.27
55	452121 408633			PRO2000 protein	3.27 3.25
	447342		Hs.19322 Hs.28288		3.24
	419229 443957		Hs.34487		3.23
<b>60</b>	452699	AW295390			3.23 3.23
60	425188 400289		Hs.15507 Hs.2258	matrix metalloproteinase 10 (stromelysin	3.21
	408524	4 D87942	Hs.4632		3.20 3.20
	437897 453927				3.19
65	45316		Hs.1462	28 ESTs	3.19 3.19
	40669		Hs.2205 Hs.1589		3.18
	43018 41620			8 MAD2 (mitotic arrest deficient, yeast, h	3.16
<b>5</b> 0	44704	8 AW39308	0 Hs.2283	20 Homo sapiens cDNA: FU23537 fis, clone L	3.14 3.14
70	40811 42546		Hs.1941 Hs.1904		3.13
	42582	6 U97698	Hs.1595	593 mucin 6, gastric	3.13 3.13
	43168				3.13
75	41921 41820		Hs.837	58 CDC28 protein kinase 2	3.12
, 5	41731	15 AI080042	Hs.180	450 ribosomal protein S24	3.11 3.11
	43300 4595			ob;zk15e04.s1 Soares_pregnant_uterus_NbH	3.11
	4501	59 AI702410	5 Hs.200	771 ESTs, Weakly similar to CAN2_HUMAN CALPA	A 3.11 3.10
80			18 Hs.583 Hs.102	482 mucin 5, subtype B, tracheobronchial	3.10
	4211 4213	79 Y15221	Hs.103	982 small inducible cytokine subfamily B (Cy	3.10 3.10
	4203		31 Hs.102		3.10

	414774 415989	X02419 Al267700	Hs.77274 Hs.111128	plasminogen activator, urokinase ESTs	3.10 3.09
	407137	T97307	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	3.09
_	407289	AA135159	Hs.203349	Homo sapiens cDNA FLJ12149 fis, clone MA	3.09
5	420297	AI628272	Hs.88323	ESTs	3.08 3.08
	447519 448045	U46258 AJ297436	Hs.23448 Hs.20166	ESTs prostate stem cell antigen	3.07
	431956	AK002032	Hs.272245	Homo sepiens cDNA FLJ11170 fis, clone PL	3.06
10	410286	AI739159	Hs.61898	DKFZPS86N2124 protein	3.05
10	409632	W74001	Hs.55279 Hs.575	serine (or cysteine) proteinase inhibito	3.05 3.05
	454034 436481	NM_000691 AA379597	Hs.5199	aldehyde dehydrogenase 3 HSPC150 protein similar to ubiquitin-con	3.05
	430573	AA744550	Hs.136345	ESTs	3.05
1.5	428987	NM_004751	Hs.194710	glucosaminyi (N-acetyl) transferase 3, m	3.04
15	424252	AK000520	Hs.143811	hypothetical protein FLJ20513	3.04 3.03
	436291 415992	BE568452 C05837	Hs.5101 Hs.145807	protein regulator of cytokinesis 1 Horno sapiens cDNA FLJ13593 fis, clone PL	3.03
	411789	AF245505	Hs.72157	Homo sapiens adlican mRNA, complete cds	3.02
20	417956	AA210704	Hs.190465	ESTs	3.02
20	408908	BE296227 D30783	Hs.48915 Hs.115263	serine/threonine kinase 15	3.01 3.01
	422330 425071	NM_013989	Hs.154424	epiregulin delodinase, iodothyronine, type II	3.00
	425761	AW664214	Hs.196729	ESTs	2.99
06	432978	AF126743	Hs.279884	DNAJ domain-containing	2.99
25	418546 425371	AA224827 D49441	Hs.155981	gb:nc32g04.s1 NCI_CGAP_Pr2 Homo sapiens mesothelin	2.99 2.99
	422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member 811	2.98
	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	2.98
20	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	2.97
30	428450	NM_014791	Hs.184339 Hs.145479	KIAA0175 gene product Homo sapiens cDNA FLJ10518 fis, clone NT	2.95 2.95
	424345 433133	AK001380 AB027249	Hs.104741	PDZ-binding kinase; T-cell originated pr	2.94
	432269	NM_002447	Hs.2942	macrophage stimulating 1 receptor (c-met	2.94
2.5	432917	NM_014125	Hs.279812	PRO0327 protein	2.94
35	433384	AI021992	Hs.124244 Hs.287820	ESTs 6bronectin 1 ,	2.93 2.93
	432731 420552	R31178 AK000492	Hs.98806	hypothetical protein	2.92
	428303	AW974476	Hs.183601	regulator of G-protein signalling 16	2.92
40	409687	T51125	Hs.8493	ESTs	2.91
40	434377	AW137148	Hs.136348	osteoblast specific factor 2 (fasciclin	2.89 2.89
	417791 457288	AW965339 AA521458	Hs.111471 Hs.192738	ESTs ESTs	2.89
	456181	L36463	Hs.1030	ras inhibitor	2.89
4.0	450190	T51387		gb:yb20e08.r1 Stratagene fetal spicen (9	2.88
45	411573	AB029000	Hs.70823	KIAA1077 protein	2.88 2.88
	430204 434808	AA618335 AF155108	Hs.146137 Hs.256150	ESTs, Weakly similar to putative [C.eleg ESTs, Highly similar to NY-REN-41 antige	2.87
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	2.87
50	418670	AA601036	Hs.285083	ESTs	2.87
50	416661	AA634543 AW885757	Hs.79440 Hs.257862	IGF-II mRNA-binding protein 3 ESTs	2.87 2.87
	409723 435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	2.86
	408660	AA525775	Hs.292523	ESTs	2.86
55	434032	AW009951	Hs.206892	ESTs	2.85
55	418216	AA662240 AI240665	Hs.283099 Hs.8895	AF15q14 protein ESTs	2.85 2.85
	453331 450221	AA328102	Hs.24641	cytoskeleton associated protein 2	2.84
	402075				2.84
60	410145	AW886300	14.00.00	gb:RC5-OT0078-100400-023-C11 OT0078 Homo	2.83 2.83
OU	410681 439867	AW246890 AA847510	Hs.65425 Hs.161292	calbindin 1, (28kO) ESTs	2.83
	443715	AI583187	Hs.9700	cyclin E1	2.83
	420005	AW271106	Hs.133294	ESTs	2.83
65	417366	BE185289	Hs.1076	small proline-rich protein 1B (comitin)	2.83
65	422283 404567	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	2.82 2.82
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	2.82
	449224	AW995911	Hs.299883		2.81
70	407584	W25945	Hs.18745	ESTs	2.81 2.81
70	453884 449032	AA355925 AA045573	Hs.36232 Hs.22900	KIAA0186 gene product nuclear factor (erythroid-derived 2)-lik	2.80
	422809	AK001379	Hs.121028		2.79
	449722	BE280074	Hs.23960	cyclin B1	2.79
75	445676	AI247763	Hs.16928	ESTs	2.79 2.78
75	424308 453028	AW975531 AB006532	Hs.154443 Hs.31442		2.78
	453028 421777	BE562088	Hs.108196		2.78
	452571	W31518	Hs.34665	ESTS	2.77
80	420759	T11832	Hs.127797		2.77 2.77
οU	422675 412723		Hs.119140 Hs.179912		2.76
	439670		Hs.59507	ESTs, Weakly similar to AC004858 3 U1 sm	2.76
	400298		Hs.61635	six transmembrane epithelial antigen of	2.76
					_

			440050	prostate cancer associated protein 1	2.76
		AF109298 AW664026	Hs.118258 Hs.59892	ESTs	2.75
		M57765	Hs.1721	interleukin 11	2.75
_	412059	AA317962	Hs.249721	ESTs	2.75 2.75
5		AW970859	Hs.269109 Hs.67709	ESTs Homo sapiens mRNA full length insert cDN	2.75
	439759 450701	AL359055 H39960	Hs.288467	Homo sapiens cDNA FLJ12280 fis, clone MA	2.75
	452940	AA029722	Hs.20279	ESTS	2.74 2.74
10	408690	AW864542		gb:PM4-SN0016-120500-003-h02 SN0016 Homo	2.73
10	407777	AA161071	Hs.71465 Hs.135657	squalene epoxidase ESTs	2.73
	432201 414416	AI538613 AW409985	Hs.76084	tamin B2	2.73
	414617	Al339520	Hs.20524	ESTs, Moderately similar to hexokinase I	2.73 2.73
	432407	AA221036	Hs.285026	HERV-H LTR-essociating 1 hypothetical protein FLJ20129	2.72
15	444301	AK000136 AA009647	Hs.10760 Hs.8850	a disintegrin and metalloproteinase doma	2.72
	450375 441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	2.72
	408298	AI745325	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	2.72 2.71
20	426711	AA383471	Hs.180669	conserved gene amplified in osteosarcoma synaptonemal complex protein 2	2.71
20	429432 450506	A1678059 NM_004460	Hs.202676 Hs.418	fibroblast activation protein, alpha	2.71
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	2.71
	418801	AA228366	Hs.115122	ESTs	2.71 2.71
25	440283	A1732892	Hs.190489	ESTs hypothetical protein FLJ10339	271
25	429486 408366	AF155827 AW511255	Hs.203963 Hs.258082	ESTs	2.70
	406399	A41311235	113.20000		2.69
	434217	AW014795	Hs.23349	ESTs	2.68 2.68
20	449785	AI225235	Hs.288300	Homo sapiens cDNA: FLJ23231 fis, clone C hypothetical protein FLJ10540	2.68
30	446269	AW263155 AI052572	Hs.14559 Hs.269864	FSTs	2.68
	443349 426514	BE616633	Hs.301122	bone morphogenetic protein 7 (asteogenic	2.67
	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	2.67 2.67
26	444754	TB3911	Hs.11881	transmembrane 4 superfamily member 4 matrix metalloproteinase 9 (gelatinase B	2.66
35	424687	J05070 AW600291	Hs.151738 Hs.6823	hypothetical protein FLJ10430	2.65
	439979 424408	AI754813	Hs.146428	collagen, type V, alpha 1	2.65
	430832	AI073913	Hs.100686	ESTs, Wealthy similar to secreted cement	2.65 2.65
40	427217	AA399272	Hs.144341	ESTs dual specificity phosphatase 4	2.64
40	429170 450400	NM_001394 AI694722	Hs.2359 Hs.279744		2.64
	435380	AA679001	Hs.19222	I ESTs	2.64
	432375	BE536069	Hs.2962	S100 calcium-binding protein P	2.63 2.63
45	453700	AB009426	Hs.560	apolipoprotein B mRNA editing enzyme, ca centromere protein A (17kD)	2.63
45	422938 453134	NM_001809 AA032211	Hs.1594 Hs.11849	3 FSTs	2.63
	420727	H75701	Hs.99886		2.62
	408868	AW292286	Hs.25505		2.62 2.62
50	414972	BE263782	Hs.77695 Hs.16056		2.62
50	440255 403055	Al932285	N\$. 10030		2.62
	443247	BE614387	Hs.47378	ESTs, Moderately similar to hypothetical	2.62 2.61
	447400		Hs.18457		2.61
55	413753		Hs.30110 Hs.25466		2.61
22	445114 422397			t myeloma overexpressed gene(in a subset o	2.60
	407366			nh:Homo saniens cin33 mRNA, partial segu	2.60 3 2.60
	432009			gb:Homo sapiens mRNA; cDNA DKFZp761G212 25 ESTs	2.60
60	440249 433220		Hs.1253 Hs.1319	33 ESTs	2.60
00	438533		Hs.1706		2.60
	436251			nucleolar protein (KKE/D repeat)	2.60 2.60
	424717		Hs.1522		2.60
65	448988 425463		Hs.2278 Hs.1579		2.60
05	435370			38 ESTs	2.59
	43221	5 AU076609		ribonucleotide reductase M1 polypeptide	2.59 2.59
	40914				2.58
70	44391' 41326				2.58
,,	40451	-			2.58
	41499	8 NM_0025		29 oxidised low density lipoprotein (lectin	2.57 2.57
	42959				2.57
75	42684 41676				2.57
, ,	41793	3 X02308	Hs.829	62 thymidylate synthetase	2.56
	43367	5 AW9776			2.56 2.56
	44138		19 Hs.288 Hs.273		2.56
80	45193 41886		Hs.894	04 msh (Drosophila) homeo box homolog 2	2.55
	44904	2 AW2949	85 Hs.301	148 potassium voltage-gated channel, lsk-rel	2.55 2.55
	41600				2.55
	4141	)Z A10U1Z3	- 113,404		27

	431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subuni	2.55
	407830	NM_001086 AF155582	Hs.587 Hs.46744	arylacetamide deacetytase (esterase) core1 UDP-galactose:N-acetytgalactosamin	2.55 2.54
_	434815 415250	F02614	Hs.27319	ESTs	2.54
5	435647	A1653240	Hs.49823	ESTs	2.54
	459306 414361	AW578452 AI086138	Hs.232988 Hs.204044	ESTs, Wealthy similar to mucin [H.sapiens ESTs	2.54 2.54
	425782	U66468	Hs.159525	cell growth regulatory with EF-hand doma	2.53
10	416984	H38765	Hs.80706	diaphorase (NADH/NADPH) (cytochrome b-5	2.53
10	431183 436043	NM_006855 AW963838	Hs.250696 Hs.168830	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic Homo sapiens cDNA FLJ12136 fis, clone MA	2.53 2.53
	456743	AI630124	Hs.7434	ESTs	2.53
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	2.52 2.52
15	424905 411734	NM_002497 AW374954	Hs.153704 Hs.71779	NIMA (never in mitosis gene a)-related k Homo sapiens DNA from chromosome 19, cos	2.52
	432657	AA831815	Hs.270940	ESTs	2.51
	434080	AI820719 AA780020	Hs.154662 Hs.136798	hypothetical protein PRO1472 ESTs	251 251
	438190 418969	W33191	Hs.28907	hypothetical protein FLJ20258	2.51
20	446405	AW451259	Hs.57851	ESTs	2.51
	450002 431808	A1679524 M30703	Hs.201629 Hs.270833	ESTs, Moderately similar to ALUS_HUMAN A amphiregulin (schwannoma-derived growth	2.51 2.51
	429093	NM_000253	Hs.195799	microsomal triglyceride transfer protein	2.50
25	447634	AW967902	Hs.5152	Homo sapiens cDNA: FLJ22618 fis, clone H	2.50 2.50
23	436393 453751	AW022213 R36762	Hs.143617 Hs.101282	ESTs Homo sapiens mRNA; cDNA DKFZp434B102 (fr	2.49
	445669	AI570830	Hs.174870	ESTs	2.49
	445865	AI262584 AW470125	Hs.145575	ESTs gb:xw60c04.x1 NCI_CGAP_Pan1 Homo sapiens	2.49 2.49
30	448437 414883	AA926960	Hs.77550	CDC28 protein kinase 1	2.49
	406747	AI925153	Hs.217493	ennexin A2	2.49
	446921 426322	AB012113 J05068	Hs.16530 Hs.2012	small inducible cytokine subfamily A (Cy transcobalamin I (vitamin B12 binding pr	2.49 2.48
	412903	BE007967	Hs.155795	ESTs	2.48
35	422515	AW500470	Hs.117950	multifunctional polypeptide similar to S	2.48 2.48
	447030 448454	AW444659 NM_005879	Hs.232184 Hs.21254	ESTs TRAF interacting protein	2.48
	419092	J05581	Hs.89603	mucin 1, transmembrane	2.48
40	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	2.48 2.48
40	409640 424639	U78722 AI917494	Hs.55481 Hs.131329	zinc finger protein 165 ESTs	2.48
	404171				2.47
	414747 407839	U30872 AA045144	Hs.77204 Hs.161566	centromere protein F (350/400kD, mitosin ESTs	2.47 2.47
45	410406	AI969703	Hs.301842	ESTS	2.47
	452220	BE158006	Hs.212296	ESTs	2.45
	427691 421493	AW194426 BE300341	Hs.20726 Hs.104925	ESTs ectodermal-neural cortex (with BTB-like	2.45 2.46
	444838	AV651680	Hs.208558	ESTs	2.46
50	413816	AW958181	Hs.189998	ESTs	2.46 2.46
	408296 436613	AL117452 AA972691	Hs.44155 Hs.192974	DKFZP586G1517 protein Homo sapiens cDNA FLJ12735 fis, clone NT	2.45
	445417	AK001058	Hs.12680	Homo samens cDNA FLJ10196 fis, clone HE	2.45
55	432874	W94322 AI807883	Hs.279651 Hs.156932	melanoma inhibitory activity ESTs	2.45 2.45
33	425268 425397	J04088	Hs.156346		2.45
	408308	AL033377	Hs.44197	hypothetical protein DKFZp564D0462	2.45
	427961 422363	AW293165 T55979	Hs.143134 Hs.115474		2.45 2.45
60	433083	AL042759	Hs.191762	ESTs	2.45
	439848	AW979249	Un 272202	gb:EST391359 MAGE resequences, MAGP Homo	2.44 2.44
	431924 431457	AK000850 NM_012211	Hs.272203 Hs.256297		2.44
	443949	AW827419	Hs.235070	ESTs	2.44
65	416498 428484	U33632 AF104032	Hs.79351 Hs.184601	potassium channel, subfamily K, member 1 solute carrier family 7 (cationic amino	2.44 2.43
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	2.43
	413833	Z15005	Hs.75573	centromere protein E (312kD)	2.43
70	407243 410044	AA058357 BE566742	Hs.74466 Hs.58169	carcinoembryonic antigen-related cell ad highly expressed in cancer, rich in leuc	2.43 2.43
. •	424273	W40460	Hs.144442	phospholipase A2, group X	2.42
	409533	AW969543	Hs.21291 Hs.252833	mitogen-activated protein kinase kinase ESTs	2.42 2.42
_	453966 427043	BE148734 AA397679	Hs.298460		2.42
75	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	2.42
	449987 433159	AW079749 AB035898	Hs.184719 Hs.150587		2.42 2.42
	439396	BE562958	Hs.74346	ESTs. Weakly similar to Iprediction	2.42
80	426427	M86699	Hs.169840		2.41 2.41
ου	434725 427719	AK000796 Al393122	Hs.4104 Hs.134726	hypothetical protein 5 ESTs	2.41
	433312	AI241331	Hs.131765	5 ESTs	2.41
	432615	AA557191	Hs.55028	ESTs	2.41

					2.41
		X65965 AA811938	Hs.291759	gb:H.sapiens SOO-2 gene for manganese su ESTs	2.40
			Hs.79361	kallikrein 6 (neurosin, zyme)	2.40
_		AA676349	Hs.190331	ESTs	2.40 2.40
5			Hs.17518	Homo sapiens cig5 mRNA, partial sequence gb:yc18b03.s1 Stratagene lung (937210) H	2.40
	416713 418322	T70174 AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	2.40
	409902	Al337658	Hs.156351	ESTs	2.40 2.40
10	443597	A)078418		gb:oz05e03.x1 Soares_fetal_liver_spleen_	2.40
10	404253 428970	BE276891	Hs.194691	retinoic acid induced 3	2.40
	443452	AI064690	Hs.171176	ESTs	2.39
	418693	AI750878	Hs.87409	thrombospondin 1 gb:EST00049 pGEM-T library Homo sapiens	2.39 2.39
15	451237	AW600293	Hs.38260	ubiquitin specific protease 18	2.39
15	407756 437935	AA116021 AW939591	Hs.5940	hypothetical protein FLJ20063	2.39
	445625	BE246743	Hs.288529	Homo sapiens cDNA: FLJ22635 fis, clone H	2.39 2.39
	435937	AA830893	Hs.119769	ESTs gb:od77b08.s1 NCI_CGAP_Ov2 Homo sapiens	2.38
20	438993 422082	AA828995 AA016188	Hs.111244	hypothetical protein	2.38
20	435849	BE305242	Hs.112442	ESTs. Weakly similar to CLDE_HUMAN CLAUD	2.38 2.38
	407242	M18728	11-04050	gb:Human nonspecific crossreacting antig regulator of G-protein signating 5	2.38
	450396	AU077002 AA954810	Hs.24950 Hs.239784	human homolog of Drosophila Scribble	2.38
25	430354 422578	AF239666	Hs.1545	caudal type horseo box transcription fact	2.38 2.38
	446342	BE298665	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (fr	2.38
	450737	AW007152 T63918	Hs.203330 Hs.182313	ESTs retinol-binding protein 2, cellular	2.38
	428070 416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (	2.37
30	433345	AI681545	Hs.152982		2.37 2.37
	427557	NM_002659	Hs.179657 Hs.1674	plasminogen activator, urokinase recepto glutamine-fructose-6-phosphate transamin	2.37
	423554 453204	M90516 R10799	Hs.191990		2.37
	453876	AW021748	Hs.110406	FSTs	2.36 2.36
35	425081	X74794	Hs.154443		2.36
	434682 439737	AA827165 AI751438	Hs.191958 Hs.41271	B ESTs Homo sapiens mRNA full length insert cDN	2.36
	414108	Al267592	Hs.75761	SFRS protein kinase 1	2.36 2.36
40	417900	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevi 1 ESTs, Moderately similar to 138022 hypot	2.36
40	428046	. AW812795 AI580252	Hs.155381 Hs.293246		2.36
	448826 441020	W79283	Hs.35962		2.36
	448019	AW947164	Hs.19564		2.36 2.36
AE	431753	X76029	Hs.2841 Hs.19284	neuromedin U 3 ESTs	2.36
45	441703 410361	AW390054 BE391804	Hs.62661	quanylate binding protein 1, interferon-	2.36
	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic	2.36 2.36
	444478	W07318	Hs.240	M-phase phosphoprotein 1 Homo sapiens cDNA FLJ11643 fis, clone HE	2.35
50	421878 428388	AA299652 AA729827	Hs.11149 Hs.10126		2.35
50	436961	AW375974		04 ESTs	2.35 2.35
	408194	AA601038	Hs.19179		2.35
	438578 429183		Hs.16416 Hs.19795	T T T T T T T T T T T T T T T T T T T	2.35
55	435663		Hs.1342	73 ESTs	2.35 2.34
	430290		Hs.1363		2.34
	423441 453900		Hs.2783 Hs.2264	THE PARTY OF THE PARTY OF THE PARTY AND THE PARTY OF THE	2.33
	450378		I Hs.1995	4 ESTs, Wealdy similar to cDNA EST yk386e1	2.33 2.33
60	432877		Hs.2924 Hs.3031		2.33
	451928 426227		Hs.3031 Hs.1681	02 Human proteinase activated receptor-2 mR	2.33
	418245			transmembrane, prostate androgen induced	2.33
	415083	3 A1632683			2.33 2.33
65	435106 43219				2.33
	45853		3 Hs.1590	083 ESTs	2.33 2.33
	44953	2 W74653	Hs.2715		2.33
70	44635 40970				2.33
70	41937	·		77 TG-interacting factor (TALE family homeo	2.32 2.32
	43560	7 W73428	Hs.875	0 uncharacterized bone marrow protein BM04	2.32
	40581		7 Hs.124	126 Homo sapiens clone 24438 mRNA sequence	2.32
75	42313 44437				2.32
	43267	5 AJ791855	5 Hs.105	884 ESTs	2.32 2.31
	41177				2.31
	44856 43477			2911 EŠTs	2.31
80	4073	78 AA29926	54	gb:EST11752 Uterus Homo sapiens cDNA 5	2.31 2.31
	4423	53 BE37959			2.31
	4226 4099			gb:zm95f04.r1 Stratagene colon HT29 (937	2.31
	4033			-	

	421677	H64092	Hs.38282	ESTs	2.31
	419493	AF001212	Hs.90744	proteasome (prosome, macropain) 26S subu	231
	424435	AB011167	Hs.146957	KIAA0595 protein	2.30 2.30
5	446880 452795	AJ811807 AW392555	Hs.108646 Hs.18878	Homo sapiens cDNA FLJ12534 fis, clone NT hypothetical protein FLJ21620	2.30
,	452834	AI638627	Hs.105685	ESTs	2.30
	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	2.30
	428125	AA393071	Hs.182579	laucine aminopeptidase	2.30 2.29
10	417655 407287	AA780791 AI678812	Hs.14014 Hs.201658	ESTs, Wealthy similar to KIAA0973 protein ESTs, Wealthy similar to ALU4_HUMAN ALU S	2.29
10	428923	BE047698	Hs.188785	ESTs	2.29
	452203	X57522	Hs.158164	ATP-binding cassette, sub-family 8 (MDR/	2.29
	409402	AF208234	Hs.695	cystatin B (stefin 8)	2.29
1.5	419359	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)	2.29 2.29
15	451999 400811	AW176401 AF219139	Hs.27424 Hs.87726	DEAD/H (Asp-Gtu-Ala-Asp/His) box polypep KIAA0154 protein; ADP-ribosylation facto	2.29
	436396	AI683487	Hs.299112	Homo sapiens cDNA FLJ11441 fis, clone HE	2.28
	442152	R39246	Hs.239666	Homo sapiens cDNA FLJ13495 fis, clone PL	2.28
20	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	2.28 2.28
20	410174 425247	AA306007 NM_005940	Hs.59461 Hs.155324	OKFZP434C245 protein matrix metalloproteinase 11 (stromelysin	2.28
	438170	AI916685	Hs.194601	ESTs	2.28
	445378	AV653564	Hs.226946	ESTs	2.28
26	428048	AA705745	Hs.185070	ESTs	2.28 2.27
25	414696 444665	AF002020 BE613126	Hs.76918 Hs.47783	Niemann-Pick disease, type C1 ESTs, Wealdy similar to T12540 hypotheti	2.27
	427660	AI741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, done C	2.27
	422128	AW881145		gb:QV0-OT0033-010400-182-a07 OT0033 Homo	2.27
20	433535	AF111106	Hs.3382	protein phosphatase 4, regulatory subuni	2.27
30	415857	AA866115	Hs.301646 Hs.102267	Homo sapiens cDNA FLJ11381 fis, clone HE	2.27 2.27
	421155 405545	H87879	ns.102201	lysyl oxidase	2.27
	449467	AW205006	Hs.197042	ESTs	2.27
~ ~	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	2.27
35	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	2.26 2.26
	423634 443868	AW959908 W88483	Hs.1690 Hs.293650	heparin-binding growth factor binding pr ESTs	2.26
	407742	AF186252	Hs.38084	sulfotransferase family, cytosolic, 1C,	2.26
40	428330	1,22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	2.26
40	432655	AA832195	Hs.292266	ESTS	2.26 2.26
	429731	AK001592	Hs.212172	beta,beta-carotene 15,15-dioxygenase ho	2.26
	400514 431846	BE019924	Hs.271580	uroplakin 19	2.26
	439521	AI808955	Hs.58248	ESTs	2.26
45	426010	AA136563	Hs.1975	Homo sapiens cDNA: FLJ21007 fis, clone C	2.26
	437641	AA811452	Hs.291911	ESTs	2.26 2.26
	418982 411393	AJ348838 AW797437	Hs.13073 Hs.69771	ESTs B-factor, properdin	2.26
	414809	Al434699	Hs.77356	transferrin receptor (p90, CD71)	2.25
50	419488	AA316241	Hs.90691	nucleophosmin/nucleoplasmin 3	2.25
	434540	NM_016045	Hs.5184	TH1 drosophila homolog	2.25 2.25
	449962 410196	AA004879 A1936442	Hs.187820 Hs.59838	ESTs hypothetical protein FLJ10808	2.25
	456844	AJ264155	Hs.152981	COP-diacytglycerol synthase (phosphatida	2.25
55	414368	W70171	Hs.75939	uridine monophosphate kinase	2.25
	408353	BE439838	Hs.44298	hypothetical protein	2.25 2.25
	439223	AW238299 AL048858	Hs.23945 Hs.224355	ESTs ESTs, Weakly similar to A39650 protein k	2.25
	448753 428479	Y00272	Hs.184572		2.24
60	432403	AA550815	Hs.124840	ESTs	2.24
	424971	AA479005	Hs.154036		2.24
	432673	AB028859	Hs.278605		2.24 2.24
	446887 452833	AI346656 BE559681	Hs.156652 Hs.30736	KIAA0124 protein	2.24
65	409432	D49372	Hs.54460	small inducible cytokine subfamily A (Cy	2.24
•	422039	BE567832	Hs.82148	hypothetical protein	2.24
	429925	NM_000786			2.24 2.23
	445413 423645	AA151342 AI215632	Hs.12677 Hs.147487	CGI-147 protein PESTs	2.23
70	447532	AK000614	Hs.18791	hypothetical protein FLJ20607	2.23
. •	423515	AA327017	Hs.162204	ESTs	2.23
	444743	AA045648	Hs.11817	nudix (nucleoside diphosphate linked moi	2.23 2.23
	434518		Hs.37372 Hs.28353	Homo sapiens DNA binding peptide mRNA, p uncharacterized bone marrow protein BM03	2.23 2.23
75	435602 449974		Hs.26940		2.23
	424927		Hs.15385	hypothetical protein C321D2.4	2.23
	457982	AW856093	Hs.18361	7 ESTs	2.23
	414420		Hs.76095		2.23 2.23
80	449019 431840		Hs.67776 Hs.2860	POU domain, class 5, transcription facto	2.23
30	452930		Hs.19409	7 ESTs	2.23
	436391	AJ227892	Hs.14627	4 ESTs	2.23
	439186	AJ697274	Hs.6487	Xq28, 2000bp sequence contg. ORF	2.23

PCT/US02/29560

27254 ALS9443 14.1727 ALS9443 14.1727 ALS94543 ALS9457 A							2.22
### ### ### ### ### ### ### ### ### ##					ESTS	saniens cDNA FLJ12169 fis, clone MA	2.22
411835 U29343					minic	hromosome maintenance deficient (S.	
1	_			Hs.72550	hyshi	ronan-mediated motility receptor (R	
### ### ### ### ### ### ### ### ### ##	5			Hs.180059	Hom	24d05 s1 Soares testis NHT Homo sap	
401919				Hs.121590	Hom	o sapiens cDNA FLJ12827 fis, clone N1	
10				Hs.293440	FST	s Moderately similar to ZIC2 protein	
41794 AV19797 H. 52533	10		AI890347	Hs.271923	Hom	o sapiens curva: FW22765 ils, Guille R	
### ### ### ### ### ### ### ### ### ##	10		AW197794	Hs.253338	EST	s	
15 49991 AK00330 hs.4885 sp. 43931 AK00330 hs.4885 sp. 43931 AK00330 hs.4885 sp. 43932 W07411 hs.118212 bypothetical protein FLJ10468 221 hypothetical protein FLJ10468 221 hypo					EST	S ONLY THE TAKERNON (IT	
ACOUSTION   ACOU							
## 193/28   MM, 006/69   Hs.3844   STR, Moderately similar to ALU3_HUMAN A   221   ## 20021   AA625599   Hs.12229   ESTs   STR   ## 27848   NA, 001955   Hs.2271   ## 27848   NA, 001955   Hs.2271   ## 27849   NA, 001955   Hs.2271   ## 27840   AA93996   Hs.18529   ESTs   221   ## 27840   AA93996   Hs.18529   ESTs   221   ## 27840   AA93996   Hs.18529   ESTs   221   ## 27840   AA937808   Hs.19780   Hs.19780   Hs.19719   Hs.2771   ## 27840   AA937808   Hs.19045   ESTs   221   ## 27840   AA937808   Hs.284295   Hs.284295   ## 27840   AA937808   Hs.284295   Hs.284295   ## 27840   AA937808   Hs.284295   ## 27840   AA937808   Hs.284295   ## 27840   AA937808   Hs.284295   ## 27840   AA937808   Hs.284295   ## 27840   AA93891   Hs.284295   ## 27840   AA93891   Hs.196594   ## 27840   AA94391   Hs.196594   ## 27840   AA94391   Hs.196594   ## 27840   AA94395   ## 27840	15				hyp	othetical protein FLJ10468	
### ### ### ### ### ### ### ### ### ##	1.5	434423	NM_006769		I IM	domain only 4	
20			W07411	Hs.118212	AFF	SX control: STAT1	2.21
AA43470			AK000404		hyp	othetical protein FLJ20397	
284349 AW34956 Hs. 2271 endothelin 1 2.21 43102 A334956 Hs. 1378 dp.;10309.rt Stratagene lung (937210) H 2.21 43499 T62489 433827 AF078866 Hs. 284295 Hs. 39495 A33627 AF078866 Hs. 284295 Horno appiens CDNA: FLJ22993 fs. chone K 2.20 42689 AW365665 Hs. 284295 Horno appiens CDNA: FLJ22993 fs. chone K 2.20 42689 AW365665 Hs. 284295 Horno appiens CDNA: FLJ22993 fs. chone K 2.20 42689 AW365665 Hs. 284295 Fls. 30212 Hs. 51945 Hs. 274290 AW355078 Hs. 274290 Hs. 51945 Hs. 274290 AW355078 Hs. 274290 AW355078 Hs. 274290 AW355078 Hs. 274290 AW355078 Hs. 27429 Hs. 51945 Hs. 274290 AW355078 Hs. 27429 Hs. 51945 Hs. 274290 AW355078 Hs. 27429 Hs. 51945 Hs. 274290 AW355078 Hs. 27429 Hs. 51940 Hs. 27429 Hs. 51940 Hs. 27429 Hs. 51940 Hs. 27429 Hs. 27429 Hs. 27429 Hs. 27429 Hs. 27429 Hs. 274290 AW355078 Hs. 27429	20						
### ### ### ### ### ### ### ### ### ##							
25					ES	Ts	
188780		421470	R27496	Hs.1378	anı	nexin A3	
A0381	25			Hs 217493			
## 453779 N35187					ES	Ts	
A	•	453779	N35187		ES	TS COMMON COMMON FOR COMMON K	
## 1792   AW206330   Hs.73239   Hs.73239   Ay206330   Hs.73239   AW306655   Hs.245997   Hs.7908   Hs.7908	20				HO CO	llanen, Ivoe V. alpha 2	2.20
### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756   ### 1756	30				hv	nothetical protein FLJ10901	
14621   18513171   18.79086   18.16994   18.16994   18.16994   18.16994   18.16994   18.16994   18.16994   18.16994   18.16994   18.16994   18.16994   18.16994   18.16994   18.16994   18.16994   18.16994   18.16994   18.16994   18.16994   18.16994   18.16994   18.16994   18.16994   18.16994   18.16994   18.16994   18.16994   18.16994   18.16994   18.16994   18.16994   18.16994   18.16994   18.16994   18.16994   18.16994   18.16994   18.16994   18.16994   18.16994   18.16994   18.16994   18.16994   18.16994   18.16994   18.16994   18.16994   18.16994   18.16995   18.16994   18.16995   18.16994   18.16994   18.16995   18.16994   18.16995   18.16994   18.16995   18.16994   18.16995   18.16994   18.16995   18.16994   18.16995   18.16994   18.16995   18.16994   18.16995   18.16994   18.16995   18.16994   18.16995   18.16995   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   18.16997   1			AW856665				
According   Acco					en:	itochondrial ribosomal protein L3	2.20
A30603	35				4 F/	AT tumor suppressor (Drosophila) homolo	
425274 BEZ81191 Hs. 155462 452679 Z42387 Hs. 4299 Hs. 452679 410619 BE512730 Hs. 65114 keratin 18 2.20 424390 AW955078 Hs. 30212 thromo sapiens cDNA: FLJ20965 fis, clone A 2.20 424490 AW955078 Hs. 30212 thromo sapiens cDNA: FLJ20965 fis, clone A 2.20 42490 Z11502 Hs. 181898 ESTs Superbor interacting protein 15 2.20 427920 Z11502 Hs. 18107 419752 AA249573 Hs. 152618 ESTs Weakly similar to ALU1_HUMAN ALU S 2.19 419752 AA249573 Hs. 152618 ESTs 2.19 413095 AA249573 Hs. 152618 ESTs 2.19 413095 AA249573 Hs. 18639 Hs. 30715 ESTs 2.19 403308 50 422596 AF063611 Hs. 118633 AK958619 Hs. 155849 Hs. 10724 A4261 AA298958 Hs. 13680 Hs. 15849 A423401 NM_001992 Hs. 134650 A4797627 Hs. 134650 A44261 AA298958 Hs. 10724 A40250 AA876179 Hs. 134650 A4797627 Hs. 134650 A44261 AA298958 Hs. 10724 A42340 Hs. 1079763 Hs. 1079763 Hs. 1079763 A44424 Hs. 1079763 Hs.	55		AA148164		о н	BV associated factor	
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40 424332 AA38919 Hs.101615 ESTS 424990 AW965078 Hs.30212 thyroid receplor interacting protein 15 220 418661 NM_001949 Hs.11898 Hs.118888 A27920 Z11502 Hs.181107 amerix A13 ame							
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43308							
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MOS023 protein   2.19	50			Lie 1186	33	7-Sotingarlenylate synthetase-like	
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55 453450 AW797627 Hs.89474 ADP-ribosylation factor if (thrombin) recepto 2.18 AW797627 Hs.89474 ADP-ribosylation factor 6 2.18 ADP-ribosylation factor 6 2			AW96861	9 Hs.1558	49	ESTs	-
ASSISTION   ANTI-197627						enanulation factor II (thrombin) recepto	2.18
Add250	55						
Add   Add   BE296785   Hs.207954   Hs.20			AA876179	Hs.1346			
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Has been solution   Has						DKFZP564J0863 protein	
Hs.71465	60	43044	1 BE39809			DKFZP434D156 protein Home series mPNA: cDNA DKF7n564B1264 (f	
A53735						souriene epoxidase	2.10
A235207				Hs.125	073	FSTs	
A21532		45049	9 AA23520			hypothetical protein UKFZp762F2U11	
NM_014398	65					hypothetical protein FLJ22969	
18				398 Hs.108	87	similar to lysosome-associated membrane	
10						interteukin 13 receptor, alpha 2	
417404	70	44420					2.17
449437 A7702038 Hs. 100057 Hormo sapiens CDNA: FUZ2802 is, Cobre NT 217 446995 A1355012 Hs. 9711 Hormo sapiens CDNA: FUZ2802 is, Cobre NT 217 431548 A1834273 Hs. 9711 Hormo sapiens CDNA: FUZ2802 is, Cobre NT 217 411127 AA668995 Hs. 218329 hypothetical protein 217	/0		· · · · · · · · · · · · · · · · · · ·			nleckstrin homology-like domain, family	
446995 AI359012 Hs.9711 Homo sapiens cDNA FLJ13018 fis, clone NT 217 75 411127 AA668995 Hs.218329 hypothetical protein 217		44943	37 AJ70203	8 Hs.10	0057	Homo sapiens cDNA: FLJ22902 fis, clone K	
75 411127 AA668995 Hs.218329 hypothetical protein 217					11	Homo sapiens cDNA FLJ13018 fis, clone NT	2.17
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439961 AA857451 Hs.269696 ESTS 2.17		4399	61 AA8574	51 Hs.26		ESTs	
429125 AA446854 HS.2/1004 ESTS 2.17							2.17
435990 AI015862 Hs.131793 ESTs		4359		62 Hs.13	11793	ESTs	
80 415116 AA160363 Hs.269956 ESTs	80	4151	16 AA160	363 Hs.26			
440052 Al633/44 Hs. 19048 E315 423961 D13666 Hs. 136348 osteoblast specific factor 2 (fasciclin 2.17						osteoblast specific factor 2 (fasciclin	2.17
431070 AW408164 Hs.249184 transcription factor 19 (SC1) 2.16						transcription factor 19 (SC1)	2.15

	443599	AJ079559	Hs.134125	ESTs	2.16
	423623	AB011117	Hs.129943	KIAA054S protein	2.16
	427258 418113	AA400091 AI272141	Hs.39421 Hs.83484	ESTs SRY (sex determining region Y)-bax 4	2.16 2.16
5	450835	BE262773	Hs.25584	hypothetical protein FLJ10767	2.16
•	428698	AA852773	Hs.297939	ESTs, Weakly similar to T17344 hypotheti	2.16
	421408	AI688223	Hs.104114	H.sapiens HCG I mRNA	216
	449057	AB037784	Hs.22941	KIAA1363 protein	2.16 2.16
10	408947 443552	AL080093 N65982	Hs.49117 Hs.109434	Homo sepiens mRNA; cDNA DKFZp564N1662 (1 ESTs	2.16
• •	448153	Y10805	Hs.20521	HMT1 (hnRNP methyltransferase, S. cerevi	2.16
	424653	AW977534	Hs.151469	calcium/calmodulin-dependent serine prot	2.16
	431341	AA307211	Hs.251531	proteasome (prosome, macropain) subunit,	2.16 2.16
15	452865 432789	AI924046 D26361	Hs.119567 Hs.3104	ESTs KIAA0042 gens product	2.16
	438580	AA811262	Hs.299202	ESTs	2.16
	422192	AA305159	Hs.113019	fts485	2.15
	425607	U09860	Hs.158333	protease, serine, 7 (enterokinase)	2.15 2.15
20	447289 447674	AW247017 BE270640	Hs.36978 Hs.19192	metanoma antigen, family A, 3 cyclin-dependent kinase 2	2.15
	441021	AW578716	Hs.7644	H1 histone family, member 2	2.15
	442432	BE093589	Hs.38178	Homo sapiens cDNA: FLJ23468 fis, clone H	2.15
	426471	M22440	Hs.170009	transforming growth factor, alpha Homo sapiens cDNA FLJ20099 fis, clone CO	2.15 2.15
25	431941 414761	AK000106 AU077228	Hs.272227 Hs.77256	enhancer of zesta (Drosophila) homolog 2	2.15
	447033	AI357412	Hs.157601	ESTs	2.15
	410407	X66839	Hs.63287	carbonic anhydrase IX	2.15
	446077 420900	BE251048 ALD45633	Hs.22579 Hs.44269	Homo sapiens clone CDABP0036 mRNA sequen ESTs	2.15 2.15
30	411975	ALD45655 AI916058	Hs.144583	ESTs, Weakly similar to gag (H.sapiens)	2.15
	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	2.15
	449571	AW016812	Hs.200266	ESTs	2.15
	452721 410491	AJ269529 AA465131	Hs. <b>30</b> 377 Hs.64001	Homo sapiens EST from clone 470080, full Homo sapiens clone 25218 mRNA sequence	2.15 2.14
35	410664	NM_006033	Hs.65370	lipase, endotheliat	2.14
	435730	AB020635	Hs.4984	KIAA0828 protein	2.14
	452835	AK001269	Hs.30738	hypothetical protein FLJ10407	2.14 2.14
	452092 401708	BE245374	Hs.27842	hypothetical protein FLJ11210	2.14
40	411400	AA311919	Hs.69851	GAR1 protein	2.14
. •	448526	AB028946	Hs.21361	KIAA1023 protein	2.14
	421175	AI879099	Hs.102397	GIOT-3 for gonadotropin inducible transc	2.14
	412338 420894	AA151527 AA744597	Hs.69485 Hs.88854	Horno sapiens cDNA FLJ12436 fis, clone NT ESTs	2.14 2.14
45	409235	AA188827	Hs.7988	ESTs, Weakly similar to endo-alpha-0-man	2.14
	412870	N22788	Hs.82407	Homo sapiens HSPC296 mRNA, partial cds	2.14
	447760	AI431328	Hs.291179		2.14 2.13
	413511 432945	AI627178 AL043683	Hs.75412 Hs.271357	Arginine-rich protein ESTs, Wealdy similar to unnamed protein	2.13
50	418592	X99226	Hs.284153	Fanconi anemia, complementation group A	2.13
	441790	AW294909	Hs.132208	ESTs	2.13
	425298	AK000209	Hs.155556	hypothetical protein FLJ20202	2.13 2.13
	450956 419569	AW193531 AI971651	Hs.205647 Hs.91143	ESTs, Moderately similar to ALU1_HUMAN A jagged 1 (Alagille syndrome)	2.13
55	421508	NM_004833	Hs.105115	absent in melanoma 2	2.13
	453975	AW009808	Hs.270829	ESTs	2.13
	413670	AB000115 AA598956	Hs.75470 Hs.120439	hypothetical protein, expressed in osteo ethanolamine kinase	2.13 2.13
	422783 444542	Al161293	Hs.146862		2.13
60	410418	D31382	Hs.63325	transmembrane protease, serine 4	2.13
	419791	AI579909	Hs.105104	ESTs methionine adenosyltransferase II, alpha	2.13 2.13
	414860 425860	BE255593 L29339	Hs.77502 Hs.1964	solute carrier family 5 (sodium/glucose	2.13
	414839	X63692	Hs.77462	DNA (cytosine-5-)-methytransferase 1	2.13
65	437050	AA766420	Hs.291606	ESTs	213
	430217	N47863	Hs.180450		2.13 2.12
	420923 409012	AF097021 AL117435	Hs.273321 Hs.49725	differentially expressed in hematopoieti DKFZP4341216 protein	2.12
	450645	AL117441	Hs.25264	DKFZP434N126 protein	2.12
70	431322	AW970622		gb:EST382704 MAGE resequences, MAGK Horno	2.12
	451356	AA748418	Hs.164577		2.12 2.12
	429534 428365	AW976987 AA295331	Hs.163327 Hs.183861		2.12
	441495	AW294603	Hs.127039		2.12
75	443564	Al921685	Hs.199713	ESTs	2.12
	410839	NM_006849		protein disulfide isomerase Homo sapiens cDNA: FLJ23538 fis, clone L	2.12 2.12
	433640 442947	AW390125 R40800	Hs.240443 Hs.21303	ESTs	2.12
00	414987	AA524394	Hs.165544	ESTs	2.12
80	450510	AA010056	Hs.242998		2.12
	427475 444670	AA403151 H58373	Hs.191605 Hs.37494	S ESTS ESTS	2.12 2.12
	452099	BE612992	Hs.27931	hypothetical protein FLJ10607 similar to	2.12

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						2.12
		R12244			33c12.r1 Soares fetal liver spleen e factor pathway inhibitor 2	2.12
	415138	C18356 R98299	Hs.78045 Hs.177502	EST:	* *	2.11
	438138 414788	X78342	Hs.77313	cvcli	n-dependent kinase (CDC2-like) 10	211
5	415474	NM_014252	Hs.78457	solut	e carrier family 25 (mitochondrial s, Moderately similar to ALU4_HUMAN A	2.11 2.11
	416472	AA180756	Hs.193094	ESI	s, Moderatery similar to ALO4_NOWAY A o sapiens cDNA: FLJ22528 fis, clone H	2.11
	412490 410718	AW803564 AI920783	Hs.288850 Hs.191435	FST	۹.	2.11
	425811	AL039104	Hs.159557	karv	onherin aloha 2 (RAG cohort 1, impor	2.11 2.11
10	433344	AI741506	Hs.186753	EST	s, Weakly similar to ALU1_HUMAN ALU S h88b01.s1 Soares placenta Nb2HP Homo	2.11
	447197	R36075	Un 162491	go:y ES1		2.11
	431621 418522	AW292329 AA505038	Hs.163481 Hs.7149	Hon	no sapiens cDNA: FLJ21950 fis, clone H	211
	433849	BE465884	Hs.280728	EST	Te	211 211
15	438038	AJ732629	Hs.194161	ES	rs, Wealdy similar to TA2R HUMAN, BETA merase (RNA) III (DNA directed) poly	2.11
	422032	AA476966	Hs.110857 Hs.56043	CC	L115 omtein	2.11
	409717 410566	AW452871 AA373210	Hs.43047	Ho	no sapiens cDNA FLJ13585 fis, clone PL	2.11
	445837	AI261700	Hs.145544	ES	Ts	2.11 2.11
20	414334	AA824298	Hs.21331	hyp	othetical protein FLJ 10036 jor histocompatibility complex, class	2.10
	436326	BE085236 BE278111	Hs.181244 Hs.134200	ma DK	FZP564C186 protein	2.10
	423880 421574	AJ000152	Hs.105924		lensin, beta 2	2.10
	437103	AW139408	Hs.152940	ES		2.10 2.10
25	435550	A1224456	Hs.4934	H.	sapiens polyA site DNA ITs, Highly similar to EWS_HUMAN RNA-BI	2.10
	450747	A1064821 AW248364	Hs.48306 Hs.5409	RI	IA nolymerase i subunit	2.10
	437033 417640	D30857	Hs.82353	-	ntoin C recentor, endothelial (EPCR)	2.10 2.10
	431120	AA492588		ab	:ng99c08.s1 NCI_CGAP_Thy1 Homo sapiens	2.10
30	430510	AW162916	Hs.241576 Hs.2471	hy K	pothetical protein PRO2577 AA0020 gene product	2.10
	429669	BE185499 AW072003	Hs.40968	he	paran sulfate (glucosamine) 3-O-sulfot	2.10
	407881 436124	AA705012	Hs.269584	l F	STs	2.10 2.10
	436415	BE265254	Hs.5181		oliferation-associated 2G4, 38kD omo sapiens cDNA FLJ13903 fis, clone TH	2.10
35	451121	AW973795	Hs.128927 Hs.62711		omo sapiens curior rus 13903 ns, ciono 111 STs	2.10
	453968 437549	AA847843 AA759149	113.02711	α	b:ah70e03.s1 Soares_testis_NHT Homo sap	2.10
	407887	AA579668	Hs.41072	S	erine (or cysteine) proteinase inhibito	2.10 2.09
	447720	AL038765	Hs.16130		STs Iomo sapiens cDNA FLJ12676 fis, clone NT	2.09
40	434769	AA648884	Hs.13427 Hs.28899		ypothetical protein FLJ20813	2.09
	429743 447815	AA804398 AJ432199	Hs.24708		STs	2.09
	441675	Al914329	Hs.5461		STS	2.09 2.09
	434274	AA628539	Hs.11625		STs, Moderately similar to ALU1_HUMAN A hypothetical protein FLJ20516	2.09
45	411571				ESTs	2.09
	442525 423750				prefoldin 2	2.09
	449199		Hs.19698	38	ESTs	2.09 2.09
50	415363		Hs.7840	5 22	phosphatidylinositol-4-phosphate 5-kinas Homo sapiens cDNA: FLJ21274 fis, clone C	2.09
50	432543 418462			6	intenrin hela 4	2.09
	432093		, , , , , , , , , , , , , , , , , , , ,	_	obivi52c03 r1 Soares breast 3NbHBst Homo	2.09 2.09
	407862	2 BE548267			Homo sapiens cDNA FLJ10934 fis, clone OV	2.09
55	434447				ESTs EST	2.09
55	44267° 42877				KIAA1069 protein	2.09
	43033		Hs.2394		KIAA0185 protein	2.08 2.08
	42508		Hs.1260 8 Hs.2662		ESTs Homo sapiens cDNA FLJ13346 fis, clone OV	2.08
60	41253 44345		B NS.2007 Hs.133		ECT-	2.08
00	41875				Homo sapiens cDNA: FLJ22938 fis, clone K	2.08 2.08
	43220	4 AI916132			Homo sapiens cDNA FLJ13123 fis, clone NT ESTs, Wealdy similar to unnamed protein	2.08
	43901				Homo sapiens cDNA: FLJ21578 fis, clone C	2.08
65	41830 43162				CD2-associated protein	2.08
05	44652		40 Hs.152		nucleolar protein 1 (120kD)	2.08 2.08
	4322	84 AA53280			ESTs low density lipoprotein receptor (famili	2.08
	4113			3269	gb:Homo sapiens breast cancer 2, early o	2.08
70	4593 4087			144	DKFZP585N0819 protein	2.08
, ,	4436	07 Al45251	2 Hs.134		ESTS	2.08 2.08
	4220	58 AA8622		222	gb:oe13g03.s1 NCI_CGAP_Ov2 Homo sapiens tumor necrosis factor receptor superfami	2.08
	4092				Engcalin 2 (oncogene 24p3)	2.08
75	_ 4295 0 4096				Homo sapiens mRNA for FLJ00036 protein.	2.08
, .	4383	94 BE3796	23 Hs.27	693	CGI-124 protein	2.08 2.08
	4130	)92 AA1268			ESTs Homo sapiens cDNA: FLJ22139 fis, clone H	2.08
	4137 4230				reolication protein A3 (14kD)	2.07
86	) 423 ) 438				Homo sapiens cDNA: FLJ21816 fis, clone H	2.07 2.07
٠,	453	379 AA035	261 Hs.61		ESTs Homo sapiens cDNA FLJ12300 fis, clone MA	2.07
	432				hypothetical protein FLJ1250	2.07
	449	J10 MNUUZ	113.23	,,,,,		

	449318	AW236021	Hs.108788	ESTs, Weakly similar to zeste (D.melanog	2.07
	450096	A1682088	Hs.223368	ESTs	2.07
	454011	M31008	Hs.37009	alkaline phosphatase, Intestinal	2.07
5	427876 422901	AM94291 R81936	Hs.111977 Hs.121576	ESTs aspartate beta-hydroxylase	2.07 2.07
	419235	AW470411	Hs.288433	neurotrimin	2.07
	449207	AL044222	Hs.23255	nucleoporin 155kD	2.07
	408243 415652	Y00787 179213	Hs.624 Hs.272073	interleukin 8 ESTs	2.07 2.07
10	446546	BE167687	Hs.156628	ESTs	2.07
	411765	H43346		gb:yp09a04.r1 Soares breast 3NbHBst Homo	2.07
	423472	AF041260	Hs.129057	breast carcinoma amplified sequence 1	2.07
	436211 456157	AK001581 AW979153	Hs.80961	polymerase (DNA directed), gamma gb:EST391263 MAGE resequences, MAGP Homo	2.07 2.06
15	407143	C14076	Hs.248968	EST	2.06
	454269	AI961060	Hs.296411	ESTs, Moderately similar to KF1A_HUMAN K	2.06
	432440	X63597 BE379794	Hs.2996 Hs.65403	sucrase-isomaltase hypothetical protein	2.06 2.06
	410668 422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	2.06
20	450434	AA166950	Hs.18645	ESTs, Weakly similar to partial CDS [C.e	2.06
	439832	T81829	Hs.14870	ESTs	2.06
	456264 431201	AW974175 AA678405	Hs.105251 Hs.8854	ESTs Human transcription unit PVT gene, exons	2.06 2.06
	445021	AK002025	Hs.12251	Homo sapiens cDNA FLJ11163 fis, clone PL	2.06
25	438714	AA814859	Hs.294112	ESTs	2.06
	445318 439951	AW500652 Al347067	Hs.200885 Hs.124636	ESTs ESTs	2.06 2.06
	433681	AI004377	Hs.200360	Homo sapiens cDNA FLJ13027 fis, clone NT	2.06
••	428307	W27393	Hs.183648	protein tyrosine phosphatase, receptor t	2.06
30	426874	N67325	Hs.247132	ESTs	2.06
	451295 432584	AI557212 AA928829	Hs.17132 Hs.47099	ESTs Homo sapiens cDNA: FLJ21212 fis, clone C	2.06 2.06
	433027	AF191018	Hs.279923	putative nucleotide binding protein, est	2.06
25	433716	AA608808	Hs.225118	ESTs	2.06
35	429412 426235	NM_006235 Al631964	Hs.2407 Hs.34447	POU domain, class 2, associating factor ESTs	2.06 2.06
	449026	BE500946	Hs.209105	ESTs	2.06
	437016	AU076916	Hs.5398	guanine monphosphate synthetase	2.06
40	400019	`A104043	11- 223/7	AFFX control: STAT1	2.06
40	408873 442547	AL046017 AA306997	Hs.23247 Hs.268362	ESTs ESTs, Weakly similar to hypothetical pro	2.06 2.06
	455778	BE088746		gb:CM2-BT0693-210300-123-d09 BT0693 Homo	2.06
	439975	AW328081	Hs.6817	Homo sapiens putative encogene protein m	2.06
45	433037 440086	NM_014158	Hs.279938 Hs.288757	HSPC067 protein v-ral simian leukemia viral oncogene hom	2.06 2.06
77	436414	NM_005402 BE264633	Hs.143638	WD repeat domain 4	2.05
	411770	NM_014278	Hs.71992	heat shock protein (hsp110 family)	2.05
	407293	AA602234	Hs.270551	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.05
50	409459 436238	D86407 AK002163	Hs.54481 Hs.301724	low density lipoprotein receptor-related ESTs, Highly similar to unnamed protein	2.05 2.05
	400517	AF242388	Hs.149585	lengsin	2.05
	439943	AW083789	Hs.124620	ESTs	2.05
	421904 417850	BE143533 AA215724	Hs.109309 Hs.82741	hypothetical protein FLJ20035 primase, polypeptide 1 (49kD)	2.05 2.05
55	417491	AW376842	Hs.1085	guanylate cyclase 2C (heat stable entero	2.05
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	2.05
	435525	AI831297	Hs.123310 Hs.74276	ESTs chloride intracellular channel 1	2.05 2.05
	412627 439702	BE391959 AW085525	Hs.134182	ESTs	2.05
60	440006	AK000517	Hs.6844	hypothetical protein FLJ20510	2.05
	432979	AA573263	Hs.120860	ESTs	2.05
	417308 432925	H50720 AAB78324	Hs.81892 Hs.192734	KIAA0101 gene product ESTs	2.05 2.05
	446311	AW007294	Hs.149795	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.05
65	427871	AW992405	Hs.59622	ESTs, Weakly similar to unknown (H.sapie	2.05
	453804 449939	AA300204 T86420	Hs.35276 Hs.272139	KIAA0852 protein ESTs	2.05 2.05
	455666	BE065813	113.272103	gb:RC2-BT0318-110100-012-a08 BT0318 Homo	2.05
70	417819	AI253112	Hs.133540	ESTs	2.04
70	427747	AW411425	Hs.180655	serine/threonine kinase 12	2.04 2.04
	415009 437829	C75253 AI358522	Hs.220950 Hs.270188	ESTs ESTs	2.04
	435381	AW136397	Hs.247572	ESTs	2.04
75	439778	AL109729	Hs.18948	ESTs, Highly similar to HPS1_HUMAN PROTE	2.04
13	428753 446475	AW939252 AI908188	Hs.192927 Hs.209245	hypothetical protein FLJ20251 ESTs	2.04 2.04
	431394	AK000692	Hs.252351	HERV-H LTR-associating 2	2.04
	423701	AA329856	Hs.143022		2.04
80	430580 422369	AW138724 AF005216	Hs.168974 Hs.115541		2.04 2.04
50	432481	AW451645	Hs.151504		2.04
	443746	AW861379	Hs.160602	ESTs	2.04
	400792	AA635062	Hs.50094	Homo sapiens mRNA; cDNA DKFZp43400515 (f	2.04

	432393			ESTs, Weakly similar to 152825 gene MAC2	2.04 2.04
	430785	Z30201		gb:HHEA22G Atrium cDNA library Human hea ESTs, Weakly similar to plakophilin 2b (	2.04
	428343 419329			S100-type calcium binding protein A14	2.04
5	452488		Hs.184389	ESTs	2.04
-	403485				2.04 2.04
	413313		Hs.75280 Hs.301280	glycyl-tRNA synthetase ESTs, Highly similar to AF241831 1 intra	2.04
	407634 433326	AW016569 Al379486	Hs.159430	FSTs	2.03
10	451129	BE072881	1.0	gb:RC2-BT0548-200300-012-e09 BT0548 Homo	2.03
••	429165	AW009886	Hs.118258	prostate cancer associated protein 1	2.03 2.03
	422963	M79141	Hs.13234	ESTs Bcl-2 binding component 3	2.03
	418684 407824	U82987 AA147884	Hs.87246 Hs.9812	FSTs	2.03
15	434551	BE387162	Hs.280858	ESTs, Highly similar to XPB_HUMAN DNA-RE	2.03
	440246	W52010	Hs.191379	ESTs	2.03 2.03
	444006	BE395085	Hs.10086	type I transmembrane protein Fn14 ESTs	2.03
	431301 452705	AA502384 H49805	Hs.151529 Hs.246005	ESTs	2.03
20	421724	AB037832	Hs.107287	KIAA1411 orotein	2.03
	420637	AW976153		gb:EST388262 MAGE resequences, MAGN Homo	2.03 2.03
	450200	AW975625	Hs.173088	ESTs ESTs	2.03
	447474 418852	AW614220 BE537037	Hs.189402 Hs.273294	hypothetical protein FLJ20069	2.03
25	445019	AI205540	Hs.281295	ESTs	2.03
	435202	AI971313	Hs.170204	KIAA0551 protein	2.03 2.03
	431842	NM_005764	Hs.271473	epithelial protein up-regulated in carci Homo sapiens cDNA FL110263 fis, clone HE	2.03
	436198	AK001125 AA352702	Hs.300922 Hs.37747	hypothetical protein FLJ12484	2.03
30	440773 443425	A1056776	Hs.133397	ESTs	2.03
50	454166	AW993356	Hs.2055	ubiquitin-activating enzyme E1 (A1S9T an	2.03 2.03
	407975	X89426	Hs.41716	endothelial cell-specific molecule 1 (NO	2.03
	428299	AL038004	Hs.29419	ESTs ESTs	2.03
35	418735 442053	N48769 R35343	Hs.44609 Hs.24968	Human DNA sequence from clone RP1-233G16	2.03
55	415757	AA830854	Hs.187810		2.03
	432559	AW452948	Hs.257631	ESTs (A. Dat and d	2.03 2.02
	425912	AL137629	Hs.162189	serine/threonine kinase with Dbl- and pl 5-aminoimidazole-4-carboxamide ribonucle	2.02
40	419395	BE268326 AA339449	Hs.90280 Hs.82285	phosphoribosylglycinamide formyltransfer	2.02
40	417576 418559	AA225048	Hs.104207		2.02
	410855	X97795	Hs.66718	RAD54 (S.cerevisiae)-like	2.02
	433906	A1167816	Hs.43355	ESTs	2.02 2.02
15	422072	AB018255	Hs.111138	kiAA0712 gene product gb:nc06c05.s1 NCI_CGAP_Pr1 Homo sapiens	2.02
45	419546 446229	AA244199 AI744964	Hs.14449	KIAA1609 protein	2.02
	450516	AA902656	Hs.21943	NIF3 (Ngg1 interacting factor 3, S.pombe	2.02
	431721	AB032996	Hs.26804	1 KIAA1170 orotein	2.02 2.02
50	419807	R77402	44-46000	gb:yi75f11.s1 Soares placenta Nb2HP Homo ESTs, Wealtly similar to paraplegin-like	2.02
50	438192 401866	A1859065	Hs.16808	E212' Mean's autility to be objective and	2.02
	443129	R16075	Hs.21668	ESTs	2.02
	426991		Hs.28580	3 Homo saciens cDNA FLJ12852 fis, clone NT	2.01 2.01
e e	414731	AI890434	Hs.77135		2.01
55	424783		Hs.15308 Hs.75270		2.01
	413293 435787			4 hypothetical protein FLI10352	2.01
	422599		Hs.11863	8 non-metastatic cells 1, protein (NM23A)	2.01 2.01
<b>60</b>	442660				2.01
60	456553			o intendo aloba 3 (antineo CD49C, alpha	2.01
	431630 431300			gb:ne26b03.s1 NCI_CGAP_Co3 Homo sapiens	2.01
	443180		Hs.7094	S ESTs	2.01
~~	450914		Hs.1425	28 ESTs	2.01 2.01
65	448275		Hs.2083	synaptic Ras GTPase activating protein 1	2.01
	405484 436469		Hs.5198	Down syndrome critical region gene 2	2.01
	45127				201
	43969	6 <b>W9</b> 5298	Hs.1718		2.01 2.01
70	43237				2.01
	41797 45366				2.01
	41998		Hs.1287	773 ESTs	2.01
	44580	8 AV65523	4 Hs.2980		2.01 2.01
75			Hs.1178		2.01
	43046 45274				2.01
	42279			33 ESTs	2.01
	44330	3 U67319	Hs.921	6 caspase 7, apoptosis-related cysteine pr	2.01
80				79 ESTs qb:zm20h12.s1 Stratagene pancreas (93720)	2.01 2.01
	41000 4489				2.00
	4407				2.00
					445

```
Hs. 168213 ESTs, Weakly similar to ALU1_HUMAN ALU S
                                                                                                               2.00
           451351
                       AW058261
                                                     Homo sapiens cDNA FLI13986 fis, clone Y7 prostaglandin E synthase
                                                                                                               2.00
           442961
                        BE614474
                                       Hs.289074
                                                                                                               2.00
           424420
407154
                       BE614743
                                       Hs.146688
                                                      gb:yu76g10.s1 Soares fetal liver spleen
                                                                                                               2.00
                       H79677
                                                                                                               2.00
2.00
           410240
                       AL157424
                                       Hs.61289
                                                      synaptojanin 2
           426830
                        AA385751
                                       Hs.160392
                                                                                                               2.00
           435014
                        BE560898
                                       Hs.10026
                                                      ribosomal protein L17 isolog
                                                                                                               2.00
           408620
                       AI918693
                                       Hs.81848
                                                      RAD21 (S. pombe) homolog
                                       Hs.57772
                                                                                                               2.00
           432829
                        W60377
                                                      ESTs
10
                        AI285598
                                       Hs.217493
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            CAT number:
                                 Gene cluster number
                                 Genbank accession numbers
            Accession:
                        CAT number
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                        116301_1
116812_1
            409965
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            410145
                                        H43346 AA248302 AA095182
170174 H79244 T69850 H79151
            411765
                        125700_1
25
                        1610889_1
            416713
                                        AA224827 T59708 T59843 BE156903
            418546
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            419546
                         185766_1
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                                        R77402 AA262462 AA250988 R06794
AW976153 AA278945 AA747691
AA862231 AA659033 AA302799 AA302798
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30
            422058
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                                         AL137424 BE007148 T52277
                         34025 1
             432009
 40
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AW857541 AW814172 H66214 AW814398 AF134164 AA243093 AA173345 AA199942 AA223384 AA227092 AA227080 T12379 AA092174 T61139
AA149776 AA699829 AW879188 AW813567 AW813538 AI267168 AA157718 AA157719 AA100472 AA100774 AA130756 AA157730
AA157715 AA053324 AW849581 AW854566 C05254 AW882836 T92637 AW812621 AA206583 AA209204 BE156909 AA226824 AI829309 AW991957
N66951 AA527374 H66215 AA045564 AI694265 H60808 AA149726 AW195620 BE081333 BE073424 AW817662 AW817705 AW817703 AW817659
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                                         AW979249 D63277 AA846968
                                          AI078418 W80626 AW387769
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                         827655 1
              450190
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              451237
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              TABLE 40C:
  65
                                   Unique number corresponding to an Eos probeset
              Pkey:
                                   Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA
              Ref:
                                   sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
                                   Indicates DNA strand from which exons were predicted.
              Strand:
                                   Indicates nucleotide positions of predicted exons.
              Nt_position:
  70
              Pkey
                                          Strand
                                                         78844-79025,80850-80991,89754-89941,93750-93891
              400514
                          9796594
                                          Minus
                                                         157315-157950
                                          Plus
              401519
                          6649315
                                                         154511-155298
                          2951946
                                          Plus
              401708
  75
              401866
                          8018106
                                           Plus
                                                         73126-73623
                                                         121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
               402075
                          8117407
                                           Plus
                                                         109532-110225
                          R74R904
               403055
                                           Minus
                                                          147706-147903,148667-148804
                          7630829
               403208
                                           Minus
               403422
                          9665041
                                                          151169-151561
                                           Minus
  80
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                          7770611
                                           Minus
                           9930793
                                                         173667-173783,176876-177055
               404171
                                           Ptus
               404253
                           9367202
                                                          55675-56055
                                           Minus
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PCT/US02/29560 WO 03/025138

5	404519	8152000	Plus	12817-13000
	404567	7249169	Minus	101320-101501
	405484	5922025	Plus	199214-199579,199672-199920,200262-200495
	405545	1054740	Plus	118677-118807,119091-119296,121626-121823
	405818	4071056	Plus	29055-29196
	406399	9256288	Minus	63448-63554

TABLE 41A: ABOUT 634 SEQUENCES UP-REGULATED IN STOMACH CANCER
Table 41A lists about 634 genes up-regulated in stomach cancer compared to normal adult tissues that are likely to be extracellular or cell-surface proteins. These were selected as Table 41A lists about 634 genes up-regulated in stomach cancer compared to normal adult tissues that are likely to be extracellular or cell-surface proteins. These were selected as Table 40A and the predicted protein contained a structural domain that is indicative of extracellular localization (e.g. ig, fn3, egf. 7tm domains). Predicted protein contained a structural domain that is indicative of extracellular localization (e.g. ig, fn3, egf. 7tm domains). 10

noted. Pkey: ExAcon: Unique Eos probeset identifier number Exemplar Accession number, Genbank accession number Unigene number Unigene gene title Protein Structural Domain Ratio of turnor to normal adult tissues

15 UnigeneID: Unigene Title: PSDomain:

	R1:	Ratio		nal adult fissues		
	KI.					R1
20	Pkey	ExAcon	UnigenelD	Unigene Title	PSDomain	30.66
	411243	AB039886	Hs.69319	CA11	SS hemopexin,Peptidase_M10,SS	16.94
	418007	M13509	Hs.83169	matrix metallop	TM	11.08
	448811	AI590371	Hs.174759	ESTs	cystatin,SS	10.38
0.5	409757	NM_001898	Hs.123114	cystatin SN cathepsin E	asp.SS	9.11
25	421110	AJ250717	Hs.1355	matrix metallop	hemopexin,Peptidase_M10,SS	8.66
	428368	BE440042	Hs.83326 Hs.272620	pregnancy speci	hemopexin, TM,	7.11
	406687	M31126	Hs.188401	annexin A10	annexin,TM,	6.86
	428651	AF 196478 M18667	Hs.1867	progastricsin (	asp,TM,SS	6.51
30	425211 423673	BE003054	Hs.1695	matrix metallop	hemopexin, Peptidase_M10,SS	6.49 6.39
30	409683	U33317	Hs.711	defensin, alpha	defensins, Defensin_propep, SS	6.25
	428664	AK001666	Hs.189095	similar to SALL	zf-C2H2,TM,SS	5.72
	408380	AF123050	Hs.44532	diubiquitin	ubiquitin,7tm_3,ANF_receptor,sushi,7tm_1,TM,	5.46
	428953	AA306610	Hs.194676	DKFZP434C013 pr	arf, TNFR_c6, DEAD, Stathmin, TM, SS	5.40
35	450685	L15533	Hs.423	pancreatitis-as	lectin_c,TM,SS	5.34
22	409187	AF154830	Hs.50966	carbamoyl-phosp	GATase,CPSase_L_chain,CPSase_sm_chain,MGS,TM,	5.16
	434206	AW136973	Hs.288516	ESTs, Weakly si	PH,TM,	5.14
	421346	Z34277	Hs.103707	аропписіл	Cys_knot,vwd,	5.06
	427585	D31152	Hs.179729	collagen, type	C1q,Collagen,TM,SS abhydrolase,SS	4.94
40	425679	X05997	Hs.159177	lipase, gastric	trefoil, trypsin, TM, SS	4.93
	421582	AI910275	Hs.1406	trefoil factor	TM	4.89
	422956	BE545072	Hs.122579	hypothetical pr	trypsin,TM,	4.84
	448105	AW591433	Hs.170675	ESTs, Weakly si	IDO,TM,	4.72
45	413385	M34455	Hs.840	indoleamine-pyr collagen, type	TSPN, Coflagen, COLFI, SS	4.68
45	417866	AW067903	Hs.82772 Hs.1247	apolipoprotein	Apolipoprotein, SS	4.48
	419278	AU076799	Hs.40098	cysteine knat s	SS	4.47
	407811	AW190902	ns.40030	Cystolic laters	SS	4.38
	403422				IL8,TM,SS	4.32 4.32
50	403776 418478	U38945	Hs.1174	cyclin-dependen	ank,TM,SS	4.32 4.30
50	428242	H55709	Hs.2250	leukemia inhibi	LIF_OSM,SS	4.30 4.30
	421341	AJ243212	Hs.279611		SS	4.13
	428434	AW363590	Hs.65551	ESTs, Wealdy si	SS	4.04
	409420	Z15008	Hs.54451	laminin, gamma	taminin_EGF,taminin_B,SS	4.04
55	431611	U58766	Hs.264428		Epimerase, TM, SS	4.03
	413719	BE439580	Hs.75498	small inducible	ILB,SS	4.01
	409956		Hs.727	inhibin, beta A	TGF-beta,TGFb_propeptide,SS	4.00
	422420		Hs.1524	turnor necrosis	TNF,TM,	3.91
	428227		Hs.2248	small inducible	IL8,TM,SS efhand,TM,	3.87
60	422168		Hs.11240		kinesin,TM,SS	3.82
	412140		Hs.73625	RAB6 interactin	ILB.SS	3.81
	414812		Hs.77367		WHEP-TRS.TM,	3.81
	419833		Hs.22069 Hs.16554		7tm_3,TM,	3.74
<b>65</b>	446232		Hs.2979	trefoil factor	trefoil,TM,SS	3.70
65	432390				GSHPx,TM,SS	3.66
	43286				serpin,TM,	3.65
	42404 41491		Hs.7222	Homo sapiens cD	TM	3.61 3.59
	45429		Hs.1340		TM	3.59 3.57
70	44257				TM	3.53
,,	42617				SS	3.48
	41886				Sema,TM,	3.45
	41805	•			Lysyl_oxidase,SRCR,SS	3.44
	44229	5 A1827248	Hs.2243	98 Homo sapiens cD		3.44
75	42592		31 Hs.1622		SNF,TM,	3.43
. •	42194	18 L42583	Hs.1117		filament,TM,	3.39
	44478	3 AK00146			PH,TM, PIPSK,TM,SS	3.37
	43752				ipocalin,SS	3.37
	4330		Hs.2822		Xink,CUB,TM,SS	3.36
80					TM	3.33
	4588		Hs.1385		asp,TM,SS	3.33
	4138		Hs.182 776 Hs.694		typsin,TM,	3.32
	4112	74 NM_002	110 115.034	CO PERMITTER TO		
					447	

	410400	X73501	Hs.84905	cytokeratin 20	Slamost TM	3.32
	418406 419559	Y07828	Hs.91096	rjud gruðas bao cymnesam so	filament, TM, zf-C3HC4,zf-B_box, TM,	3.32
	423217	NM_000094	Hs.1640	collagen, type	fn3,Coflagen,Kunitz_BPTI,vwa,SS	3.31
•	411558	AA102670	Hs.70725	gamma-aminobuty	neur_chan,TM,SS	3.30
5	427722	AK000123	Hs.180479 Hs.98370	hypothetical pr cytochrome P540	PH,SS p450,SS	3.30 3.30
	422310 411263	AA316622 BE297802	Hs.69360	kinesin-like 6	p430,55 kinesin,TM,	3.29
	443426	AF098158	Hs.9329	chromosome 20 o	TM	3.28
	452121	NM_004081	Hs.70936	deteted in azoo	TM	3.27
10	447342	AI199268	Hs.19322	ESTs	TM,SS	3.25
	452699 425188	AW295390 AK002052	Hs.213062 Hs.155071	ESTs hypothetical pr	TM TM	3.23 3.23
	400289	X07820	Hs.2258	matrix metalion	hemopexin, SS	3.21
	408524	D87942	Hs.46328	fucosyltransfer	Glyco_transf_11,TM,SS	3.20
15	437897	AA770561	Hs.146170	hypothetical pr	ŢM	3.20
	453922	AF053306	Hs.36708	budding uninhib	TM	3.19 3.19
	406690 416209	M29540 AA236776	Hs.220529 Hs.79078	carcinoembryoni MAD2 (mitotic a	ig,TM,SS HORMA,SS	3.16
	408113	T82427	Hs.194101	Homo sapiens cD	7tm_3,TM,	3.14
20	425465	L18964	Hs.1904	protein kinase	Ski_Sno,DAG_PE-bind,OPR,pkise,pkise_C,TM,SS	3.13
	419216	AU076718	Hs.164021	small inducible	ILB,TM,SS	3.13 3.12
	418203 417315	X54942 AI080042	Hs.83758 Hs.180450	CDC28 protein k ribosomal prote	CKS,TM, TM,SS	311
	433001	AF217513	Hs.279905	ctone HQ0310 PR	TMSS	3.11
25	459587	AA031956		gb:zk15e04.s1 S	LIM,TM,	3.11
	421379	Y15221	Hs.103982	small inducible	ILB,TM,SS	3.10
	414774	X02419	Hs.77274	plasminogen act	kringle, trypsin, SS	3.10 3.09
	407289 447519	AA135159 U46258	Hs.203349 Hs.23448	Homo sapiens cD ESTs	TM histone,Ribosomal_L22e,TM,	3.08
30	448045	AJ297436	Hs.20166	prostate stem c	TMSS	3.07
50	431956	AK002032	Hs.272245	Homo sapiens cD	RA,SS	3.06
	409632	W74001	Hs.55279	serine (or cyst	serpin,TM,	3.05
	454034	NM_000691	Hs.575	aldehyde dehydr	aldedh,TM,	3.05 3.05
35	436481	AA379597	Hs.5199	HSPC150 protein	UQ_con,TM, Branch.TM.SS	3.04
33	428987 424252	NM_004751 AK000520	Hs.194710 Hs.143811	glucosaminyl (N hypothetical pr	casein_kappa,SS	3.04
	436291	8E568452	Hs.5101	protein regulat	TM	3.03
	411789	AF245505	Hs.72157	Homo sapiens ad	ig,LRRCT,SS	3.02
40	417956	AA210704	Hs.190465	ESTs	sushi,SS	3.02 3.01
40	408908	BE296227	Hs.48915	serine/threonin	pkise,TM,SS EGF,TM,SS	3.01
	422330 425071	D30783 NM_013989	Hs.115263 Hs.154424	epiregulin deiodinase, iod	T4_deiodise,TM,SS	3.00
	425761	AW664214	Hs.196729	ESTs	SH3,TM,	2.99
	432978	AF126743	Hs.279884	DNAJ domain-con	DJ,TM,	2.99
45	418546	AA224827		gb:nc32g04.s1 N	vwa.integrin_A,FG-GAP,TM,SS	2.99 2.99
	425371	D49441	Hs.155981	mesothelin	TM,SS	2.99 2.98
	422440 439453	NM_004812 BE264974	Hs.116724 Hs.6566	aldo-keto reduc thyroid hormone	aldo_ket_red,TM, AAA,TM,	2.98
	413278	BE563085	Hs.833	interferon-stim	ubiquitin,TM,	2.97
50	428450	NM_014791	Hs.184339	KIAA0175 gene p	ptrise,KA1,TM,	2.95
	424345	AK001380	Hs.145479	Homo sapiens cD	TMSS	2.95 2.94
	433133	AB027249	Hs.104741	PDZ-binding kin	pkise,TM, pkise,Sema,Plexin_repeat,TIG,TM,SS	2.94
	432269 432917	NM_002447 NM_014125		macrophage stim PRO0327 protein	TM	2.94
55	432731	R31178	Hs.287820	fibronectin 1	SS	2.93
	420552	AK000492	Hs.98806	hypothetical pr	SS	2.92
	428303	AW974476	Hs.183601	regulator of G-	RGS,TM,	2.92
	409687 457288	T51125 AA521458	Hs.8493 Hs.192738	ESTs ESTs	Ets,SAM_PNT,TM, TM	2.91 2.89
60	456181	L36463	Hs.1030	ras inhibitor	RAVPS9.TM.SS	2.89
	450190	T51387		gb:yb20e08.r1 S	SH3,TM,	2.88
	430204	AA618335	Hs.146137	ESTs, Weakly si	TM	2.88
	434808	AF155108	Hs.256150		TM	2.87 2.87
65	450983	AA305384	Hs.25740 Hs.285083	ERO1 (S. cerevi ESTs	SS TM	2.87
03	418670 416661	AA601036 AA634543	Hs.79440	IGF-II mRNA-bin	KH-domain,TM,	2.87
	435099	AC004770	Hs.4756	flap structure-	XPG_I,XPG_N,TM,	2.86
	402075			•	serpin,TM,	2.84
70	410681	AW246890	Hs.65425	calbindin 1, (2	efhand,FHA,BRCT,adh_short,adh_short_C2,TM,	2.83 2.83
70	439867	AA847510	Hs.161292	ESTs cyclin E1	TM cyclin,TM,SS	2.83
	443715 417366	AI583187 BE185289	Hs.9700 Hs.1076	small proline-r	Cornifin, TM.	2.83
	422283	AW411307	Hs.114311		CDC45,TM,SS	2.82
	404567			·	HECT,zf-UBR1,TM,	2.82
75	422158	L10343	Hs.112341		wap,SS	2.82
	449224	AW995911	Hs.299883		fa3,TM, PK,SS	2.81 2.81
	407584 453884	W25945 AA355925	Hs.18745 Hs.36232	ESTs KIAA0186 gene p	TM	2.81
	449032	AA045573	Hs.22900	nuclear factor	bZIP,Chromo_shadow,TM,SS	2.80
80	422809	AK001379	Hs.121028	hypothetical pr	IQ,TM,	2.79
	449722	BE280074	Hs.23960	cyclin 81	cyclin,TM,	2.79 2.78
	453028 421777	AB006532 BE562088	Hs.31442 Hs.108196	RecQ protein-ti HSPC037 protein	DEAD,helicase_C,TM, TM	2.78
	421111	DLJ02000	rs.100130	, no our process	• 🖚	

						2.77
	452571		Hs.34665	ESTs	TM eIF-5a,TM,	2.77
	422675	BE018517	Hs.119140 Hs.61635	eukaryotic tran six transmembra	TM	2.76
	400298 414569	AA032279 AF109298	Hs.118258	prostate cancer	TM	2.76 2.75
5	449378	AW664026	Hs.59892	ESTs	TM	2.75
	423903	M57765	Hs.1721	interleukin 11 ESTs	TM,SS Sema,TM,SS	2.75
	431104 452940	AW970859 AA029722	Hs.269109 Hs.20279	ESTs	7tm_1,TM,SS	2.74
	432340	AI538613	Hs.135657	ESTs	trypsin,TM,	2.73 2.73
10	414617	AI339520	Hs.20524	ESTs, Moderatel	hexokise,TM, LRR,TM,	2.72
	444301	AK000136	Hs.10760	hypothetical pr conserved gene	TM	2.71
	426711 429432	AA383471 AJ678059	Hs.180669 Hs.202676	synaptonemal co	TM	2.71
	450506	NM_004460	Hs.418	fibroblast acti	Peptidase_S9,DPPIV_N_term,SS	2.71 2.71
15	427528	AU077143	Hs.179565	minichromosome	MCM,TM,SS	271
	418801	AA228366	Hs.115122	ESTs hypothetical pr	integrin_A,FG-GAP,TM,SS SNF2_N,heticase_C,TM,	2.71
	429486 408366	AF155827 AW511255	Hs.203963 Hs.258082	ESTs	SS	2.70
	406399	A11311233	110.20000		kazal,TM,SS	2.69 2.68
20	446269	AW263155	Hs.14559	hypothetical pr	TM TGF-beta,TGFb_propeptide,TM,SS	2.67
	426514	BE616633	Hs.301122	bone morphogene interleukin 1 r	IL1.SS	2.67
	417079	U65590 T83911	Hs.81134 Hs.11881	transmembrane 4	TM,SS	2.67
	444754 424687	J05070	Hs.151738	matrix metallop	fn2,hemopexin,Peptidase_M10,SS	2.66 2.65
25	439979	AW600291	Hs.6823	hypothetical pr	TM TM ES	2.65
	430832	AI073913	Hs.100686	ESTs, Weakly si	TM,SS DSPc.Rhodanese,TM,	2.64
	429170	NM_001394	Hs.2359 Hs.279744	dual specificit ESTs	TM	2.64
	450400 435380	AI694722 AA679001	Hs.192221		Occludin,TM,SS	2.64 2.63
30	432375	BE536069	Hs.2962	S100 calcium-bi	S_100,efhand,TM,SS dCMP_cyt_deam,sugar_tr,TM,SS	2.63
	453700	AB009426	Hs.560	apolipoprotein	histone.TM.	2.63
	422938	NM_001809 AA032211	Hs.1594 Hs.118493	centromere prot ESTs	adh_short,TM,SS	2.63
	453134 420727	H75701	Hs.99886	complement comp	sushi,	2.62 2.62
35	408868	AW292286	Hs.255058		TM	2.62
•	414972	BE263782	Hs.77695	KIAA0008 gene p	TM fitament,TM,SS	2.62
	403055	AK000322	Hs.18457	hypothetical pr	zf-C3HC4,TM,	2.61
	447400 413753	U17760	Hs.30110		laminin_EGF,laminin_Nterm,SS	2.61 2.60
40	433220	AJ076192	Hs.13193		TM	2.60
	436251	BE515065	Hs.5092	nucleolar prote	Nop,TM,SS neur_chan,TM,SS	2.60
	448988	Y09763	Hs.22785 Hs.15798	gamma-aminobuty 6 hypothetical pr	TM	2.60
	425463 435370		Hs.22583		EGF,fn3,fibrinogen_C,TM,SS	2.59 2.59
45	432215		Hs.2934	ribonucleotide	ribonucleo_red_ribonuc_red_lg,TM,	2.59
	409142	AL136877	Hs.50758		SMC_N,TM,SS adh_short,TM,SS	2.58
	443919		Hs.13522		RGS,TM,	2.58
	413268 404519		Hs.75256	i leginara a o	defensins,SS	2.58 2.57
50	414998		3 Hs.77729	oxidised low de	TM	2.57
	429597	NM_00381	6 Hs.2442	a disintegrin a	TM,SS æp,TM,SS	2.57
	426841		Hs.1937	6 ESTs regenerating is	lectin_c,SS	2.57
	416768 41793		Hs.1032 Hs.8296		thymidylat_synt,SS	2.56
55	44138			60 protease, serin	TM	2.56 2.56
•	45193		Hs.2731		PAC,PAS,BPL,BPL_C,TM, homeobox,TM,	2.55
	41886		Hs.8940		TM	2.55
	41606 43189		Hs.7899 Hs.2719		wwa,integrin_A,FG-GAP,TM,SS	2.55
60	40783	•		arytacetamide d	COesterase,7tm_1,TM,SS	2.55 2.54
•	43481	5 AF155582	2 Hs.4674		SS TM	2.54
	43564				TM,SS	2.54
	45930 41438				TM	2.54
65	42578		Hs.159		SS	2.53 2.53
	41698		Hs.807			2.53
	4311				TM	2.53
	45674				TM	2.52
70	4102 4249				pkise,TM,	2.52 2.51
,,	4326			940 ESTs	TM	2.51
	4340	80 AI82071			DJ_CXXCXGXG,TM,SS SH3,TM,	2.51
	4189				EGF,TM,SS	2.51
75	4318 > 4290				Vitellogenin_N,TM,SS	2.50
/ -	, 4290 4476			2 Homo sapiens cl	D TM	2.50 2.50
	4363	93 AW0222	13 Hs.14	617 ESTs	Galactosyl_T_2,TM,SS	2.49
	4537				ir TM SS	2.49
80	4458					2.49
0(	() 4148 4067			7493 annexin A2	TM	2.49 2.49
	446	921 AB0121	13 Hs.16	530 small inducible	IL8,SS Cobdomin hind TM SS	2.48
	426		Hs.20	12 transcobalamin	Coballamin_bind,TM,SS	

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	422515	AW500470	Hs.117950	multifunctional	AIRC, SAICAR_SYNLTM,	2.48
	447030	AW444659	Hs.232184	ESTs	TM	2.48
	448454	NM_005879	Hs.21254	TRAF interactin	zl-C3HC4,TM,	2.48
_	419092	J05581	Hs.89603	mucin 1, transm	SEATMSS	2.48
5	409640	U78722	Hs.55481	zinc finger pro	zl-C2H2,SCAN,TM,	248
	404171				sodle,TM,	2.47
	414747	U30872	Hs.77204	centromere prot	SS	2.47 2.47
	410406 452220	Al969703 BE158006	Hs.301842 Hs.212296	ESTs ESTs	FGGY,TM, FG-GAP,TM,SS	2.46
10	421493	BE300341	Hs.104925	ectodermal-neur	BTB,Kelch,TM,	2.46
10	444838	AV651680	Hs.208558	ESTs	integrin_A,FG-GAP,TM,SS	2.46
	413816	AW958181	Hs.189998	ESTs	AMP-binding,G_glu_transpept,TM,	2.46
	436613	AA972691	Hs.192974	Homo sapiens cD	TM,SS	2.45
	432874	W94322	Hs.279651	melanoma inhibi	SH3,SS	2.45
15	425397	J04088	Hs.156346	topoisomerase (	HATPase_c,SS	2.45 2.45
	422363	T55979	Hs.115474	replication fac	TM SH3.TM,	2.45
	431924 431457	AK000850 NM_012211	Hs.272203 Hs.256297	Homo sapiens cO integrin, alpha	FG-GAP,vwa,TM,SS	244
	416498	U33632	Hs.79351	potassium chann	TM	244
20	428484	AF104032	Hs.184601	sotute carrier	aa permeases,TM,	2.43
	431958	X63629	Hs.2877	cadherin 3, typ	cadherin,Cadherin_C_term,TM,SS	2.43
	413833	Z15005	Hs.75573	centromere prot	kinesin,TM,	2.43
	407243	AA058357	Hs.74466	carcinoembryoni	TM,SS	2.43
25	410044	BE566742	Hs.58169	highly expresse	TMSS	2.43 2.42
25	424273	W40460	Hs.144442	phospholipase A	phoslip,TM,SS TM,SS	242
	409533 419741	AW969543 NM_007019	Hs.21291 Hs.93002	mitogen-activat ubiquitin carri	UQ_con,efhand,TM,SS	2.42
	449987	AW079749	Hs.184719	ESTs, Weakly si	ABC_tran,ABC_membrane,TM,	2.42
	433159	AB035898	Hs.150587	kinesin-like pr	kinesin, Myosin_tail, TM, SS	2.42
30	439396	BE562958	Hs.74346	ESTs, Weakly si	SS	2.42
	426427	M86699	Hs.169840	TTK protein kin	pkise,TM,	2.41
	434725	AK000796	Hs.4104	hypothetical pr	TM	241
	433312	AI241331	Hs.131765	ESTs	zf-C2H2,SS	2.41 2.41
35	407047	X65965	Lin 201750	gb:H.sapiens SO	sodle,TM, TM,SS	2.40
20	419220 416530	AA811938 U62801	Hs.291759 Hs.79361	ESTs kallikrein 6 (n	trypsin.pro_isomerase,TM,SS	2.40
	435219	AA676349	Hs.190331	ESTs	TM	2.40
	418322	AA284166	Hs.84113	cyclin-dependen	SS	2.40
	404253				histone,TM,SS	2.40
40	428970	BE276891	Hs.194691	retinoic acid i	7tm_3,TM,	2.40
	418693	AI750878	Hs.87409	thrombospondin	EGF,TSPN,tsp_1,tsp_3,vwc,SS	2.39
	451237	AW600293		gb:EST00049 pGE	TM	2.39 2.39
	407756	AA116021	Hs.38260 Hs.5940	ubiquitin speci	UCH-1,UCH-2,SS TM,SS	2.39
45	437935 445625	AW939591 BE246743	Hs.288529	hypothetical pr Homo sapiens cD	TM	2.39
73	435937	AA830893	Hs.119769	ESTs	TM	2.39
	438993	AA828995		gb:od77b08.s1 N	integrin_B,TM,SS	2.38
	422082	AA016188	Hs.111244	hypothetical pr	TM	2.38
50	450396	AU077002	Hs.24950	regulator of G-	RGS,TM,	2.38
50	422578	AF239666	Hs.1545	caudal type hom	homeobox,SS	2.38 2.38
	428070 416111	T63918 AA033813	Hs.182313 Hs.79018	retinol-binding chromatin assem	lipocalin,TM, TM,SS	2.37
	433345	AI681545	Hs.152982		TM	2.37
	427557	NM_002659	Hs.179657		UPAR_LY6,SS	2.37
55	423554	M90516	Hs.1674	glutamine-fruct	GATase_2,SIS,TM,SS	2.37
	453204	R10799	Hs.191990		TM	2.37
	425081	X74794	Hs.154443		MCM,TM,	2.36
	434682	AA827165	Hs.191958	ESTs SFRS protein ki	TM pkise,TM,	2.36 2.36
60	414108 417900	AI267592 BE250127	Hs.75761 Hs.82906	CDC20 (cell div	WD40,TM,	2.36
50	428046	AW812795	Hs.155381		ank,SS	2.36
	448019	AW947164	Hs.195641		TM	2.36
	431753	X76029	Hs.2841	neuromedin U	NMU,TM,SS	2.36
	410361	BE391804	Hs.62661	guanylate bindi	GBP,TM,SS	2.36
65	418526	BE019020	Hs.85838	solute carrier	MCT,TM,SS	2.36 2.36
	444478	W07318	Hs.240	M-phase phospho ESTs	kinesin,SS TM	2.35
	436961 408194	AW375974 AA601038	Hs.156704 Hs.191797		TM	2.35
	438578	AA811244	Hs.164168		formyl_transf,AIRS,GARS,TM,	2.35
70	429183	AB014604	Hs.197955		TM	2.35
	453900	AW003582	Hs.226414		ТМ	2,33
	432877	AW974111	Hs.292477		EIS,SAM_PNT,TM,	233
	451928	AI823801	Hs.30315		TM	2.33 2.33
75	418245	AA088767	Hs.83883	transmembrane,	kdi_recept_a,TM,SS TM	2.33
,,	435106 432193	AA100847 AA372264	Hs.193380 Hs.273193		TM,SS	2.33
	432133	W74653	Hs.271593		TM	2.33
	409703	NM_006187			NTP_transf_2,TM,SS	2.33
~~	419373	NM_003244	Hs.90077	TG-interacting	homeobox,SS	2.32
80	435607	W73428	Hs.8750	uncharacterized	SS	2.32
	405818	00010001	U_ 000	fadband b 144	TM,SS	2.32 2.32
	444371	8E540274 AI791855	Hs.239 Hs.10588	forkhead box M1 4 ESTs	Fork_head,SS PDEase,TM,	2.32
	432675	WI 2 1000	ns.10300		r vcaso, rmi	

						2.31
	411773			orotease, serin	trypsin,SS .	2.31
	434775			ESTs ucosyltransfer	TM,SS SS	2.31
	422611 419493			proteasome (pro	SS	2.31
5	424435			KIAA0595 protei	TM	2.30 2.30
	409262			hypothetical pr	WD40,TM,SS Peotidase_M17,TM,SS	2.30
	428125	AA393071 AA780791		leucine aminope ESTs, Weakly si	TM	2.29
	417655 407287	AI678812		ESTs, Weakly si	ras,TM,SS	2.29 2.29
10	428923	BE047698	Hs.188785	ESTs	TM,SS	2.29
	452203	X57522		ATP-binding cas	ABC_tran_ABC_membrane,TM, cystatin,SS	2.29
	409402	AF208234 AL043202	Hs.695 Hs.90073	cystatin B (ste chromosome segr	TM.SS	2.29
	419359 451999	AW176401	Hs.27424	DEAD/H (Asp-Glu	TM,SS	2.29 2.29
15	400811	AF219139	Hs.87726	KIAA0154 protei	Cobalamin_bind,SS	2.28
	420931	AF044197	Hs.100431	small inducible	IL8,TM,SS hemopexin,Peptidase_M10,TM,SS	2.28
	425247	NM_005940 AI916685	Hs.155324 Hs.194601	matrix metallop ESTs	2-Hacid_DH,TM,	2.28
	438170 445378	AV653564	Hs.226946	ESTs	TM	2.28 2.28
20	428048	AA705745	Hs.185070	ESTs	AMP-binding,TM,	2.27
	414696	AF002020	Hs.76918	Niemann-Pick di	Patched,TM,SS TM	2.27
	433535	AF111106 H87879	Hs.3382 Hs.102267	protein phospha lysyl oxidase	Lysyl_oxidase,SS	2.27
	421155 405545	1101013	113.102207	1,5,1,435555	ABC_tran,ABC_membrane,TM,SS	2.27 2.27
25	445537	AJ245671	Hs.12844	EGF-like-domain	EGF,S\$	2.26
	423634	AW959908	Hs.1690	heparin-binding	TM,SS Sutfotransfer,SS	2.26
	407742	AF186252	Hs.38084	sulfotransferas matrix metallop	Peptidase_M10,SS	2.26
	428330 429731	L22524 AK001592	Hs.2256 Hs.212172	beta,beta-carot	TM	2.26
30	400514	A1001332	110.212112		p450,TM,SS	2.26 2.26
20	431846	BE019924	Hs.271580	uroplakin 1B	transmembrane4,TM,SS	2.26
	426010	AA136563	Hs.1975	Homo sapiens cD	TM TM	2.26
	437641	AA811452	Hs.291911	ESTs B-factor, prope	sushi,trypsin,vwa,DEAD,mm,EGF,fn3,ffbrinogen_C,SS	2.26
35	411393 414809	AW797437 AI434699	Hs.69771 Hs.77356	transferrin rec	PA,Ribosomal_S2,TM,	2.25
55	419488	AA316241	Hs.90691	nucleophosmin/n	SS	2.25 2.25
	434540	NM_016045	Hs.5184	TH1 drosophila	TM	2.25
	410196	AI936442	Hs.59838	hypothetical pr	UBACT_repeat,TM, Cytidylyttrans,TM,	2.25
40	456844	A1264155 BE439838	Hs.152981 Hs.44298	CDP-diacy/glyce hypothetical pr	Ribosomal_S17,TM,	2.25
40	408353 448753	AL048858	Hs.224355	ESTs, Weakly si	TM	2.25 2.24
	428479	Y00272	Hs.184572	cell division c	pkise,TM,SS	2.24
	424971	AA479005	Hs.154036	tumor suppressi	ion_trans,PH,TM, DJ,DJ_C,TM,SS	2.24
45	432673	AB028859	Hs.278605 Hs.54460	ER-associated D small inducible	ILB,TM,SS	2.24
43	409432 429925	D49372 NM_000786			p450,TM,SS	2.24
	445413		Hs.12677	CGI-147 protein	UPF0099,TM,SS	2.23 2.23
	447532		Hs.18791	hypothetical pr	TM SS	2.23
50	423515		Hs.162204 Hs.11817	ESTs nudix (nucleosi	mutT,TM,	2.23
30	444743 434518		Hs.37372	Homo sapiens DN	TM	2.23
	435602		Hs.283532	uncharacterized	TM,SS	2.23 2.23
	449974				TM,SS TM	2.23
55	424927		Hs.153850 Hs.76095	) hypothetical pr immediate early	TM	2.23
33	414420 431840		Hs.2860	POU domain, cla	homeobox,pou,TM,SS	2.23
	452930				SS	2.23 2.23
	436391		Hs.14627		SS Epimerase,SS	2.23
60	439186		Hs.6487 Hs.77152	Xq28, 2000bp se minichromosome	MCM.TM.	2.22
00	414732 411835		Hs.72550		TM	2.22
	43822			gb:aj24d05.s1 S	myosin_head,TM,	2.22 2.22
	45014	9 AW969781	1 Hs.29344	0 ESTs, Moderatel	TM Glament,TM,	2.22
65	40151		4 Hs.25333	8 ESTs	manen, rm, ank,TM,	2.22
03	44179 40890				TM	2.21
	43442			LIM domain only	LIM,TM,	2.21 2.21
	43214	0 AK000404	Hs.27268		SS	2.21
70	42345				Granin,CDP-OH_P_transf,TM, endothelin,TM,SS	2.21
70			55 Hs.2271 Hs.1378	endothelin 1 annexin A3	annexin,TM,SS	2.21
	42147 44038	•			TM,SS	2.20
	45377		Hs.4338	B ESTs	TMSS	2.20 2.20
7.	43362	27 AF07886			SURF4,TM, COLFI,Collagen,vwc,TM,SS	2.20
75				5 collagen, type gb:RC3-CT0297-2		2,20
	42268 44849		oo Hs.2459		TM,SS	2.20
	4261		Hs.1669	94 FAT tumor suppr	EGF,cadherin,laminin_G,TM,SS	2.20 2.20
	4306	03 AA14816			zi-C3HC4,TM, MCM,TM,	2.20
80						2.20
	4526 4106		Hs.4299 10 Hs.6511		filament,TM,	2.20
	4243				SS	2.20

						2.20
	418661	NM_001949	Hs.1189	Human mRNA for	E2F_TDP,TM,SS	2.20
	419341	N71463	Hs.118888 Hs.181107	ESTs, Wealtly si annexin A13	UPF0016,TM,SS annexin,TM,	2.19
	427920 403208	Z11502	ns.101107	Silledii A13	lectin_c,TM,SS	2.19
5	422596	AF063611	Hs.118633	Z-S'ofigoadeny	ubiquifin,SS	2.19
,	444261	AA298958	Hs.10724	MDS023 protein	TM	2.19
	423401	NM_001992	Hs.128087	coagulation fac	7tm_1,TM,SS	2.18
	453450	AW797627	Hs.89474	ADP-ribosylatio	SS	2.18
	444334	BE296785	Hs.10848	KIAA0187 gene p	SS	2.18
10	437616	A1797163	Hs.207954	ESTs	SMC_N,TM,SS	2.18
• -	451807	W52854	Hs.27099	DKFZP564J0863 p	TM	2.18
	430441	BE398091	Hs.6880	DKFZP434D156 pr	TM	2.18
	411678	Al907114	Hs.71465	squalene epoxid	Monooxygese,TM,	2.18
	452291	AF015592	Hs.28853	CDC7 (cell divi	pkise,TM,	2.18
15	444342	NM_014398	Hs.10887	similar to lyso	Lamp,TM,SS	2.18
	451099	R52795	Hs.25954	interleutin 13	fn3,TM,SS	218
	425873	NM_013390	Hs.160417	transmembrane p	TM	2.17
	417404	NM_007350	Hs.82101	pleckstrin homo	TM	2.17
••	446995	Al355012		gb:qu16d10.x1 N	TM	2.17
20	439961	AA857451	Hs.269696	ESTs	TM	2.17
	429125	AA446854	Hs.271004	ESTs	TM	2.17
	407103	AA424881	Hs.256301	ESTs	TM	2.17 2.17
	415116	AA160363	Hs.269956	ESTs	ER_turnen_recept,TM,SS	2.17
0.5	440052	AI633744	Hs.195648	ESTs	PAC,TM,SS	2.17
25	423961	D13666	Hs.136348	osteoblast spec	Fascidin,TM,SS	2.17
	431070	AW408164	Hs.249184	transcription (	FHASS	2.16
	443599	AI079559	Hs.134125	ESTs	TM	2.16
	427258	AA400091	Hs.39421	ESTs	TM	2.16
20	418113	AJ272141	Hs.83484	SRY (sex determ	HMG_box,TM,	2.16
30	450835	BE262773	Hs.25584	hypothetical pr	ArfGap,SS	2.16
	449057	AB037784	Hs.22941	KIAA1363 protei	TM	2.16
	448153	Y10805	Hs.20521	HMT1 (hnRNP met	TM,SS Guanytate_kin,PDZ,pkise,SH3,TM,	2.16
	424653	AW977534	Hs.151469	calcium/calmodu		2.16
25	431341	AA307211	Hs.251531	proteasome (pro	proteasome,TM,	2.16
35	452865	AI924046	Hs.119567	ESTS	PMP22_Claudin,TM,SS	2.16
	432789	D26361	Hs.3104	KIAA0042 gene p	TM	2.16
	438580	AA811262	Hs.299202	ESTs	pkise,TM, SS	2.15
	422192	AA305159	Hs.113019	fis485	kdl_recept_a,trypsin,CUB,SRCR,MAM,SEA,TM,SS	2.15
40	425607	U09860	Hs.158333	protease, serin	3Beta_HSD,Epimersse,MAGE,TM,	2.15
40	447289	AW247017	Hs.36978	melanoma antige	pkise,TM,	2.15
	447674	BE270640	Hs.19192	cyclin-dependen		2.15
	441021	AW578716	Hs.7644	H1 histone fami	linker_histone,TM, EGF,TM,SS	2.15
	426471	M22440	Hs.170009		pkise, Furin-like, TM, SS	2.15
45	431941	AK000106	Hs.272227		SET,TM,	2.15
43	414761	AU077228	Hs.77256	enhancer of zes carbonic anhydr	carb_anhydrase,TM,SS	2.15
	410407	X66839	Hs.63287 Hs.44269	ESTs	Ald_Xan_dh_C,FAD_binding_5,TM,	2.15
	420900	AL045633 AA468183	Hs.184598		TM	2.15
	419239 452721	AJ269529	Hs.30377	Homo sapiens ES	TM	2.15
50	432721	NM_006033	Hs.65370	lipase, endothe	Ribosomal_L22,lipase,PLAT,TM,SS	2.14
20	452835	AK001269	Hs.30738	hypothetical pr	TM	2.14
	452092	BE245374	Hs.27842	hypothetical pr	Acytransferase,TM,SS	2.14
	401708	DEETSOIT	16.27042	ii) posioooo p	SS	2.14
	411400	AA311919	Hs.69851	GAR1 protein	TM	2.14
55	448526	AB028946	Hs.21361	KIAA1023 protei	TM	2.14
	421175	AI879099	Hs.102397		z1-C2H2,KRAB,TM,SS	2.14
	413511	AI627178	Hs.75412	Arginine-rich p	TM	2.13
	432945	AL043683	Hs.271357	•	PK,SS	2.13
	418592	X99226	Hs.284153		TM	2.13
60	425298	AK000209	Hs.155556		TM	2.13
	450956	AW193531	Hs.205647		pkise,TM,SS	2.13
	419569	AI971651	Hs.91143	jagged 1 (Alagi	EGF,DSL,TM,SS	2.13
	421508	NM_004833			TM	2.13
	413670	AB000115	Hs.75470	hypothetical pr	TM	2.13
65	422783	AA598956	Hs.120439	ethanolamine ki	Choline_kise,TM,	2.13
	410418	D31382	Hs.63325	transmembrane p	trypsin,ldl_recept_a,TM,SS	2.13
	414860	BE255593	Hs.77502	methionine aden	S-AdoMet_synt,SS	2.13
	425860	L29339	Hs.1964	solute carrier	SSF,Ribosomal_S17e,TM,	2.13
	414839	X63692	Hs.77462		zi-cxxc,bah,tm,ss	2.13
70	437050	AA766420	Hs.291600		TM	2.13
	430217	N47863	Hs.18045		TM,SS	2.13
	409012	AL117435	Hs.49725		RhoGEF,TM,	2.12
	428365	AA295331	Hs.18386		TM	2.12
~~	410839	NM_006849			thiored,TM,	2.12 2.12
75	450510	AA010056	Hs.24299		TM,SS	2.12
	427475	AA403151	Hs.19160		SS AND hinding Yea	2.12
	433748	R12244		gb:yf33c12.r1 S	AMP-binding, TM,	2.12
	415138		Hs.78045		Kunitz_BPTI,G-gamma,TM,SS	211
90	414788		Hs.77313		pkise,TM,SS	2.11
80	415474				mito_carr,TM,	2.11
	416472		Hs.19309		TM cae pey three	2.11
	410718		Hs.19143		SOS_PSY,TM,SS	211
	425811	AL039104	Hs.15955	7 karyophesin alp	Armadillo_seg,IBB,TM,SS	£11

						2.11
	447197	R36075		gb:yh88b01.s1 S	SDF,TM,	2.11
	431621	AW292329	,	ESTS	PH,Band_41,TM,SS SS	2.11
	433849 438038	BE465884 AI732629	Hs.280728 Hs.194161	ESTs ESTs, Weakly si	Cytidylyltrans,TM,	2.11 2.11
5	422032	AA476966	Hs.110857	polymerase (RNA	TFIIS,TM,SS	2.11
•	409717	AW452871	Hs.56043	CGI-115 protein	TM TM	2.11
	445837	AI261700	Hs.145544 Hs.134200	ESTs DKFZP564C186 pr	TM	2.10
	423880 421574	BE278111 AJ000152	Hs. 134200 Hs. 105924	defensin, beta	Defensin_beta,TM,SS	2.10 2.10
10	437103	AW139408	Hs.152940	ESTs	Chaline_kise,TM,	2.10
	450747	AI064821	Hs.48306	ESTs, Highly si	rm,TM, TM	2.10
	437033	AW248364	Hs.5409	RNA polymerase protein C recep	TM.SS	2.10
	417640 431120	D30857 AA492588	Hs.82353	gb:ng99c08.s1 N	TM,SS	2.10 2.10
15	430510	AW162916	Hs.241576	hypothetical pr	TM	2.10
1.5	429669	BE185499	Hs.2471	KIAA0020 gene p	TM SS	2.10
	407881	AW072003	Hs.40968 Hs.5181	heparan sulfate proliferation-a	Peptidase_M24,TM,SS	2.10
	435415 407887	8E265254 AA579668	Hs.41072	serine (or cyst	serpin,TM,	2.10 2.09
20	447815	Al432199	Hs.247084	ESTs	UM,TM,	2.09
	434274	AA628539	Hs.116252	ESTs, Moderatel	rm,TM,SS SS	2.09
	411571	AA122393	Hs.70811 Hs.145945	hypothetical pr ESTs	pkise,TM,	2.09
	442525 423750	AF150282 AF165883	Hs.132415	prefoldin 2	TM	2.09 2.09
25	449199	AI990122	Hs.196988	ESTs	ras,TM,	2.09
	415363	AI670947	Hs.78406	phosphatidylino	P1P5K,pkise,TM,SS integrin_B,fn3,TM,SS	2.09
	418462	BE001596	Hs.85266	integrin, beta KIAA0185 protei	S1,TM,	2.08
	430335 443450	D80007 N66045	Hs.239499 Hs.133529	ESTs	TM	2.08 2.08
30	418753	BE217818	Hs.87016	Homo sapiens cD	TM	2.08
	439018	AW300887	Hs.26638	ESTs, Wealdy si	TM,SS SH3.SS	2.08
	431628	AF146277	Hs.265561 Hs.15243	CD2-associated nucleolar prote	No.1 No.2 Sun,TM,	2.08
	446528 411372	AU076640 AI147861	Hs.19243 Hs.213289		EGF,ldl_recept_a,ldl_recept_b,TM,SS	2.08 2.08
35	459319	NM_000059		gb:Homo sapiens	BRCA2_repeat,TM,	2.08
	408730	AV660717	Hs.47144	DKFZP586N0819	p TM,SS TNFR_c6,death,TM,	2.08
	409220	BE243323	Hs.51233	tumor necrosis lipocalin 2 (on	lipocalin, SS	2.08
	429504	X99133 AK000002	Hs.204238 Hs.55879	Homo sapiens mi	AND AND HARMON THE	2.08
40	409686 413092		Hs.11866		EGF,TM,SS	2.08 2.08
70	413715			Homo sapiens cD	) cyclin,TM, TM	2.07
	423020		Hs.1608	replication pro Homo sapiens co		2.07
	438378					2.07 2.07
45	432125 449370			·	TM,SS	2.07
,,,	454011		Hs.37009		alk_phosphatase,TM,SS TM	2.07
	427876		Hs.11197		SS	2.07
	42290° 44920°		Hs.12157 Hs.23255		TM,SS	2.07 2.07
50	40824		Hs.624	interleukin 8	IL8,TM,SS	2.07
	44654	6 BE167687			Sulfotransfer,TM,SS TM	2.07
	42347					2.07
	43621 45615			gb:EST391263		2.06 2.06
55	40714		~ Hs.2489	68 EST	TM	2.06
	43244	o x63597	Hs.2996		Glyco_hydro_31,trefoil,TM,SS TM	2.06
	41066				BIR,TM,	2.06
	42276 43983		Hs.1487		SS	2.06 2.06
60	4453	-			TM	2.06
	4399	51 AI347067			TM,SS TM	2.06
	4283		Hs.1839 Hs.4709			2.06
	4325 4330			-		2.06 2.06
65	4337			118 ESTs	TM	2.06
	4294	12 NM_006			da TM TM	2.06
	4490				0.40 - 1.0.714	2.06
	4370 4425				si SS	2.06 2.06
70	4557			gb:CM2-BT069		2.06
	4399	75 AW3280	081 Hs.681			2.06
	4330					2.06
	440					2.05
7:	436 5 411			192 heat shock pro	M HSP70,TM,	2.05 2.05
, ,	409	459 D86407	1 Hs.544	181 low density lip		2.05
	436				SI MMR_NORT, IM,	2.05
	400 421				r SS	2.05
8	0 417	850 AA215		741 primase, poly	pe SS	2.05 2.05
•	417	491 AW376	842 Hs.10	85 guanytate cyc		2.05
		775 NM_00			TM	2.05
	435	525 AI8312	:ar ms.12	3310 ESTs		

	412627	BE391959	Hs.74276	chloride intrac	G-patch.ig,MutS_C.TM.	2.05
	439702	AW085525	Hs.134182	ESTs .	A2M,SS	2.05
	440006	AK000517	Hs.6844	hypothetical pr	TM	2.05 2.05
5	417308 446311	H60720 AW007294	Hs.81892 Hs.149795	KIAA0101 gene p ESTs, Wealdy si	TM pkise,TM,	2.05
•	427871	AW992405	Hs.59622	ESTs, Wealthy si	SS	2.05
	453804	AA300204	Hs.35276	KIAA0852 protei	TM,SS	2.05
	449939	T86420	Hs.272139	ESTs	DIL,myosin_head,TM,SS	2.05
10	417819	AJ253112	Hs.133540	ESTs	TM	2.04 2.04
10	427747	AW411425	Hs.180655	serine/threonin ESTs	pkise,TM, TM	2.04
	415009 437829	C75253 AI358522	Hs.220950 Hs.270188	ESTs	TM	2.04
	428753	AW939252	Hs.192927	hypothetical pr	TM	2.04
	446475	AI908188	Hs.209245	ESTs .	OPR,TM,	2.04
15	431394	AK000692	Hs.252351	HERV-H LTR-asso	ig,TM,SS	2.04
	423701	AA329856	Hs.143022	ESTs	TM	2.04 2.04
	422369 432481	AF005216 AW451645	Hs.115541 Hs.151504	Janus kinase 2 Homo saoiens cD	SH2,pkise,TM, TSPN,Cotlagen,TM,SS	2.04
	443746	AW861379	Hs.160602	ESTs	TM	2.04
20	400792	AA635062	Hs.50094	Homo sapiens mR	zf-C3HC4,CARD,BIR,TM,	2.04
	428343	AL043021	Hs.12705	ESTs, Wealty si	TM	2.04
	419329	AY007220	Hs.288998	S100-type calci	TM	2.04
	403485			4 . 4 . 499.444	filament,TM,	2.04 2.04
25	413313	NM_002047 AI379486	Hs.75280	glycyl-tRNA syn ESTs	WHEP-TRS,7tm_2,TM,SS TM	2.03
23	433326 440246	W52010	Hs.159430 Hs.191379	ESTs	serpin,TM,	2.03
	444006	BE395085	Hs.10086	type I transmem	TM,SS	2.03
	452705	H49805	Hs.246005	ESTs	TM	2.03
20	421724	AB037832	Hs.107287	KIAA1411 protei	TM	2.03
30	447474	AW614220	Hs.189402	ESTs	SS	2.03
	418852	BE537037	Hs.273294	hypothetical pr	TM TM,SS	2.03 2.03
	431842 440773	NM_005764 AA352702	Hs.271473 Hs.37747	epithelial prot hypothetical pr	TM	2.03
	443425	AI056776	Hs.133397	ESTs	TM,SS	2.03
35	407975	X89426	Hs.41716	endothelial cel	IGFBP,SS	2.03
	428299	AL038004	Hs.29419	ESTs	TM,SS	2.03
	415757	AA830854	Hs.187810	ESTs	TM	2.03
	432559	AW452948	Hs.257631	ESTs	PAC,TM,SS	2.03 2.02
40	425912 419395	AL137629 BE268326	Hs.162189 Hs.90280	serine/threonin 5-aminoimidazol	fn3,ig,PH,RhoGEF,TM,SS AICARFT_IMPCH28,MGS,TM,	2.02
70	417576	AA339449	Hs.82285	phosphoribosylg	AIRS,formyl_transf,GARS,TM,	2.02
	418559	AA225048	Hs.104207	ESTs	TM	2.02
	410855	X97795	Hs.66718	RAD54 (S.cerevi	SNF2_N,helicase_C,TM,	2.02
45	422072	AB018255	Hs.111138	KIAA0712 gene p	TM	2.02
45	419546	AA244199	N= 21012	gb:nc06c05.s1 N	Y_phosphatase,TM,	2.02 2.02
	450516 419807	AA902656 R77402	Hs.21943	NIF3 (Ngg1 inte gb:yi75f11.s1 S	DUF34,TM, TM	2.02
	438192	A1859065	Hs.16808	ESTs, Weakly si	TM,SS	2.02
	401866	,,,,,,,,,,		20.0,,	filament,TM,SS	2.02
50	443129	R16075	Hs.21668	ESTs	TM,SS	2.02
	424783	AA913909	Hs.153088	TATA box bindin	TM	2.01
	413293	AL047483	Hs.75270	GTP-binding pro	ras,TM,SS	2.01 2.01
	435787 422599	AW162767 BE387202	Hs.100914 Hs.118638	hypothetical pr non-metastatic	SS NDK.SS	2.01
55	431630	NM_002204		integrin, alpha	FG-GAP integrin_A TM,SS	2.01
	448275	BE514434	Hs.20830	synaptic Ras GT	kinesin,PHD,abhydrolase_2,TM,SS	2.01
	405484			•	filament, SS	2.01
	436469	AK001455	Hs.5198	Down syndrome c	IM	2.01 2.01
60	451273 432378	NM_014811		KIAA0649 gene p ESTs	TM TM	201
UU	419981	AJ493046 AA897581	Hs.146133 Hs.128773	ESTS	Ski_Sno,SS	2.01
	445808	AV655234	Hs.298083		sushi, TM, SS	2.01
	435767	H73505	Hs.117874		Peptidase_S8,P,TM,	2.01
/-	430466	AF052573	Hs.241517		TM	2.01
65	422790	AA809875	Hs.25933	ESTs	TM	2.01
	443303	U67319	Hs.9216	caspase 7, apop	ICE_p10,1CE_p20,TM, FG-GAP,TM,SS	2.01 2.01
	410008 440774	AA079552 AI420611	Hs.127832	gb:zm20h12.s1 S ESTs	zi-mynd,tm,ss	2.00
	442961	BE614474	Hs.289074		TM	2.00
70	424420	BE614743	Hs.146688		MAPEG,TM,SS	2.00
	410240	AL157424	Hs.61289	synaptojanin 2	TM	2.00
	435014	BE560898	Hs.10026	ribosomal prote	Ribosomal_L17,TM,	2.00
	406752	A1285598	Hs.217493	annexin A2	TM	2.00
75	TABLE 4	IIR.				
, 5	Pkey:		ique Eas arabe	set identifier number		
	CAT nur	nber: Ge	ene cluster num	ber		
	Accessic	on: Ge	enbank accessio	on numbers		
80	~	CAT				
ου	Pkey 410008	CAT numbe 116812_1		BE142525 BE142527		
	418546	176677_1		T59708 T59843 BE156903		
	419546	185766_1		AA244272 H57440		

```
R77402 AA262462 AA250988 R06794
         419807
                     188252_1
                                   AW856665 AA315006 AW954733
          422689
                    219896 1
                                   AA492588 AA492498 AA492571
                     328264 1
          431120
                                   R12244 H71290 Al110858 AF090916 AF075357 AA011531
          433748
                     37385_1
                                   AA781171 AI202139 AI202098
  5
          438223
                     452646_1
                                   AA828995 AA834879 AI926361
          438993
                     467651_1
                                   Al355012 AW812856
                     702707.1
          446995
                                   R36075 Al366546 R36167
T51387 AW191595 T51271 Al686285
                     711623_1
          447197
          450190
                     827655_1
                                    AW600293 AI767468
10
          451237
                     863269 1
                                    BE088746 BE088802 BE088755 BE088876 BE088947 BE088881 BE088952
                     1364506 1
          455778
                                    AW979153 AA176967 AA826015
                      158261_1
          456157
          TABLE 41C:
                             Unique number corresponding to an Eos probeset
15
                              Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA
          Pkey:
Ref:
                              sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
                              Indicates DNA strand from which exons were predicted.
           Strand:
                              Indicates nucleotide positions of predicted exons.
           Nt position:
20
                                                 Nt position
                                     Strand
                                                 78844-79025,80850-80991,89754-89941,93750-93891
                      9796594
           400514
                                     Minus
                                                 157315-157950
154511-155298
                      6649315
                                     Pius
           401519
                      2951946
                                     Plus
           401708
 25
                                                  73126-73623
                       8018106
                                     Plus
           401866
                                                  121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
           402075
                      8117407
                                     Plus
                                                  109532-110225
                      8748904
                                     Minus
           403055
                                                  147706-147903.148667-148804
                       7630829
                                     Minus
           403208
                                                  151169-151561
            403422
                       9665041
                                     Minus
 30
                                                  2888-3001,3198-3532,3655-4117
                       9966528
                                     Plus
            403485
                                                  1414-1513,1624-1756
173667-173783,176876-177055
            403776
                       7770611
                       9930793
                                     Plus
            404171
                                                  55675-56055
            404253
                       9367202
                                     Minus
                                                  12817-13000
                       8152000
                                     Plus
            404519
                                                  101320-101501
 35
                       7249169
                                     Minus
            404567
                                                  199214-199579.199672-199920,200262-200495
            405484
                        5922025
                                     Plus
                                                  118677-118807,119091-119296,121626-121823
            405545
                        1054740
                                     Plus
                                                  29055-29196
                        4071056
            405818
                                     Plus
                        9256288
                                                  63448-63554
            406399
  40
            TABLE 42A: ABOUT 561 GENES UP-REGULATED IN STOMACH CANCER
            Table 42A lists about 561 genes up-regulated in stomach cancer compared to normal stomach. These were selected as for Table 40A except using various non-malignant stomach
            specimens in determining the denominator value.

Pkey: Unique Eos probeset identifier number
  45
                                Exemplar Accession number, Genbank accession number
             ExAccn:
                                Unigene number
             UnigenelD:
                                Unigene gene title
             Unigene Title:
                                Ratio of tumor to normal fissue
   50
                                       UnigeneID
             Pkey
428368
                        FxAccn
                                                                                                       60.4
                                                   matrix metalloproteinase 3 (stromelysin
                        BE440042
                                       Hs.83326
                                                   Homo sapiens cDNA: FLJ23537 fis, clone L
                                                                                                       28.6
                                       Hs 228320
             448693
                        AW004854
                                                   similar to SALL1 (sal (Drosophila)-like
                                                                                                       26.8
                                       Hs.189095
             428664
                        AK001666
   55
                                       Hs.115263
                                                    epiregulin
                        D30783
             422330
                                                                                                       21.2
             415989
                         AI267700
                                       Hs_111128
                                                    ESTs
                                                    hypothetical protein FLJ 10430
                                                                                                       190
             439979
                         AW600291
                                       Hs.6823
                                                                                                       17.1
                                                    interleukin 13 receptor, alpha 2
                                       Hs.25954
             451099
                         R52795
              403776
                                                                                                        14.8
                                                    NIMA (never in mitosis gene a)-related k
   60
                         NM_002497
                                       Hs.153704
              424905
                                                                                                        14.2
                                       He ARARO
                                                    ESTs
              414132
                         A1801235
                                                                                                        14.0
                                                    a disintegrin and metalloproteinase doma
                         AA009647
                                       Hs.8850
             450375
453922
                                                                                                        13.B
                                                    budding uninhibited by benzimidazoles 1
                         AF053306
                                       Hs.36708
                                                                                                        13.1
                         AA150797
                                        Hs.109276
                                                    tatexin protein
              436032
                                                    collagen, type X, alpha 1 (Schmid metaph
IGF-II mRNA-binding protein 3
   65
                                                                                                        12.5
              427585
                         D31152
                                        Hs.179729
                                                                                                        12.2
                         AA634543
                                        Hs.79440
              416661
                                                                                                        10.6
                         BE263782
                                        Hs.77695
                                                     KIAA0008 gene product
              414972
                                                     Homo sapiens clone 24787 mRNA sequence
                                                                                                        10.5
              445900
                         AF070526
                                        Hs.13429
                                                     secreted phosphoprotein 1 (osteopontin,
                                                                                                        10.5
               446619
                         AU076643
                                        Hs.313
                                                                                                        10.2
    70
                          BE218239
                                        Hs.202656
               AA1377
                                                     KIAA0007 protein
                          D26488
                                        Hs.90315
               419423
                                                                                                        9.6
                                                     tissue factor pathway inhibitor 2
               415138
                          C18356
                                        Hs.78045
                                                                                                        9.4
                          AI917494
                                        Hs.131329
                                                     ESTs
               424639
                                                                                                        9.2
                          AW975398
                                        Hs.293836
               412472
                                                     Homo sapiens cDNA: FLJ23537 fis, clone L
                                                                                                        8.9
    75
                          AW393080
                                        Hs.228320
               447048
                                                                                                        8.8
                                                     fidgetin-like 1
                          AA218940
                                        Hs.137516
               418379
                                                     replication protein A3 (14kD)
                                                                                                        8.6
                                        Hs 1608
               423020
                          AA383092
                                                                                                        8.5
                                                     serine/threonine kinase 15
                          BE296227
                                        Hs.48915
               408908
                                                                                                         8.3
                          AB041035
                                        Hs.93847
                                                     NADPH oxidase 4
               419948
                                                                                                         8.3
    80
                                                     KIAA0112 protein; homolog of yeast ribos
               411750
                          BE562298
                                        Hs.71827
                                                     gb:IL3-CT0214-291299-052-A12 CT0214 Homo
                                                                                                        8.1
               411479
                          AW848047
                                                                                                         8.0
                          AL045633
                                         Hs.44269
                                                     FSTs
               420900
               449347
                          AV549748
                                         Hs.295901
                                                     ESTs
```

	409041	AB033025	Hs.50081	KIAA1199 protein	8.0
	450480	X82125	Hs.25040	zinc finger protein 239	7.6
	417655	AA780791 AW964440	Hs.14014	ESTs, Wealdy similar to KIAA0973 protein ESTs	7.6 7.6
5	453878 430403	AF039390	Hs.19025 Hs.241382	tumor necrosis factor (ligand) superfami	7.5
-	427961	AW293165	Hs.143134	ESTs	7.4
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matritysin,	7.3
	426235 452291	AI631964 AF015592	Hs.34447 Hs.28853	ESTs CDC7 (cell division cycle 7, S. cerevisi	7.1 7.0
10	418205	L21715	Hs.83760	troponin I, skeletal, fast	7.0
	409757	NM_001898	Hs.123114	cystatin SN	6.9
	430044	AA464510 AK001468	Hs.152812 Hs.62180	ESTs anillin (Drosophila Scraps homolog), act	6.6 6.5
	444783 416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	6.5
15	449020	AJ621170	Hs.192699	ESTs	6.3
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	5.8
	434699 424345	AA643687 AK001380	Hs.149425 Hs.145479	Homo sapiens cDNA FLJ11980 fis, clone HE Homo sapiens cDNA FLJ10518 fis, clone NT	5.7 5.6
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	5.4
20	434551	BE387162	Hs.280858	ESTs, Highly similar to XPB_HUMAN DNA-RE	5.3
	427660 424960	A1741320 BE245380	Hs.114121 Hs.153952	Homo sapiens cDNA: FLJ23228 fis, clone C 5' nucleotidase (CD73)	5.0 4.9
	400268	60243000	113.133332	3 (100-3)	4.8
25	408427	AW194270	Hs.177236	ESTs	4.7
25	453785 411274	AI368236 NM_002776	Hs.283732 Hs.69423	ESTs katlikrein 10	4.7 4.7
·	424717	H03754	Hs.152213	wingless-type MMTV integration site fami	4.7
	415752	BE314524	Hs.78776	putative transmembrane protein	4.6
30	434370	AF130988	Hs.58346	downless (mouse) homolog	4.6 4.6
30	431806 400205	AF186114	Hs.270737	tumor necrosis factor (ligand) superfami	4.6
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	4.5
	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	4.4 4.4
35	453160 423871	AI263307 AA331906	Hs.146228	ESTs gb:EST35805 Embryo, 8 week I Homo sapien	4.4
-	431211	M86849	Hs.5566	gap junction protein, beta 2, 26kD (conn	4.4
	446638	AL133063	Hs.15783	Homo sapiens mRNA; cDNA DKFZp434P1115 (f	4.3
	406741 411560	AA058357 AW851186	Hs.74466	carcinoembryonic antigen-related cell ad gb:IL3-CT0220-150200-071-H05 CT0220 Homo	4.3 4.1
40	433159	AB035898	Hs.150587	kinesin-like protein 2	4.1
	446142	A1754693	Hs.145968	ESTs	4.1
	414727 422285	BE466904 AI803103		gb:hz28f03.x1 NCI_CGAP_GC6 Homo sapiens gb:tc14e06.x1 Soares_NhHMPu_S1 Homo sapi	4.1 4.1
	451807	W52854	Hs.27099	DKFZP564J0863 protein	4.1
45	411558	AA102670	Hs.70725	gamma-aminobutyric acid (GABA) A recepto	4.0
	415701 409420	NM_003878 215008	Hs.78619 Hs.54451	gamma-glutarnyl hydrolase (conjugase, fol taminin, gamma 2 (nicein (100kD), kalini	4.0 3.9
	452909	NM_015368	Hs.30985	pannexin 1	3.9
50	443211	A1128388	Hs.143655	ESTs	3.9
50	442896 407788	R37725 BE514982	Hs.261108 Hs.38991	ESTs S100 calcium-binding protein A2	3.8 3.8
	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	3.8
	421155	H87879	Hs.102267	lysyl oxidase	3.8
55	420552 420727	AK000492 H75701	Hs.98806 Hs.99886	hypothetical protein complement component 4-binding protein,	3.8 3.7
33	422665	AJ011812	Hs.119018	transcription factor NRF	3.7
	447425	AI963747	Hs.18573	acylphosphatase 1, erythrocyte (common)	3.7
	417715	AW969587	Hs.86366 Hs.137011	ESTs Homo sapiens mRNA; cDNA DKFZp547P134 (fr	3.7 3.6
60	406076 452281	AL390179 T93500	Hs.28792	Homo sapiens cONA FLJ11041 fis, clone PL	3.6
	412723	AA648459	Hs.179912	ESTs	3.6
	452461	N78223	Hs.108106	transcription factor	3.6 3.6
	453331 406434	A1240665	Hs.8895	ESTs	3.6
65	417956	AA210704	Hs.190465	ESTs	3.6
	410102	AW248508	Hs.279727		3.6
	426471 425782	M22440 U66468	Hs.170009 Hs.159525		3.5 3.5
	442556	AL137761	Hs.8379	Homo sapiens mRNA; cDNA DKFZp586L2424 (f	3.5
70	426957	AA393676	Hs.97459	ESTs, Weakly similar to KIAA0819 protein	3.5
	448105 414998	AW591433 NM_002543	Hs.170675 Hs.77729	ESTs, Wealtly similar to TMS2_HUMAN TRANS oxidised low density lipoprotein (lectin	3.5 3.5
	442942	AW167087	Hs.131562		3.4
75	416391	AI878927	Hs.79284	mesoderm specific transcript (mouse) hom	3.4
75	420230 408243	AL034344 Y00787	Hs.298020 Hs.624	Homo sapiens cDNA FLJ11796 fis, clone HE interteukin 8	3.4 3.4
	412978	AI431708	Hs.820	homeo box C6	3.4
	412851	AI826502	Hs.106149		3.4
80	417720 414812	AA205625 X72755	Hs.208067 Hs.77367	ESTs monotine induced by gamma interferon	3.4 3.4
30	453884	AA355925	Hs.36232	KIAA0186 gene product	3.4
	436396	AI583487	Hs.299112		3.4
	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitte	3.4

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					3.3
				ESTs absent in melanoma 1 like	3.3
			Hs.278359 Hs.108301	nuclear receptor subfamily 2, group C, m	3.3
				ESTs	3.3
5			Hs.152475	ESTs	3.3 3.3
	452826			ESTs, Moderately similar to PEX6_HUMAN P	3.3
	414821	M63835	Hs.77424 Hs.194290	Fc fragment of IgG, high affinity Ia, re ESTs	3.3
	413339 448756	AI818080 AI739241	Hs.171480	ESTs	3.3
10	421948	L42583	Hs.111758	karatia 6A	3.3
••	431453	AW753917		gb:RC0-CT0299-291199-031-F02 CT0299 Homo	3.3
	438538	AA832203	Hs.291955	ESTS	3.3 3.3
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	3.3
15	431721 436391	AB032996 AJ227892	Hs.268044 Hs.146274	KIAA1170 protein ESTs	3.3
13	442025	AW887434	Hs.11810	ESTs, Weakly similar to CD4.2 [C.elegans	3.3
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	3.2 3.2
	411678	AI907114	Hs.71465	squalene epoxidase	3.2
20	422956	BE545072 AI694722	Hs.122579 Hs.279744	hypothetical protein FLJ10461 ESTs	3.2
20	450400 453857	AL080235	Hs.35861	DKFZP586E1621 protein	3.2
	423528	AB011137	Hs.129740	KIAA0565 gene product	3.2
	440659	AF134160	Hs.7327	claudin 1	3.2 3.2
25	441085	AW136551	Hs.181245	Homo sapiens cDNA FLJ12532 fis, clone NT	3.2
25	412022	A1005043 X54942	Hs.24143 Hs.83758	ESTs CDC28 protein kinase 2	3.1
	418203 416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (	3.1
	408633	AW963372	Hs.46677	PRO2000 protein	3.1
	445808	AV655234	Hs.298083	ESTs	3.1 3.1
30	414618	A1204600	Hs.96978	ESTs decay accelerating factor for complement	3.1
	421340	F07783 AW856665	Hs.1369	gb:RC3-CT0297-290100-013-d03 CT0297 Homo	3.1
	422689 456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	3.1
	420759	T11832	Hs.127797	ESTs	3.1
35	452637	AW971231	Hs.291020	ESTs	3.1 3.1
	415857	AA866115	Hs.301646		3.1
	439451 424051	AF086270 AL110203	Hs.278554 Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	3.1
	440138	AB033023	Hs.6982	hynothetical protein FLJ10201	3.1
40	454456	AW850984		gb:IL3-CT0220-150200-068-H08 CT0220 Homo	3.0
	429125	AA446854	Hs.271004	ESTs	3.0 3.0
	408031	AA081395	Hs.42173	Homo sapiens cDNA FLJ10366 fis, clone NT CGI-124 protein	3.0
	438394 409361	BE379623 NM_005982	Hs.27693 Hs.54416	sine oculis homeobox (Drosophila) homolo	3.0
45	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	3.0
75	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	3.0 3.0
	422746	NM_004484			3.0
	424947	R77952	Hs.239625 Hs.35120		3.0
50	453775 449386	NM_002916 AA001308	Hs.193213		3.0
50	430687	BE274217	Hs.249247	heterogeneous nuclear protein similar to	29
	428862	NM_000346	Hs.2316	SRY (sex-determining region Y)-box 9 (ca	2.9 2.9
	401747			2 SMC1 (structural maintenance of chromoso	2.9
55	429682 444735		6 Hs.21160 Hs.24312		2.9
"	413385		Hs.840	indoteamine-pyrrole 2,3 dioxygenase	2.9
	436222		Hs.12281	0 Homo sapiens cDNA FLJ11489 fis, clone HE	2.9 2.9
	442961		Hs.28907	4 Homo sapiens cDNA FLJ13986 fis, clone Y7 gb:PM3-ST0307-241299-002-g03 ST0307 Homo	2.9
60	454798 421650		Hs.12258		2.9
UU	421650		Hs.3838	serum-inducible kinase	2.9
	420153		Hs.75277		2.9
	435706		Hs.7045	GL004 protein	2.9 2.9
65	416065		Hs.78996 Hs.12584		2.8
03	423250 423493		Hs.1296		2.8
	430242		Hs.2366	12 3-hydroxvisobutyryl-Coenzyme A hydrolase	2.8
	43641	1 AW67435	2	gb:ba63c07.y1 NIH_MGC_12 Homo sapiens cD	2.8
70	411770			2 heat shock protein (hsp110 family) gb:nz36g03.s1 NCI_CGAP_GC81 Homo sapiens	2.8 2.8
70	43783		Hs.8387		2.8
	40044 44474				2.8
	42872			2 ESTs	2.8
	41777	1 AA80469	3 Hs.8254	7 retinoic acid receptor responder (tazaro	2.8 2.8
75	44942				2.8
	43392				2.8
	43028 42334				2.8
	40782	4 AA14788	4 Hs.9812	ESTS .	2.8
80	40848	2 NM_0006			2.8 2.8
	42518				2.8
	45699 40887				2.8
	-10001			•	

	407839	AA045144	Hs.161566	ESTs	27
	409012	AL117435	Hs.49725	OKFZP434I216 protein	2.7
	410762 426925	AF226053 NM 001196	Hs.66170 Hs.172894	HSKM-8 protein BH3 interacting domain death agonist	2.7 2.7
5	410116	AW630671	Hs.58636	squamous cell carcinoma antigen recogniz	2.7
•	428398	A1249368	Hs.98558	ESTs	2.7
	400048	44240004	/ <b>3000</b> F	AFFX control: YEL002cW8P1	2.7 2.7
	412140 435664	AA219691 AX032087	Hs.73625 Hs.269819	RAB6 interacting, kinesin-like (rabkines ESTs	2.7
10	405695	700200	15.20013	2010	2.7
	456655	AI376736	Hs.111779	secreted protein, acidic, cysteine-rich	2.7
	408670 422576	AF160967 BE548555	Hs.46784 Hs.118554	potassium large conductance calcium-acti CGI-83 protein	2.7 2.7
	431379	AA504264	Hs.182937	peptidytprotyl isomerase A (cyclophilin	2.7
15	429540	M85776		gb:EST02297 Fetal brain, Stratagene (cat	2.7
	425874	N67325	Hs.247132	ESTs	2.7 2.7
	433183 409902	AF231338 Al337658	Hs.222024 Hs.156351	transcription factor BMAL2 ESTs	2.7
	422336	AI761322	Hs.115285	dihydrolipoamide S-acetyttransferase (E2	2.7
20	408434	AW195317	Hs.107716	Homo sapiens cDNA: FLJ22344 fis, clone H	2.7
	432328 407633	AI572739 NM_007069	Hs.195471 Hs.37189	6-phosphofructo-2-kinase/fructose-2,6-bi similar to rat HREV107	2.7 2.6
	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	2.6
06	422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38	2.6
25	445564 401644	AB028957	Hs.12896	KIAA1034 protein	26 26
	417479	AJ057052	Hs.133554	ESTs	26
	434217	AW014795	Hs.23349	ESTs	2.6
30	426514	BE616633 BE538690	Hs.301122	bone morphogenetic protein 7 (osteogenic gb:601064676F1 NIH_MGC_10 Homo sapiens c	26 26
30	414800 400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	26
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	2.6
	421246	AW582962	Hs.300961	ESTs, Highty similar to AF151805 1 CGI-4	2.6
35	430397 428048	AI924533 AA705745	Hs.105607 Hs.185070	ESTs ESTs	2.6 2.6
55	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	2.6
	440052	AI633744	Hs.195648	ESTs	26
	433077	AA314262	Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone H	2.6 2.6
40	432407 452401	AA221036 NM_007115	Hs.285026 Hs.29352	HERV-H LTR-associating 1 turnor necrosis factor, alpha-induced pro	2.6
. •	451813	NM_016117	Hs.27182	phospholipase A2-activating protein	2.6
	410889	X91662	Hs.66744	twist (Drosophila) hornolog (acrocephalos	2.6
	440100 413746	BE382685 AA133243	Hs.158549 Hs.171553	ESTs ESTs	26 26
45	414737	A1160386	Hs.125087	ESTs	26
	422063	BE156476		gb:QV0-HT0368-040100-082-c05 HT0368 Homo	2.6
	418250 437641	U29926 AA811452	Hs.83918 Hs.291911	adenosine monophosphate deaminase (isofo ESTs	2.6 2.6
	436027		Hs.39972	ESTs, Weakly similar to I38588 reverse t	2.6
50	444381	BE387335	Hs.283713	ESTs, Weakly similar to CA54_HUMAN COLLA	2.6
	452571	W31518 AW378065	Hs.34665 Hs.8687	ESTs ESTs	2.6 2.6
	452862 411984	NM 005419	Hs.72988	signal transducer and activator of trans	2.6
	446440	AV658411	Hs.42656	Homo sapiens cDNA FLJ12667 fis, clone NT	2.6
55	448663	BE614599	Hs.106823	H.sapiens gene from PAC 42616, similar t	2.6 2.6
	426427 445848	M86699 AA774824	Hs.169840 Hs.13377	TTK protein kinase Homo sapiens clone 23649 and 23755 unkno	2.6
	420022	AA256253	Hs.120817	ESTs	2.6
60	451418	BE387790	Hs.26369 Hs.194676	hypothetical protein FLJ20287	2.6 2.6
UU	428953 424008	AA306610 R02740	Hs.194676 Hs.137555	DKFZP434C013 protein putative chemokine receptor; GTP-binding	2.6
	417863	AB000450	Hs.82771	vaccinia related kinase 2	2.6
	414987	AA524394	Hs.165544	ESTs	2.6 2.6
65	440249 407966	A1246590 AA295052	Hs.125325 Hs.38516	ESTs ESTs	2.5
05	406685	M18728	14.55514	gb:Human nonspecific crossreacting antig	2.5
	403204				2.5
	436961 422260	AW375974 AA315993	Hs.156704 Hs.105484		2.5 2.5
70	444471	AB020684	Hs.11217	KIAA0877 protein	2.5
	430290	Al734110	Hs.136355	ESTs	2.5
	413670 421928	AB000115 AF013758	Hs.75470 Hs.109643	hypothetical protein, expressed in osteo polyadenylate binding protein-interactin	2.5 2.5
	439580	AF086401	Hs.293847		2.5
75	439963	AW247529	Hs.6793	platelet-activating factor acetyfhydrola	2.5
	457065	AJ476318	Hs.192480 Hs.58248	ESTs ESTs	2.5 2.5
	439521 426711	AI808955 AA383471	Hs.180669		2.5
00	422631	BE218919	Hs.118793	hypothetical protein FLJ10688	2.5
80	417866	AW067903	Hs.82772		2.5 2.5
	416975 415947	NM_004131 U04045	Hs.1051 Hs.78934	granzyme B (granzyme 2, cytotoxic T-lymp mutS (E. coli) homolog 2 (colon cancer,	2.5 2.5
	454678	AW813089		gb:RC3-ST0186-240400-111-b05 ST0186 Harno	2.5

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	424000	AW189983	Hs.139119		2.5
				hynothetical grolein FLJ11183	2.5
		AW445167	Hs.126036		2.5 2.5
_				ESTs, Weakly similar to ALU1_HUMAN ALU S hypothetical protein FL110512	2.5
5	408750 451177		He 13034	FSTs	2.5
	449318	AW236021	He 108788	ESTs. Weakly similar to zeste (D.melanog	2.5
	434414	A1798376		gb:tr34b07.x1 NCI_CGAP_Ov23 Homo sapiens	2.5 2.5
10	400240		11- 424705	ESTs	2.5
10	410519	AW612264 AI683036	Hs.131705 Hs.124135	KIAA1618 protein	2.5
	440953 421190	U95031	Hs.102482	mucin 5, subtype B, tracheobronchial	25
	444478	W07318	Hs.240	Munhasa ohosphoorotein 1	2.5 2.5
4.5	442295	AJ827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	25
15	420894	AA744597 BE147897	Hs.88854 Hs.58593	ESTs general transcription factor IIF, polype	2.4
	410094 413998	AW103807	Hs.243933	ESTs	2.4
	412281	AI810054	Hs.14119	ESTs ·	2.4 2.4
••	418105	AW937488	Hs.178000	ESTs protein phosphatase 1, regulatory (inhib	2.4
20	447335	8E617695	Hs.286192 Hs.257479	ESTs, Wealdy similar to AF147747 1 BOG25	2.4
	446852 408915	AW451643 NM_016651	Hs.48950	heptacellular carcinoma novel gene-3 pro	24
	442991	BE281238	Hs.8886	hypothetical protein FLJ20424	2.4 2.4
~-	410193	AJ132592	Hs.59757	zinc finger protein 281	2.4
25	410664	NM_006033	Hs.65370 Hs.196105	lipase, endothefial ESTs	2.4
	449264 423453	A1637649 AW450737	Hs.128791	CGI-09 protein	2.4
	433757	Al949974	Hs.152670	ESTs	2.4 2.4
	411598	BE336654	Hs.70937	H3 histone family, member K ESTs, Weakly similar to B34087 hypotheti	2.4
30	431657	A1345227	Hs.105448 Hs.211587	phospholipase A2, group IVA (cytosolic.	24
	429663 428242	M68874 H55709	Hs.2250	leukemia inhibitory factor (cholinergic	2.4
	419559	Y07828	Hs.91096	ring finger protein	2.4
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	2.4 2.4
35	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi ESTs	2.4
	413281 402819	AA861271	Hs.34396	2018	2.4
	431457	NM_012211	Hs.256297	integrin, alpha 11	2.4
	422564	AI148006	Hs.222120	ESTs	2.4 2.4
40	443683	BE241717	Hs.9676	uncharacterized hypothalamus protein HT0 gb:Human nonspecific crossreacting antig	2.4
	407242	M18728 AA188827	Hs.7988	ESTs, Weakly similar to endo-alpha-D-man	2.4
	409235 408938	AA059013	Hs.22607	FSTs	2.4
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	2.4 2.4
45	423217	NM_000094		collagen, type VII, alpha 1 (epidermolys	2.4
	408321	AW405882 NM_000216	Hs.44205 Hs.89591	cortistatin Kallmann syndrome 1 sequence	2.4
	419086 452945	AW978187	Hs.31086		2.4
	452234	AW084176	Hs.223296	6 ESTs	24 24
50	427722	AK000123	Hs.18047		24
	430399	AI916284	Hs.19967 Hs.20333	n ESTe	2.4
	450737 428513	AW007152 BE220806	Hs.18469		2.4
	405454				2.4 2.3
55	422168		Hs.11240		2.3
	421462		Hs.10462 Hs.30150		2.3
	403416 422039		Hs.82148	hypothetical protein	2.3
	448988		Hs.22785	gamma-aminobutyric acid (GABA) A recepto	2.3 2.3
60	429145		Hs.49031		2.3 2.3
	423198		Hs.1634 Hs.99519		2.3
	442914 449042				2.3
	421308			43 ESTs	2.3
65	41992	5 AW90099	2 Hs.9379	6 DKFZP586D2223 protein	2.3 2.3
	429993		Hs.2273		2.3
	44060		Hs.1266 Hs.1655		2.3
	44623 41017			1 DKFZP434C245 protein	2.3
70	45211		Hs.2800		2.3
	42249	3 AW47418	3 Hs.2338	116 ESTs	2.3 2.3
	40704		M. COFF	gb:H.sapiens SOD-2 gene for manganese su mitochondrial intermediate peptidase	2.3
	41109		Hs.6858 7 Hs.1699	R65 chimerin (chimaerin) 1	2.3
75	42645 44202			se neural precursor cell expressed, develop	2.3
, ,	44654		Hs.164	192 ESTs, Wealthy similar to Y161_HUMAN HYPOT	2.3 2.3
	42209	4 AF12953			2.3 2.3
	42193		Hs.1096 Hs.9899		23
80	43000 42080		Hs.133		2.3
50	4020			•	23 23
	4156	66 H72693		gb:yu03c11.r1 Soares fetal liver spleen	2.3
	4327	43 Al14696	6 Hs.101	656 ESTs	

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					••
	433409 408330	AJ278802 AW182602	Hs.25661 Hs.249954	ESTs ESTs	2.3 2.3
	407807	AL031427	Hs.40094	Human DNA sequence from clone 167A19 on	2.3
•	436972	AA284679	Hs.25640	claudin 3	2.3
5	436747 433730	AW977192 AK002135	Hs.291343 Hs.3542	ESTs hypothetical protein FLJ11273	2.3 2.3
	414839	X63692	Hs.77462	DNA (cytosine-5-)-methyttransferase 1	2.3
	438192	AJ859065	Hs.16808	ESTs. Weatily similar to paraplegin-like	2.3
10	415339	NM_015156	Hs.78398	KIAA0071 protein	2.3 2.2
10	449539 412651	W80363 AA115333	Hs.58446 Hs.107968	ESTs ESTs	2.2
	450956	AW193531	Hs.205647	ESTs, Moderately similar to ALU1_HUMAN A	2.2
	430335	D80007	Hs.239499	KIAA0185 protein	2.2
1.5	417849	AW291587	Hs.82733	nidogen 2	2.2
15	454946	AW846376	Lln 72017	gb:QV0-CT0179-090200-090-09 CT0179 Homo small inducible cytokine A3 (homologous	2.2 2.2
	412326 408349	R07566 BE546947	Hs.73817 Hs.44276	homeo box C10	2.2
	424704	AI263293	Hs.152096	cytochrome P450, subfamily IIJ (arachido	2.2
20	419433	AA814807	Hs.7395	hypothetical protein FLJ23182	2.2
20	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	2.2 2.2
	415323 417531	BE269352 NM_003157	Hs.949 Hs.1087	neutrophil cytosolic factor 2 (65kD, chr serine/threonine kinase 2	2.2
	403137	M.M000101			2.2
25	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	2.2
25	430200	BE613337	Hs.234896	gerninin	2.2 2.2
	433745 425390	AF075320 Al092634	Hs.28980 Hs.156114	Homo sapiens clone HQ0270 protein tyrosine phosphalase, non-recept	2.2
	408380	AF123050	Hs.44532	diubiquitin	2.2
20	422424	AI186431	Hs.116577	prostate differentiation factor	2.2
30	431548	AI834273	Hs.9711	Homo sapiens cDNA FLJ13018 fis, clone NT six transmembrane epithelial antigen of	2.2 2.2
	400298 428771	AA032279 AB028992	Hs.61635 Hs.193143	KIAA1069 protein	2.2
	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	2.2
2.5	442573	н93366	Hs.7567	Homo sapiens cDNA: FLJ21962 fis, clone H	2.2
35	412802	U41518	Hs.74602 Hs.266273	aquaporin 1 (channel-forming integral pr	2.2 2.2
	412530 414761	AA766268 AU077228	Hs.77256	Homo sapiens cDNA FLJ13346 fis, clone OV enhancer of zeste (Drosophila) homolog 2	22
	408432	AW195262	1.5.77.250	gb:xn67b05.x1 NCI_CGAP_CML1 Homo sapiens	2.2
40	440283	A1732892	Hs.190489	ESTs	2.2
40	429568	AI088691	Hs.208414	Homo sapiens mRNA; cDNA DKFZp564D0472 (f Homo sapiens BAC clone RP11-120J2 from 7	2.2 2.2
	424003 425300	BE274717 AW601773	Hs.137506 Hs.270259	ESTs	2.2
	448568	AA149121	Hs.71947	ESTs	2.2
	419229	AI827237	Hs.282884	ESTs	2.2
45	420982	AW576160	Hs.100729	KIAA0692 protein	2.2 2.2
	403258 439653	AW021103	Hs.6631	hypothetical protein FLJ20373	2.2
	426827	AW067805	Hs.172665	methylenetetrahydrofolate dehydrogenase	2.2
	444514	AI682905	Hs.270431		2.2
50	426298	AW965058	Hs.111583		2.2 2.2
	425322 421662	U63630 NM 014141	Hs.155637 Hs.106552		2.2
	412505	AA974491	Hs.21734	ESTs	2.2
	438788	AA825716		gb:od29e10.s1 NCI_CGAP_GCB1 Homo sapiens	2.2
55	429058	AF138863	Hs.194827		2.2 2.2
	423104	AJ005273 AI969703	Hs.123647 Hs.301842		2.2
	410406 443180	AI969703 R15875	Hs.70945	ESTS	2.2
	419235	AW470411	Hs.288433		2.2
60	421379	Y15221	Hs.103982	· · · · · · · · · · · · · · · · · · ·	2.2
	422809 415058	AK001379 AW902848	Hs.121028 Hs.273829		2.2
	418049	AA211467	Hs.190488		2.2
	436209	AW850417	Hs.254020	ESTs, Moderately similar to unnamed prot	2.2
65	408042	AL049233	Hs.42244	Homo sepiens mRNA; cDNA DKFZp564A023 (fr	2.2 2.2
	425692 409665	D90041 NM_006731	Hs.155956 Hs.55777	N-acetytransferase 1 (arylamine N-acety Fukuyama type congenital muscular dystro	2.2
	409005	AI738719	Hs.298668		2.2
~^	410480	R97457	Hs.63984	cadherin 13, H-cadherin (heart)	2.2
70	429732	U20158	Hs.2488	tymphocyte cytosolic protein 2 (SH2 doma	2.2 2.2
	414747 425843	U30872 BE313280	Hs.77204 Hs.159627	centromere protein F (350/400kD, mitosin death associated protein 3	2.2
	425843 445299	AI910382	Hs.118727		2.1
~-	436251	BE515065	Hs.5092	nucleolar protein (KKE/O repeat)	2.1
75	430066	AI929659	Hs.237825		21
	422516		Hs.117950 Hs.40719		2.1 2.1
	407870 416109		Hs.126550		2.1
	427528	AU077143	Hs.17956	5 minichromosome maintenance deficient (S.	2.1
80	448089	Al467945	Hs.17369		2.1 2.1
	441790 400022		Hs.13220	B ESTs AFFX control: STAT1	2.1
	428728		Hs.19138		2.1
		•			_

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	414366	BE549143	11- 177610	gb:601076456F1 NIH_MGC_12 Homo sapiens c	2.1 2.1
	409929 405264		Hs.172619	•	2.1
5	445625 408949	BE246743 AF189011	Hs.288529 Hs.49163	Homo sapiens cDNA: FLJ22635 fis, clone H putative ribonuclease III	2.1 2.1
,	424513	BE385864	Hs.149894	mitochondrial translational initiation f	2.1
	433683 442952	AI817723 AI743261	Hs.22678 Hs.131860	hypothetical protein FLJ21832 ESTs	2.1 2.1
	441020	W79283	Hs.35962	ESTs	2.1
10	446770	AV660309	Hs.154986	ESTs, Weakly similar to AF137386 1 plasm	2.1 2.1
	432378 447769	A1493046 AW873704	Hs.146133 Hs.48764	ESTs ESTs	2.1
	412654	AI093480	Hs.29263	Homo sapiens cDNA FLJ11896 fis, clone HE	2.1 2.1
15	445669 417979	AI570830 AU077284	Hs.174870 Hs.83081	ESTs GTP cyclohydrolase I feedback regulatory	2.1
13	433849	8E465884	Hs.280728	ESTs	2.1
	437928	NM_005476	Hs.5920	UDP-N-acetylglucosamine-2-epimerase/N-ac gb:QV1-HT0639-150500-198-e03 HT0639 Homo	2.1 2.1
	457341 452833	BE181716 BE559681	Hs.30736	KIAA0124 protein	2.1
20	403055			FOT	2.1 2.1
	414581 432840	AA256213 AK001403	Hs.72010 Hs.279521	ESTs hypothetical protein FLJ20530	2.1
	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecul	2.1
25	440908	A1915225	Hs.126735	ESTs interferon-induced, hepatitis C-associat	21 21
23	417621 436895	AV654694 AF037335	Hs.82316 Hs.5338	carbonic anhydrase XII	2.1
	455716	BE070263		gb:QV4-BT0407-280100-090-e07 BT0407 Homo	2.1 2.1
	408420 435849	NM_006915 BE305242	Hs.299481 Hs.112442	Homo sapiens mRNA; cDNA DKFZp58680118 (f ESTs, Wealdy similar to CLDE_HUMAN CLAUD	21
30	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	2.1
	433644	AW342028	Hs.256112	ESTs AFFX control: STAT1	2.1 2.1
	400020 434064	AL049045	Hs.180758	hypothetical protein PRO0082	2.1
25	410660	AI061118	Hs.65328	Fanconi anemia, complementation group F	2.1 2.1
35	404076 441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) hornolog (E coli Re	2.1
	422515	AW500470	Hs.117950	multifunctional polypeptide similar to S	2.1 2.1
	444863	AW384082 AF272663	Hs.301323 Hs.13405	ESTs gephyrin	2.1
40	445867 441021	AP 27 2003 AW 5787 16	Hs.7644	H1 histone family, member 2	2.1
	446595	T57448	Hs.15467	hypothetical protein FLJ20725	2.1 2.1
	417515 412429	L24203 AV650262	Hs.82237 Hs.75765	ataxia-telangiectasia group D-associated GRO2 oncogene	2.1
4.5	449207	AL044222	Hs.23255	nucleoporin 155kD	2.1 2.1
45	412095 400861	AI624707	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	2.1
	448826	AI580252	Hs.293246		21
	440591	AA431599 AA371422	Hs.132799 Hs.69844		2.1 2.1
50	426181 452880	AA029332	Hs.87549	ESTs	21
	421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE phosphodiesterase 4B, cAMP-specific (dun	2.1 2.1
	442104 427224	L20971 AL135554	Hs.188 Hs.10193	7 sine oculis homeobox (Drosophila) homolo	2.1
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	2.1 2.1
55	432487 429534	AA550988 AW976987	Hs.221477 Hs.16332		2.1
	446051	BE048061	Hs.15331	5 ESTs	2.1
	447760	AI431328 BE018517	Hs.29117 Hs.11914		21 21
60	422675 415173	AW501735	Hs.25301	5 ESTs	2.1
	425170		Hs.15497		2.1 2.1
	453751 426283	R36762 NM_00393	Hs.10128 7 Hs.16913	9 kynureninase (L-kynurenine hydrolase)	2.1
	417874	BE616160	Hs.82829	protein tyrosine phosphatase, non-recept	21 21
65	449555 439699		Hs.19539 Hs.18756		2.1
	427413	BE547647	Hs.17778	31 superoxide dismutase 2, mitochondrial	2.1
	424673		Hs.29409 Hs.39913		2.1 2.0
70	407802 452834		Hs.10568	BS ESTs	20
	438899	AW007021		4 ESTs	2.0 2.0
	446035 406981		8 Hs.13569 Hs.2968		2.0
	427001	NM_00648	2 Hs.1731	35 dual-specificity tyrosine-(Y)-phosphoryl	2.0
75	439223 432343				2.0 2.0
	43234	) BE281095	Hs.7757	3 uridine phosphorylase	2.0
	423019	A1640185	Hs.2258		2.0 2.0
80	43590 42227				2.0
	43960	8 AW86469	6 Hs.2619	8 Homo sapiens cDNA: FLJ23363 fis, clone H	2.0 2.0
	43211 40554		Hs.2255	97 ESTs	20

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			11-00440	Maria anciena abilia. El Ibrara el Irra	20
	418201	AA214345	Hs.98445	Homo sapiens cDNA: FLJ21652 fis, clone C	2.0 2.0
	442528 446237	AF150317 AW270515	Hs.134217 Hs.149596	ESTs ESTs	2.0
	428074	BE387770	Hs.182378	colony stimulating factor 2 receptor, al	20
5	423430	AF112481	Hs.128501	RAD54, S. cerevisiae, homolog of, B	20
•	435767	H73505	Hs.117874	ESTs	2.0
	432945	AL043683	Hs.271357	ESTs, Weakly similar to unnamed protein	20
	428792	BE535955	Hs.193602	chromosome condensation protein G	20
	404170				20
10	410286	AI739159	Hs.61898	DKFZPS86N2124 protein	20
	434565	T52172		gb:yb22d01.s1 Stratagene fetal spleen (9	20
	422610	AF153820	Hs.1547	potassium inwardly-rectilying channel, s	20 20
	417933	X02308	Hs.82962	thymidylate synthetase	20
15	441384	AA447849 AI208149	Hs.288660 Hs.121196	protease, serine, 23 ESTs	2.0
13	437403 412673	AL042957	Hs.31845	ESTS	20
	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	20
	438426	AA835936	Hs.269763	ESTs	2.0
	413943	AW294416	Hs.144687	ESTs	2.0
20	449001	AI619957	Hs.189854	ESTs	20
	427674	NM_003528	Hs.2178	H2B histone family, member Q	2.0
	435425	H16263	Hs.31416	ESTs	2.0
	433364	AI075407	Hs.296083	ESTs	20
25	429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain	20
25	417366	BE185289	Hs.1076	small proline-rich protein 1B (comifin)	2.0 2.0
	426746	J03626	Hs.2057	uridine monophosphate synthetase (orotat	20
	411943	BE502436	Hs.7962	ESTs, Weakly similar to putative [C.eleg	20
	414266 432677	BE267834 NM_004482	Hs.278611	gb:601124428F1 NIH_MGC_8 Homo sapiens cD UDP-N-acetyl-alpha-D-galactosamine:polyp	20
30	450534	AI570189	Hs.25132	KIAA0470 gene product	20
50	446715	AI337735	Hs.173919		20
	410110				
	TABLE 42	<b>8</b> :			
	Pkey:	Unic	que Eos probes	set identifier number	
35	CAT numl	per. Gen	e cluster numb	er	
	Accession	: Gen	bank accessio	n numbers	
	Pkey	CAT number		D07000 A11/044000	
40	408432	1058667_1	AW195262	R27868 AW811262	121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069 AW848905
40	411479	1247077_1	AW848214	AND40202 AND40031 AND40142 AND40102 AND40	TEL MICHOGE MICHOLINA INC.
	411560	1249443_1		AW996967 BE143456	
	411366	1430984_1		BE514180 BE514096	
	414366	1438636_1		BE390613 BE277344	
45	414727	1481204_1	BE466904		
15	414800	1491863_1	BE538690		
	415666	1543492_1		18673 H72694 F20990 R08580	
	422063	210852_1	BE156476	BE156473 BE156474 BE156475 AA302839	•
	422285	214669_1	AI803103 A	A1885143 AW470793 AW450703 A1090784 AW271587	AW236950 AW242783
50	422689	219896_1		AA315006 AW954733	
	423871	232749_1	AA331906		
	429540	305828_1		A454535 AA456208 H90189	
	431453	333457_1	AW753917	BE152926 AA505333 BE155673	7858232 AW861851 AW858362 AA232351 AA218567 AA055556 AW858231
55	434414	38585_1	A17983/63	546400 AW811617 AW811616 WUUDDY BE 19229D AF   AMB	AA173345 AA199942 AA223384 AA227092 AA227080 T12379 AA092174 T61139
22			AVV63/343	AACDODDO AWGDOLGO AWG13567 AWG13538 AI2671	S8 AA157718 AA157719 AA100472 AA100774 AA130756 AA157705 AA157730
			AA157715	AANS3524 AWRAGSRI AWRSASSS COS254 AWRR2R36	T92637 AW812621 AA206583 AA209204 BE156909 AA226824 AI829309 AW991957
			NEEDS1 A	AS27174 HEE215 AAA45564 AIE94265 HEOROR AA149	726 AW195620 BE081333 BE073424 AW817662 AW817705 AW817703 AW817659
			BE081531		
60	434565	38898_1		147324 T52248	
-	436411	419334_1	AW67435	ΣΔΔ715374 725205	
	437834	443674_1	AA769294	AW749299 AW749302 AW749295 AW749304 AW74	293 AW749298 AW749294 AW749288 AW749291 AW749297 AW749292 AW749296
				9 AW749287 BE535498	
	438788	465159_1	AA825716	AW978859 AA828841	
65	454456	1207088_1	AW85098	4 AW752836 M86124	
	454678	1228915_1	AW81308	9 W28102	
	454798	1235104_1	AW82129	5 AW821272 AW821282	
	454946	1245753_1	AW84637	6 AW846375 AW846434 AW846287 AW846365 AW84	6554 AW846384 AW84629U AW846396 AYV846474
70	455716	1352695_1	BE070263	BE070195 BE070265 BE070202 BE070233 BE07035	9 8E0/0203
70	457341	322221_1	BE181716	3 AW948314 AW801848 AW948320 AW983981 AA484	444
	TABLE	nc.			
	TABLE 4		iana armhar a	orresponding to an Eos probeset	
	Pkey:	Ç1	raine universe a	The 7 digit numbers in this column are Genbank Ide	ntifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA
75	Ref:	36	quence of him	ian chromosome 22" Dunham, et al. (1999) Nature 402	:489-495.
, ,	Strand:	tn	ficates DNA st	rand from which exons were predicted.	
	Nt_posit			ide positions of predicted exons.	
				•	
	Pkey	Ref	Strand	Nt_pasition	
80	400861	9757506	Plus	163855-164016	
	401544	8576138	Plus	82655-83959	20422-120990,130161-130381,130468-130593,131097-131258,131866-31932,132451-
	401747	9789672	Minus		20122-120334, 130 101-13030 1, 130400-130333, 131431-131230, 131000-31332, 132431-
				132575,133580-134011	
					ā

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62703-63179
          402053
                     8083229
                                    Plus
                                                 29217-29422
                                    Plus
          402819
                     6729581
                                    Minus
                      8748904
          403055
                                                  92349-92572,92958-93084,93579-93712,93949-94072,94591-94748,95214-95337
                      9211494
           403137
                                     Minus
  5
                                                  16214-16439
           403204
                      7622392
                                    Plus
                                                  156251-156619
                                     Minus
           403258
                      7770439
                      7770611
                                                  1414-1513,1624-1756
                                     Minus
           403776
                      9931752
                                     Minus
                                                  3848-3967
168836-169248
           404076
           404170
                      9930793
                                     Plus
                                                  28556-28684
10
                                     Plus
           405264
                      7329374
                                                   133807-134053
           405454
                      7656675
                                     Plus
                                                   118677-118807,119091-119296,121626-121823
                      1054740
           405545
                                                  51860-52162
           405695
                      4309958
                                     Plus
                                                   17803-17931
           406434
                      9256651
                                     Minus
15
           TABLE 43A: ABOUT 339 GENES UP-REGULATED IN STOMACH CANCER
           Table 43A lists about 339 genes up-regulated in stomach cancer compared to normal stomach that are likely to be extracellular or cell-surface proteins. These were selected as for Table 42A and the predicted protein contained a structural domain that is indicative of surface or extracellular localization (e.g. ig, In3, egf, 7tm domains). Predicted protein domains
20
           are noted.
                               Unique Eos probeset identifier number
            Pkey:
                               Exemplar Accession number, Genbank accession number
            ExAccn:
                               Unigene number
            UnigenelD:
            Unigene Title:
                                Unigene gene title
 25
            PSDomain:
                                Protein Structural Domain
                                Ratio of turnor to normal tissue
            R1:
                                                                              PSDomain
                                      UnigenelD
Hs.83326
                                                   Unigene Title
                       ExAccn
            Pkey
                                                                              hemopexin,Peptidase_M10,,SS
                                                   matrix metallog
            428368
                        BE440042
                                                                              71-C2H2.TM.SS
                                      Hs.189095
                                                   similar to SALL
 30
                        AK001666
            428664
                                                                                                                                  22.0
                                                                              FGF.TM.SS
                                       Hs.115263
                                                   epiregulin
                        D30783
            422330
                                                                                                                                   19.0
                       AW600291
                                       Hs.6823
                                                   hypothetical pr
             439979
                                                                                                                                   17.1
                                                    interleukin 13
                                                                              m3,TM,SS
                                      Hs.25954
             451099
                        R52795
                                                                                                                                   14.9
                                                                              IL8.TM.SS
             403776
                                                                                                                                   14.8
                                       Hs.153704
                                                    NIMA (never in
                                                                              pkinase,TM,
  35
                        NM 002497
             424905
                                                                                                                                   13.8
             453922
                                       Hs.36708
                                                    budding uninhib
                                                                               TM
                        AF053306
                                                                                                                                   13.1
                                       Hs.109276
                                                                               TM
                                                    latexin protein
                        AA150797
             436032
                                                                                                                                   12.5
                                                                               C1q,Collagen,TM,SS
                                                    collagen, type
                                       Hs.179729
             427585
                        D31152
                                                                                                                                   12.2
                                                                               KH-domain,TM,
                        AA634543
                                       Hs.79440
                                                    IGF-II mRNA-bin
             416661
                                                                                                                                   10.6
                                                                               TM
  40
                        BE263782
                                       Hs.77695
                                                    KIAA0008 pene p
             414972
                                                                                                                                   10.5
                                                                               Osteopontin, TM, SS
                        AU076643
                                       Hs.313
                                                    secreted phosph
             446619
                                                                                                                                   9.6
                                                                               Kunitz_BPTI,G-gamma,TM,SS
                                                    tissue factor p
             415138
                        C18356
                                       Hs 78045
                                                                                                                                   86
                                                                               TM
                        AA383092
                                       Hs.1608
                                                    replication pro
             423020
                                                                               pkinase,TM,SS
                                                                                                                                   8.5
                        BE296227
                                        Hs.48915
                                                     serine/threonin
             408908
                                                                                                                                    8.3
                                                                                Ferric_reduct,TM,SS
  45
                         AB041035
                                       Hs.93847
                                                     NADPH oxidase 4
              419948
                                                     KIAA0112 protei
                        BE562298
AL045633
                                        Hs 71827
              411750
                                                                               Ald_Xan_dh_C,FAD_binding_5,TM,
                                                                                                                                    8.0
                                        Hs.44269
                                                     ESTs
              420900
                                                                               zl-C2H2,TM,SS
                                                                                                                                    7.6
                                                     zinc finger pro
                         X82125
                                        Hs.25040
              450480
                                                                                                                                    7.6
                                                                                TM
                                                     ESTs, Weakly si
                         AA780791
                                        Hs.14014
              417655
                                                                                TM,SS
   50
                                        Hs 241382
                                                     tumor necrosis
              430403
                         AF039390
                                                                                                                                    7.3
                                                                                Peptidase_M10,,SS
                                        Hs.2256
                                                     matrix metallop
                         1 22524
              428330
                                                                                                                                    7.0
                         AF015592
                                        Hs.28853
                                                     CDC7 (cell divi
                                                                                nkinase.TM.
              452291
                                                                                                                                    7.0
                                                                                Troponin,,SS
                                        Hs.83760
                                                     troponin I, ske
              418205
                         L21715
                                                                                                                                    6.9
                                                                                cystatin.,SS
                         NM_001898
AK001468
                                        Hs.123114
                                                     cystatin SN
              409757
                                                                                                                                    6.5
                                                                                PH.TM.
                                        Hs.62180
                                                     anillin (Drosop
   55
              444783
                                                                                HORMA, SS
                                                                                                                                    6.5
5.8
              416209
                         AA236776
                                        Hs.79078
                                                      MAD2 (mitotic a
                                                                                cadherin,Cadherin_C_term,TM,SS
              431958
                         X63629
                                        Hs.2877
Hs.145479
                                                      cadherin 3, typ
                                                     Homo sapiens cD
                                                                                 TM,SS
              424345
                         AK001380
                                                                                IL8,TM,SS
                                                                                                                                    5.4
                                                      small inducible
                                        Hs.2248
                         AA321649
              428227
                                                                                 5_nucleotidase,TM,SS
                                                                                                                                    49
   60
                                         Hs.153952
                                                      5 nucleotidase
              424960
                          BE245380
                                                                                                                                    4.8
                                                                                 Myosin_tail,,SS
              400268
                                                                                 trypsin,TM,
                                        Hs.69423
                                                      kallikrein 10
                          NM 002776
              411274
                                                                                                                                     4.6
                                         Hs.78776
                                                      putative transm
              415752
                         8E314524
                                                                                                                                     4.6
                                                                                 TM,SS
                                         Hs.270737
                                                      tumor necrosis
                          AF186114
              431806
                                                                                                                                     4.6
                                                                                 SS
   65
               400205
                          NM 001809
                                         Hs.1594
                                                      centromere prot
               422938
                                                                                                                                     4.4
4.4
4.4
                                                                                 hemopexin,TM,
                                         Hs.272620
                                                      pregnancy speci
                          M31126
               406687
                                                       gb:EST35805 Emb
                          AA331906
                                                                                 TM
               423871
                                                                                 connexin,TM,
                           M86849
                                         Hs.5566
                                                       gap junction pr
               431211
                                                                                                                                     4.3
    70
                          AI 133063
                                         Hs 15783
                                                       Homo sapiens mR
               446638
                                                                                 ig,TM,SS
TM
                                                                                                                                     4.3
                                         Hs.74466
                                                       carcinoembryoni
                           AA058357
               406741
                                                                                                                                     4.1
4.1
                           AW851186
                                                       gb:IL3-CT0220-1
               411560
                                                                                 kinesin, Myosin_tail, TM, SS
               433159
                           AB035898
                                          Hs.150587
                                                       kinesin-like pr
qb:tc14e06.x1 S
                                                                                                                                      4.1
4.1
                                                                                  TM,SS
               422285
                           AIB03103
                                          Hs.27099
                                                       OKFZP564J0863 p
                                                                                 TM
    75
                           W52854
               451R07
                                                                                  neur_chan,TM,SS
                                                                                                                                      4.0
                                                       gamma-aminobuty
                           AA102670
                                          Hs.70725
               411558
                                                                                                                                      4.0
                                                       gamma-olutamvi
                           NM_003878
                                          Hs.78619
                415701
                                                                                                                                      3.9
                                                                                  laminin_EGF,taminin_B,,SS
                                                       laminin, gamma
                                          Hs.54451
               409420
452909
                           715008
                                                                                                                                      3.9
                                                       pannexin 1
                           NM_015368
                                          Hs.30985
                                                                                  TM
                                                                                  efhand,S_100,TM,SS
                                                                                                                                      3.8
     80
                           BE514982
                                          Hs.38991
                                                       $100 calcium-bi
                407788
```

Lysyl_oxidase,.SS

sushi..

tysyt oxidase

hypothetical pr

complement comp

Hs.102267

Hs.98806

Hs.99886

421155

420552

420727

H87879

H75701

AK000492

3.8

3.8

					22 MT 200 BTD COLD	3.7
	422665 447425	AJ011812 AJ963747	Hs.119018 Hs.18573	transcription f acylphosphatase	R3H,G-patch,GTP_CDC,TM,SS Acytohosphatase,TM,	3.7
	406076	AL390179	Hs.137011	Homo sapiens mR	TM	3.6
	406434	AC030113	113.13.011	That is depicted in a	heme_1,TM,	3.6
5	417956	AA210704	Hs.190465	ESTs	sushi,,SS	3.6
•	410102	AW248508	Hs.279727	Homo sapiens cD	TM,SS	3.6
	426471	M22440	Hs.170009	transforming gr	EGF,TM,SS	3.5
	425782	U56458	Hs.159525	cell growth reg	SS	3.5
10	426957	AA393676	Hs.97459	ESTs, Weakly si	SS The	3.5 3.5
10	448105	AW591433	Hs.170675	ESTs, Weakly si	trypsin,TM, TM	3.5
	414998	NM_002543	Hs.77729	oxidised low de	pkinase,TM,SS	3.4
	442942 416391	AW167087 AI878927	Hs.131562 Hs.79284	mesoderm specif	abhydrolase,TM,SS	3.4
	420230	AL034344	Hs.298020	Homo sapiens cD	Fork_head,TM,	3.4
15	408243	Y00787	Hs.624	interleukin 8	ILB,TM,SS	3.4
	412978	AJ431708	Hs.820	homeo box C6	homeobox,TM,	3.4
	412851	AI826502	Hs.106149	ESTs	TM,SS	3.4
	414812	X72755	Hs.77367	monokine induce	nla_ss	3.4
	453884	AA355925	Hs.36232	KIAA0186 gene p	TM	3.4
20	425921	NM_007231	Hs.162211	solute carrier	SNF,TM,	3.4
	421787	AA227068	Hs.108301	nuctear recepto	TM	3.3
	447342	A1199268	Hs.19322	ESTs	TM,SS	3.3 3.3
	452826	BE245286	Hs.301636	ESTs, Moderatel	AAA,TM, ig,TM,SS	3.3
25	414821	M63835 Al739241	Hs.77424 Hs.171480	Fc fragment of ESTs	TM	3.3
23	448756 421948	L42583	Hs.111758	keratin 6A	filament,TM,	3.3
	438538	AA832203	Hs.291955	ESTs	TM	3.3
	436391	AJ227892	Hs.146274	ESTs	SS	3.3
	418007	M13509	Hs.83169	matrix metallop	hernopexin,Peptidase_M10,,SS	3.2
30	411678	AI907114	Hs.71465	squatene epoxid	Monooxygenase,TM,	3.2
•	422956	BE545072	Hs.122579	hypothetical pr	TM	3.2
	450400	AI694722	Hs.279744	ESTs	TM	3.2
	440659	AF134160	Hs.7327	claudin 1	PMP22_Claudin,TM,SS	3.2
	418203	X54942	Hs.83758	CDC28 protein k	CKS,TM,	3.1
35	416111	AA033813	Hs.79018	chromatin assem	TM,SS	3.1
	445808	AV655234	Hs.298083	ESTs	sushi,TM,SS	3.1 3.1
	421340	F07783	Hs.1369	decay accelerat	sushi,,SS	3.1
	422689	AW856665	U- 270564	gb:RC3-CT0297-2	SNF2_N,TM, chromo,Chromo_shadow.,SS	3.1
40	439451	AF086270	Hs.278554	heterochromatin gb:IL3-CT0220-1	fn3,TM,SS	3.0
40	454456 429125	AW850984 AA446854	Hs.271004	ESTs	TM	3.0
	409361	NM_005982	Hs.54416	sine oculis hom	homeoboxSS	3.0
	439453	BE264974	Hs.6566	thyroid hormone	AAA,TM	3.0
	414696	AF002020	Hs.76918	Niemann-Pick di	Patched,TM,SS	3.0
45	422746	NM_004484	Hs.119651	glypican 3	Glypican, TM, SS	3.0
	453775	NM_002916	Hs.35120	replication fac	AAA,TM,SS	3.0
	428862	NM_000346	Hs.2316	SRY (sex-determ	HMG_box,TM.	29
	401747				filament,TM,	2.9
<b>~</b> ^	429682	NM_006306	Hs.211602	SMC1 (structura	SMC_C,SMC_N,TM,	2.9
50	413385	M34455	Hs.840	indoteamine-pyr_	IDO,TM,	2.9 2.9
	442961	BE614474	Hs.289074	Homo sapiens cD	TM TM	2.9
	421650	AA781795	Hs.122587	ESTs serum-inducible	pkinase,POLO_box,TM,	2.9
	434398	AA121098	Hs.3838 Hs.7045	GL004 protein	PDEase,TM,	2.9
55	435706 416065	W31254 BE267931	Hs.78996	proliferating c	TM	2.9
))	423493	AIB15965	Hs.129683	ubiquitin-conju	UQ_con,,SS	2.8
	430242	U66669	Hs.236642		TM	2.8
	411770	NM_014278		heat shock prot	HSP70,TM,	2.8
	400440	X83957	Hs.83870	nebulin	TM	2.8
60	444743	AA045648	Hs.11817	nudix (nucleosi	mutT,TM,	2.8
	417771	AA804698	Hs.82547	retinoic acid r	TM	2.8
	430287	AW182459	Hs.125759		TM,SS	2.8
	408482	NM_000676		adenosine A2b r	7tm_1,TM,SS	2.8
15	425188	AK002052	Hs.155071		TM	2.8 2.8
65	456999	AA319798	Hs.172247		SS ' TM	2.8
	408875	NM_015434		DKFZP434B168 pr DKFZP434I216 pr	RhoGEF,TM,	2.7
	409012	AL117435	Hs.49725 Hs.66170	HSKM-8 protein	zf-MYND,,SS	2.7
	410762 426925	AF226053 NM_001196			TM	2.7
70	410115	AW630671	Hs.58636	squamous cell c	TM,SS	2.7
, 0	428398	A1249368	Hs.98558	ESTs	SS	2.7
	412140	AA219691	Hs.73625	RAB6 interaction	kinesin,TM,SS	2.7
	456655	AJ376736	Hs.111779	secreted protei	kazal, SS	27
	408670	AF160967	Hs.46784	potassium large	TM,SS	2.7
75	422576	BE548555	Hs.118554		tactamase_B,,SS	2.7
	431379	AA504264	Hs.182937		TM	2.7
	433183		Hs.22202		HLH,PAS,TM,SS	2.7 2.7
	432328	AI572739	Hs.19547		PGAM,6PF2K,TM,	2.6
80	407633				TM,SS ILB,TM,SS	2.6
٥V	419216		Hs.16402		TM	2.6
	422363 401644		Hs.11547	T TOPHNOOUT 100	zi-CZH2,TM,	26
	417479		Hs.13355	4 ĖSTs	CARD,TM,	2.6
	711773					

					41 71400	2.6
	426514	BE616633		one morphogene	TGF-beta,TGFb_propeptide,TM,SS	2.6
		X07820		natrix metallop	hemopexin,,SS ank,TM,SS	2.6
		U38945		yclin-dependen ESTs, Highly si	PolyA_pol,TM,	2.6
5	421246 428048	AW582962 AA705745		STs	AMP-binding,TM,	2.6
,	452092	BE245374		rypothetical pr	Acytransferase,TMLSS	2.6 2.6
	440052	AI633744		ESTs	PAC,TM,SS	2.6
	452401	NM_007115		turnor necrosis	Xtink,CUB,TM,SS WD40,,SS	2.6
10	451813	NM_016117		phospholipase A lwist (Drosophi	HLH,TM,	2.6
10	410889 422063	X91662 BE156476		gb:QV0-HT0368-0	\$S	2.6
	418250	U29926		adenosine monop	A_deaminase,TM,	2.6 2.6
	437641	AA811452		ESTs	TM	2.6
	452571	W31518		ESTs	TM SH2.STAT.,SS	2.6
15	411984	NM_005419		signal transduc TTK protein kin	pkinase,TM,	2.6
	426427 445848	M86699 AA774824	Hs.169840 Hs.13377	Homo sapiens ci	TM	2.6
	420022	AA256253	Hs.120817	ESTs	SS	2.6 2.6
	451418	BE387790	Hs.26369	hypothetical pr	TM	2.6
20	428953	AA306610	Hs.194676	DKFZP434C013 pr	arf,TNFR_c6,DEAD,Stathmin,TM,SS	2.6
	424008	R02740	Hs.137555	putative chemok vaccinia relate	7tm_1,TM, pkinase,TM,SS	2.6
	417863	AB000450 AW375974	Hs.82771 Hs.156704	ESTs	TM	2.5
	436961 413670	AB000115	Hs.75470	hypothetical pr	TM	2.5
25	421928	AF013758	Hs.109643	polyadenylate b	SS THE PARTY OF TH	2.5 2.5
	439963	AW247529	Hs.6793	ptatelet-activa	PAF-AH,HMG_box,pkinase,TM,	2.5
	426711	AA383471	Hs.180669	conserved gene	TM TM	2.5
	422631	BE218919	Hs.118793 Hs.82772	hypothetical pr collagen, type	TSPN,Collagen,COLFI,,SS .	2.5
30	417866 416975	AW067903 NM_004131	Hs.1051	granzyme B (gra	trypsin,,SS	2.5
50	415947	U04045	Hs.78934	mutS (E. coli)	Muts_C,Muts_N,TM.	2.5 2.5
	454678	AW813089		gb:RC3-ST0186-2	TPR,Ribosomal_S5,TM,SS	2.5 2.5
	426572	AB037783	Hs.170623	hypothetical pr	PH,FYVE,TM, TM	2.5
25	428264	AA424839	Hs.98484	ESTs, Weakly si M-phase phospho	kinesin,,SS	2.5
35	444478 442295	W07318 A1827248	Hs.240 Hs.224398	Homo sapiens cD	Collagen, COLFI, vwc, TM, SS	2.5
	410094	BE147897	Hs.58593	general transcr	TFIIF_beta,TM,	2.4 2.4
	413998	AW103807	Hs.243933	ESTs	TPR,TM,SS	24
40	412281	AI810054	Hs.14119	ESTs	Ribosomal_S7e,TM,	2.4
40	446852	AW451643	Hs.257479	ESTs, Weakly si	TM TM,SS	2.4
	408915	NM_016651 BE281238	Hs.48950 Hs.8886	heptacellular c hypothetical pr	TM	2.4
	442991 410193	AJ132592	Hs.59757	zinc finger pro	zt-C2H2,TM,	2.4
	410664	NM_006033		lipase, endothe	Ribosomal_L22,lipase,PLAT,TM,SS	2.4 2.4
45	423453	AW450737	Hs.128791	CGI-09 protein	Granin,CDP-OH_P_transf,TM,	2.4
	411598	BE336654	Hs.70937	H3 histone fami	histone,,SS C2,PLA2_B,TM,	2.4
	429663	M68874 H55709	Hs.211587 Hs.2250	phospholipase A leukemia inhibi	LIF_OSM.,SS	2.4
	428242 419559	Y07828	Hs.91096	ring finger pro	zf-C3HC4,zf-B_box,TM,	24
50	419839	U24577	Hs.93304	phospholipase A	SS	2.4 2.4
	402819				IBR,TM, FG-GAP,vwa,TM,SS	2.4
	431457	NM_01221		integrin, alpha uncharacterized	DUF157,TM,	2.4
	443683		Hs.9676 Hs.112341		wap,,SS	24
55	422158 423217			collagen, type	fn3,Collagen,Kunitz_BPTI,vwa,,SS	2.4 2.4
	408321			cortistatin	TM	2.4
	419086			Kalimann syndro	fn3,wap.,SS	24
	427722		Hs.180479	hypothetical pr	PH,,SS TM	2.4
60	405454 422168		Hs.11240	8 S100 calcium-bi	ethand,TM,	2.3
00	421462				MIP,TM,	2.3
	403416				SS THE STATE OF	2.3 2.3
	448988		Hs.22785		neur_chan,TM,SS Rhodanese,,SS	2.3
65	423198		Hs.1634	cell division c DKFZP586D2223		2.3
65	419920					2.3
	429993 44623				7tm_3,TM,	2.3
	42249			6 ESTs	TM.	23 23
	40704			gb:H.sapiens SO	sodfe,TM, Peptidase_M3,,	23
70	41109		Hs.68583		DAG_PE-bind,RhoGAP,TM.	2.3
	42645				TM	2.3
	44654 42209				TM	23
	42193		Hs.1096	55 sex comb on mid	SAM,TM,	2.3 2.3
75	43000	1 AI580058	5 Hs.9899	2 ESTs	TM TM	2.3
	42080		Hs.1334	v-myb avian mye	TM gpdh,,SS	2.3
	40205		6 Hs.1016	56 ESTs	SS	2.3
	43274 4334(				PWWP,PHD,bromodomain,TM,	23
80	4083		02 Hs.2499	54 ESTs	TM,SS	2.3 2.3
	4078	07 AL03142			ue T4_deiodinase,TM, PMP22_Claudin,TM,SS	2.3
	4369				TM,SS	2.3
	4337	JU ANUUKI	35 Hs.3542	· · · · · · · · · · · · · · · · · · ·		

	414839	X63692	Hs.77462	DNA (cytosine-5	zf-CXXC,BAH,TM,SS	2.3
	438192	AI859065	Hs.16808	ESTs, Wealthy si	TM.SS	2.3
	415339	NM_015156	Hs.78398	KIAA0071 protei	ELM2,TM,	2.3
_	449539	W80363	Hs.58446	ESTs	phinase, Funn-like, Recep_L_domain, TMLSS	2.2
5	450956	AW193531	Hs.205647	ESTs, Moderatel	pkinase,TM,SS	2.2
	430335	080007	Hs.239499	KIAA0185 protei	S1,TM,	2.2
	417849	AW291587	Hs.82733	nidogen 2	EGF,ktl_recept_b,thyroglobulin_1,TM,SS	22
•	412326	R07566	Hs.73817	small inducible	ILB,,SS	2.2 2.2
10	408349 424704	BE546947 AI263293	Hs.44276	homeo box C10	homeobax,TM, p450,,SS	2.2
10	409632	W74001	Hs.152096 Hs.55279	cytochrome P450 serine (or cyst	serpin,TM,	2.2
	415323	BE269352	Hs.949	neutrophil cyto	SH3,TPR,TM,	2.2
	417531	NM_003157	Hs.1087	serine/threonin	pkinase,TM,	2.2
	403137				rm,TM,SS	2.2
15	428479	Y00272	Hs.184572	cell division c	pkinase, TM, SS	2.2
	430200	BE613337	Hs.234896	geminin	TM,SS	2.2
	425390	Al092634	Hs.156114	protein tyrosin	ig,Opiods_neuropep,TM,SS	2.2
	408380	AF123050	Hs.44532	diubiquitin	ubiquitin,7tm_3,ANF_receptor,sushi,7tm_1,TM,	2.2
20	422424	A1186431	Hs.116577	prostate differ	TGF-beta,,SS	2.2 2.2
20	400298 411571	AA032279 AA122393	Hs.61635 Hs.70811	six transmembra hypothetical pr	TM SS	2.2
	412802	U41518	Hs.74602	aquaporin 1 (ch	MIP,TM,	2.2
	414761	AU077228	Hs.77256	enhancer of zes	SET,TM,	2.2
	408432	AW195262		gb:xn67b05.x1 N	TM,SS	2.2
25	429568	AI088691	Hs.208414	Homo sapiens mR	mito_carr,TM,	2.2
	425300	AW601773	Hs.270259	ESTs	TM	2.2
	439653	AW021103	Hs.6631	hypothetical pr	TM,SS	2.2
	426827	AW067805	Hs.172665	methylenetetrah	THF_DHG_CYH,FTHFS,TM,	2.2
30	444514	AI682905	Hs.270431	ESTs, Wealdy si	cNMP_binding,TM,SS	2.2 2.2
30	425322	U63630	Hs.155637	protein kinase,	MCM,TM, laminin_G,TM,SS	2.2
	421662 438788	NM_014141- AA825716	Hs.106552	cell recognitio gb:od29e10.s1 N	ank,death,RHD,TM,	2.2
	429058	AF138863	Hs.194827	hypothetical pr	TM	2.2
	423104	AJ005273	Hs.123647	antigenic deter	TM	2.2
35	410406	AJ969703	Hs.301842	ESTs	FGGY,TM,	2.2
	421379	Y15221	Hs.103982	small inducible	IL8,TM,SS	2.2
	422809	AK001379	Hs.121028	hypothetical pr	IQ,TM,	2.2
	418049	AA211467	Hs.190488	hypothetical pr	TM	2.2
40	436209	AW850417	Hs.254020	ESTs, Moderatel	TM,SS	2.2 2.2
40	408042	AL049233	Hs.42244	Homo sapiens mR	TM Apphdropers TM	2.2
	425692 409665	D90041 NM_006731	Hs.155956 Hs.55777	N-acetyltransfe Fukuyama type c	Acetytransf2,TM, SS	2.2
	428157	AI738719	Hs.298668	ESTs	hexokinase,TM,	2.2
	410480	R97457	Hs.63984	cadherin 13, H-	cadherin,TM,SS	2.2
45	429732	U20158	Hs.2488	lymphocyte cyto	SH2,TM,	2.2
	414747	U30872	Hs.77204	centromere prot	SS	2.2
	425843	BE313280	Hs.159627	death associate	TM	2.2
	445299	AI910382	Hs.118727	Homo sapiens cD	HLH,TM,	2.1
50	436251	BE515065	Hs.5092	nucleolar prote	Nop,TM,SS	2.1 2.1
50	430066	AI929659 AU077143	Hs.237825 Hs.179565	signal recognit minichromosome	TPR,SS MCM,TM,SS	2.1
	427528 448089	A1467945	Hs.173696	ESTs	TM,SS	21
	428728	NM_016625	Hs.191381	hypothetical pr	TM	2.1
	409929	R38772	Hs.172619	KIAA1106 protei	TM	21
55	405264			•	SS	21
	445625	BE246743	Hs.288529	Homo sapiens cD	TM	2.1
	408949	AF189011	Hs.49163	putative ribonu	Ribonuclease_3,TM,SS	21
	424513	BE385864	Hs.149894	mitochondrial t	GTP_EFTU,IF2,TM,	21 2.1
60	433683 442952	AI817723 AI743261	Hs.22678 Hs.131860	hypothetical pr ESTs	SS TM	2.1
00	432378	A1493046	Hs.146133	2 1 1	TM	2.1
	417979	AU077284	Hs.83081	GTP cyclohydrol	TM,SS	2.1
	433849	BE465884	Hs.280728	ESTs	SS	2.1
	437928	NM_005476	Hs.5920	UDP-N-acetylglu	ROK,Epimerase_2,TM,	2.1
65	403055			· -	filament,TM,SS	2.1
	432840	AK001403	Hs.279521	hypothetical pr	TM	2.1
	418994	AA296520	Hs.89546	selectin E (end	EGF,lectin_c,sushi,TM,SS	21
	440908	AI915225	Hs.126735		ŢM	2.1
70	417621	AV654694 AF037335	Hs.82316 Hs.5338	interferon-indu carbonic anhydr	TM carb_anhydrase,TM,SS	21 21
70	436895 408420	NM_006915			TM	21
	434064	AL049045	Hs.180758		cadherin,TM,SS	2.1
	404076			,,,	RmaAD,TM,	2.1
	422515	AW500470	Hs.117950	multifunctional	AIRC, SAICAR_synt, TM,	2.1
75	445867	AF272663	Hs.13405	gephyrin	MoCF_biosynth,TM,	2.1
	441021	AW578716	Hs.7644	H1 histone lami	linker_histone,TM,	2.1
	446595	T57448	Hs.15467	hypothetical pr	TM,SS	21
	417515	L24203	Hs.82237	ataxia-telangie GRO2 oncogene	zf-B_box.,SS ILB,TM,SS	21 21
80	412429 449207	AV650262 AL044222	Hs.75765 Hs.23255	nucleoporin 155	TM,SS	2.1
50	412095	AI624707	Hs.5921	Homo sapiens cO	TM,SS	2.1
	400861				pkinase,TM,	2.1
	440591	AA431599	Hs.132799	Homo sapiens cD	TM	2.1

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phosphodiestera
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         442104
                   L20971
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                                              small inducible
                                                                      IL8.SS
                                 Hs.16530
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                   AB012113
                                                                      Reprolysin, Pep_M12B_propep, TM, SS
                                 Hs.153315
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                                              eukaryotic tran
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2.1
2.1
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                                                                       TM
                                              transcription f
                    AU077315
                                 Hs.154970
         425170
                                              Homo sapiens mR
                                                                       TM
                                  Hs.101282
                   R36762
NM 003937
         453751
                                              kynureninase (L
                                                                       TM
                                 Hs.169139
         426283
                                                                       Y_phosphatase,TM,
                    BE616160
                                  Hs.82829
                                              protein tyrosin
ESTs
         417874
                                                                                                                        2.1
2.1
                                  Hs.195390
Hs.187561
                                                                       ΤM
         449555
                    AW450288
                                                                       TM
                                              ESTs, Moderatel
10
          439699
                    AF086534
                                                                                                                        2.1
                                                                       sodie,TM,
                                              superoxide dism
                                  Hs.177781
                    BE547647
          427413
                                                                                                                       2.0
2.0
2.0
2.0
2.0
                                              novel RGD-conta
                                                                       hexapep,TM,SS
                    D84145
                                  Hs.39913
          407802
                                                                       TM
                                              Sam68-like phos
          446035
                     NM_006558
                                  Hs.13565
                                                                       COesterase, TM, SS
                                              Acetylcholinest
                                  Hs.296844
          406981
432343
                     571129
                                                                        S_100,efhand,TM,SS
                                               S100 calcium bi
                     NM_002960
                                  Hs.2961
15
                                                                        PNP_UDP_1,TM,SS
                                              uridine phospho
                     BE281095
                                  Hs.77573
          414890
                                                                                                                        2.0
2.0
                                  Hs.225816
                                               ESTs
          423019
                     AI640185
                                                                        Fz.Frizzled,TM,SS
                                               frizzled (Droso
                                  Hs.114218
                     AF072873
          422278
                                                                        ABC_tran,ABC_membrane,TM,SS
                                                                                                                        2.0
2.0
          405545
                                                                        bZIP,TM,
                                               ESTs
20
          446237
                     AW270515
                                   Hs.149596
                                               colony stimulat
                                                                        SS
                                   Hs 182378
           428074
                     BE387770
                                                                                                                         20
                                                                        SNF2_N,helicase_C,TM,
                                               RAD54, S. cerev
                                                                                                                        20
20
20
20
                                   Hs.128501
                     AF112481
           423430
                                                                        Peptidase_S8,P,TM,
                     H73505
                                   Hs.117874
                                               ESTs
           435767
                                                                        PK,SS
                                               FSTs. Wealdy si
                     AL043683
                                   Hs.271357
           432945
                                                                        sodie TM
 25
           404170
                                                                         IRK,TM,
                                                potassium inwar
                     AF153820
                                   Hs.1547
           422610
                                                                                                                         20
                                                                         thymidylat_synt,.SS
                                   Hs.82962
                                                thymidylate syn
                      X02308
           417933
                                                                                                                         2.0
                                               protease, senn
small inducible
                                   Hs.288660
                      AA447849
           441384
                                                                                                                         2.0
                                                                         IL8..SS
                                   Hs.75703
           414020
                      NM_002984
                                                                                                                         2.0
                                                                         histone,TM,SS
                      NM 003528
                                    Hs.2178
                                                H2B histone fam
 30
           427674
                                                                         TM
                      H16263
                                    Hs.31416
                                                ESTs
                                                                                                                         2.0
           435425
                                                                         nm,NTF2,,SS
                                                Ras-GTPase-acti
                                    Hs.220689
                      NM_005754
            429782
                                                small profine-r
                                                                         Comifin.TM.
                                    Hs.1076
                      BE185289
            417366
                                                                         Pribosyltran, OMPdecase, TM,
                                    Hs.2057
                                                 undine monopho
                      J03626
                                                                                                                          2.0
            426746
                                                                         Glycos_transf_2,Ricin_B_lectin,TM,
                      NM_004482
                                    Hs.278611
                                                UDP-N-acetyl-al
 35
            432677
            TABLE 438:
                              Unique Eos probeset identifier number
           Pkey:
CAT number:
                              Gene cluster number
                              Genbank accession numbers
  40
            Accession:
                       CAT number
                                     AW195262 R27868 AW811262
            408432
                       1058667_1
                                     AW851186 AW996967 BE143456
            411560
                       1249443_1
                                     BE156476 BE156473 BE156474 BE156475 AA302839
  .45
                       210852 1
             422063
                                     AI803103 AI885143 AW470793 AW450703 AI090784 AW271587 AW236950 AW242783
             422285
                       214669 1
                                     AW856665 AA315006 AW954733
                       219896_1
             422689
                                     AA331906 AA332484
             423871
                       232749_1
                                     AA825716 AW978859 AA828841
                        465159_1
             438788
                                     AW850984 AW752836 M86124
   50
                        1207088 1
             454456
                                      AW813089 W28102
             454678
                        1228915 1
                         Unique number corresponding to an Eos probeset
Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of
             TABLE 43C:
             Pkey:
Ref:
   55
                          human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
                          Indicates DNA strand from which exons were predicted.
             Strand:
             Nt position: Indicates nucleotide positions of predicted exons.
                                                   Nt position
    60
                                      Strand
              Pkey
                                                   163855-164016
                         9757506
                                      Plus
              400861
                                                   82655-83959
                                                   Plus
                         8576138
              401644
                         9789672
              401747
                                                   131932,132451-132575,133580-134011
                         8083229
    65
                                       Plus
              402053
                                                   29217-29422
109532-110225
                         6729581
                                       Plus
               402819
                                       Minus
                         8748904
                                                   92349-92572,92958-93084,93579-93712,93949-94072,94591-94748,95214-95337
               403055
                         9211494
                                       Minus
               403137
                                                    1414-1513,1624-1756
                         7770611
                                       Minus
               403776
                                                    3848-3967
     70
                         9931752
                                       Minus
               404076
                                                    168836-169248
                          9930793
               404170
                                       Plus
                                                    28556-28684
               405264
                          7329374
                                       Phis
                                                    133807-134053
               405454
                          7656675
                                       Plus
                                                    118677-118807,119091-119296,121626-121823
                          1054740
                                       Plus
               405545
                                                    17803-17931
     75
                          9256651
                                       Minus
               406434
```

TABLE 44A: ABOUT 314 GENES DOWN-REGULATED IN STOMACH CANCER

Table 44A lists about 314 genes significantly down-regulated in stomach cancer compared to normal stomach. These were selected as for Table 42A, except that the numerator and 80 denominator were switched.

Unique Eos probeset identifier number Pkey:

Exemplar Accession number, Genbank accession number ExAccn:

UnigenelD: Unigene number

	Unigene Title:		Unigene gene title		
	R1:	Retic	of turnor to nom	nal tissue	
	Pkey	ExAcon	UnigenatD	Unigene Title	R1
5	412859	NM_000705	Hs.813	ATPase, H+/K+ exchanging, beta polypepti	0.01
_	415447	297171	Hs.78454	myocilin, trabecular meshwork inducible	0.05
	427469	AA403084	Hs.269347	ESTs	0.05
	407485	S69741		gb:hSCG-3=stomach cancer gene-3 (oncogen	0.06
• •	428602	AL137479	Hs.186655	Homo sapiens mRNA; cDNA DKFZp434M0223 (f	0.06
10	402761	BE387621	Hs.108809	chaperonin containing TCP1, subunit 7 (e	0.07
	443547	AW271273	Hs.23767	Homo sapiens cDNA FLJ12666 fis, clone NT	0.07
	430130	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (	0.07
	435473	N53550	Hs.260881	EST&	0.07
15	455826	BE144228		gb:MR0-HT0165-140200-009-d04 HT0165 Homo	0.07
15	402015	********			0.08
	430664	AW969834	11- 400070	gb:EST381912 MAGE resequences, MAGK Horno	0.09
	444515 429201	AW204908	Hs.169979	ESTs	0.09
	434424	X03178 AI811202	Hs.198246 Hs.125365	group-specific component (vitamin D bind	0.10 0.10
20	450940	AI744943	Hs.300744	Homo sapiens cDNA: FLJ23523 fis, clone L ESTs, Moderately similar to ALU7_HUMAN A	0.10
20	400811	AF219139	Hs.87726	KIAA0154 protein; ADP-ribosylation facto	0.10
	424596	AB020639	Hs.151017	estrogen-related receptor gamma	0.11
	403670	, 2020000	113.131911	carage in caches gained	0.11
	410234	NM_003837	Hs.61255	fructose-1,6-bisphosphatase 2	0.12
25	407462	AJ252011		gb:Homo sapiens partial mRNA for amilori	0.13
	405110			• , ,	0.13
	402760				0.13
	408947	AL080093	Hs.49117	Homo sapiens mRNA; cDNA DKFZp564N1662 (f	0.13
20	413724	AA131466	Hs.23767	Homo sapiens cDNA FLJ12666 fis, clone NT	0.14
30	431514	AW972363		gb:EST384454 MAGE resequences, MAGL Horno	0.14
	451103	R52804	Hs.25956	DKFZP564D206 protein	0.14
	452033	AW273741	Hs.246977	ESTs	0.16
	440058 405645	Al932662	Hs.164073	ESTs	0.16 0.17
35	429093	NM_000253	Hs.195799	microsomal triglyceride transfer protein	0.17
55	445627	AW818475	Hs.7363	ESTs	0.19
	425679	X05997	Hs.159177	lipase, gastric	0.19
	417296	L36196	Hs.81884	suffotransferase family, cytosolic, 2A,	0.19
40	443537	D13305	Hs.203	cholecystokinin B receptor	0.20
40	435654	AW139612	Hs.131041	ESTs	0.20
	406326				0.20
	454120	AB032990	Hs.40719	hypothetical protein KIAA1164	0.20
	455541	AW993005		gb:RC2-BN0032-160200-013-d04 BN0032 Homo	0.21
45	453989	M63962	Hs.36992	ATPase, H+/K+ exchanging, alpha polypept	0.23
77	407261 451062	L03172 AL110125	Hs.25910	gb:Homo sapiens cell-type T-cell immunog	0.23 0.23
	429350	ALT 10123 AI754634	Hs.131987	Homo sapiens mRNA; cDNA DKFZp564C1416 (f ESTs	0.23
	411021	F00055	Hs.172004	tiún	0.24
_	441212	AW242447	Hs.146182	ESTs, Weakly similar to lactase phlorizi	0.24
50	450572	AI700863	Hs.202494	Homo sapiens cDNA FLJ13245 fis, clone OV	0.25
	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	0.26
	421562	AA530994	Hs.105803	ghrefin precursor	0.26
	457432	NM_005136	Hs.268538	potassium voltage-gated channel, tsk-rel	0.26
55	418421	R58620	Hs.85050	phospholamban	0.26
55	424104	AA669515	Hs.144950	ESTs	0.26
	422582	AA312660	11- 000400	gb:EST183335 Jurkat T-cells VI Horno sapi	0.26
	417332	AW972717	Hs.288462	Homo sapiens cDNA: FLJ21511 fis, clone C	0.27
	432440 448520	X63597 AB002367	Hs.2996 Hs.21355	sucrase-isomatiase doublecortin and CaM kinase-like 1	0.27 0.28
60	401989	AB002361	ns.21333	CONTROL OF THE COMMUNICATION OF THE PROPERTY O	0.28
•	452528	AA742457	Hs.291479	ESTs	0.28
	412569	H63789	Hs.296288	ESTs, Weakly similar to KIAA0638 protein	0.28
	434779	AF153815	Hs.50151	potassium inwardly-rectifying channel, s	0.28
	406255				0.29
65	419293	AA746282	Hs.255659	ESTs	0.29
	428649	AL045716	Hs.188228	Homo sapiens cDNA FLJ11003 fis, clone PL	0.29
	410036	R57171	Hs.57975	calsequestrin 2, cardiac muscle	0.29
	414502	AL133721	Hs.224680	ESTs	0.29
70	432113	AA935065	Hs.152385	ESTs	0.29
70	413808	J00287	Hs.182183	caldesmon 1	0.29
	451406 434745	A1694320 AW974445	Hs.6295 Hs.185155	ESTs, Weakly similar to T17248 hypotheti ESTs, Weakly similar to HuEMAP (H.sapien	0.29 0.30
	420444	AI905985	Hs.111805	ESTs	0.30
	445200	AA084460	Hs.12409	somatostatin	0.30
75	415314	N88802	Hs.5422	glycoprotein M68	0.30
	427019	AA001732	Hs.173233	hypothetical protein FLJ 10970	0.30
	431152	AW970998		gb:EST383083 MAGE resequences, MAGK Homo	0.30
	432306	Y18207	Hs.274315	protein phosphatase 1, regulatory (inhib	0.31
80	401775	****	No present	FOT-	0.31
οU	440059	AW467335	Hs.257676	ESTs ESTs	0.31
	436089 447071	AA804957 AW236867	Hs.119840 Hs.244376	ESTs	0.31 0.32
	435604	AA625279	Hs.26892	uncharacterized bone marrow protein BM04	0.32
				440	

					0.32
			Hs.136529	solute carrier family 23 (nucleobase tra	0.32
			Hs.201217 Hs.103253	ESTs perilipin	0.32
	421296 427138		Hs.173717	phosphatidic acid phosphatase type 28	0.33
5	449916		Hs.299221	ESTs	0.33 0.33
	446393	AW014174	Hs.151707	ESTs diacylglycerol kinase, eta	0.33
	446632 428070	Al333565 T63918	Hs.159073 Hs.182313	retinol-binding protein 2, cellular	0.33
	421451	AA291377	Hs.50831	ESTs	0.33 0.33
10	405817			gb:RC2-ST0301-120200-011-f12 ST0301 Homo	0.33
	454790	AW820852		gb:RC1-HT0370-120100-012-009 HT0370 Homo	0.34
	413679 404121	BE156765		BOING I-MIDDIO-120100-012 000	0.34
	433084	M18079	Hs.282265	fatty acid binding protein 2, intestinal	0.34 0.34
15	413079	BE064382		gb:RC4-BT0310-110300-015-c12 BT0310 Homo	0.35
	403059	***********	Hs.205386	ESTs	0.35
	458987 429609	AW750067 AF002246	Hs.210863	cell adhesion molecule with homology to	0.35
	423371	AU076819	Hs.1650	solute carrier family 26, member 3	0.35 0.35
20	424765	AA428211	Hs.284256	hypothetical protein FLJ14033 similar to gb:ts54f01.x1 NCI_CGAP_Kid8 Homo sapiens	0.35
	451818	AIB19018 T06430	Hs.6194	chondroifin suffate proteoglycan BEHAB/b	0.35
	438380 405742	100430	16.0154		0.35
	403429				0.35 0.36
25	443622	AI911527	Hs.11805	ESTs	0.36
	404973	AV654020	Hs.184261	ESTs, Weakly similar to putative type II	0.36
	444567 412228	AW503785	Hs.73792	complement component (3d/Epstein Barr vi	0.36 0.36
	407110	AA018042	Hs.95078	ESTs	0.36
30	411671	BE049094	Hs.278567	ESTs gastrin	0.36
	430800	NM_000805 AW807281	Hs.2681	gb:MR4-ST0062-240300-003-g01 ST0062 Homo	0.36
	454560 444536	A1161068	Hs.14780	ESTs	0.36
	454042	H22570	Hs.172572	hypothetical protein FLJ20093	0.37 0.37
35	444102	AV647953	Hs.282379	ESTs ESTs	0.37
	424122 452093	AA335593 AA447453	Hs.116147 Hs.27860	Homo sapiens mRNA; cDNA DKFZp586M0723 (f	0.37
	436277	R88520	Hs.120917	ESTs	0.37 0.37
4.0	456350	BE246762	Hs.89499	arachidonate 5-lipoxygenase	0.37
40	451027	AW519204	Hs.40808 Hs.172216	ESTs chromogranin A (parathyroid secretory pr	0.38
	426784 410023	U03749 AB017169	Hs.57929	slit (Drosophila) homolog 3	0.38
	436802	N34486	Hs.170504	ESTs	0.38 0.38
	448142	AI521768	Hs.164586	ESTs	0.38
45	442378	R54033	Hs.21245 Hs.25248	ESTs ESTs	0.38
	446406 455753	AI553681 BE075124	N3.23240	oh-PM1_RT0585-110200-003-h02 BT0585 Homo	0.38
	424903	T26477	Hs.22883	ESTs, Weakly similar to ALU8_HUMAN ALU S	0.38 0.39
	406714		Hs.283108	hemoglobin, gamma G ESTs	0.39
50	434340		Hs.128685	ESIS	0.39
	406036 431078		Hs.249195	homeo bax A13	0.39 0.39
	457663	AW371946		ESTs	0.39
	451880		Hs.209387	ESTs carboxypeptidase A2 (pancreatic)	0.39
55	419219 446414		Hs.89717 Hs.59187	ESTs	0.39
	442317		Hs.129225	ESTs	0.39 0.39
	447261	NM_00669		lymphatic vessel endothelial hyaluronan CEGP1 protein	0.39
60	439569 433485		i Hs.222399 Hs.78183	aldo-keto reductase family 1, member C1	0.40
OU	433465	04.40		PRO0593 protein	0.40
	420200		Hs.88142	ESTs	0.40 0.40
	42186		Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr eukaryotic translation initiation factor	0.40
65	453956 40740			ab Homo saniens interleukin-1 type I rec	0.40
05	41073			ab:PM3-HN0010-050400-001-h12 HN0010 Homo	0.40 0.40
	45827	2 AI797360		ESTS, Weakly similar to ALU3_HUMAN ALU S	0.40
	40151			gb:AF147186 Homo sapiens library (Schere ESTs	0.40
70	43636 43444			ESTs	0.40
70	41327			ESTs	0.40
	40968	1 N51508	Hs.143718	ESTs gb:RC0-CT0210-280999-021-c10 CT0210 Homo	0.40 0.40
	45455			gb:RCO-C10210-280999-021-c10 C10210 Forms ESTs, Wealdy similar to neuroguin-4 sho	0.40
75	45089 45207			ESTs	0.41
, ,	41927		9 Hs.1247	apolipoprotein A-IV	0.41 0.41
	4336	37 AW0242		ESTs gb:601111034F1 NIH_MGC_16 Homo sapiens c	0.41
	4499		i1 Hs.80691	creatine kinase, mitochondriai 2 (sarcom	0.41
80	4169 4531			ESTs	0.41
50	4086	14 AL13769	8 Hs.46531	Homo sapiens mRNA; cDNA DKFZp434C1915 (f	0.41 0.41
	4379		8 Hs.145274	ESTs	0.41
	4027	<b>3</b> 3		469	

	450888	AW021446	Hs.80714	ESTs .	0.41
	417318	AW953937	Hs.12891	ESTs	0.41 0.41
	407244 424884	M10014 AW299437	Hs.75431 Hs.225717	fibrinogen, gamma polypeptide ESTs	0.41
5	439024	R96696	Hs.35598	ESTS	0.42
_	423732	AF058056	Hs.132183	solute carrier family 16 (monocarboxylic	0.42
	409300	AA126190	U= 0043	gb:zm78f03.r1 Stratagene neuroepithefium Human DNA sequence from clone RP4-788L20	0.42 0.42
	444237 425860	AA336878 L29339	Hs.9842 Hs.1964	solute carrier family 5 (sodium/glucose	0.42
10	447021	AI356564	Hs.161406	ESTs	0.42
	422270	AF114494	Hs.114062	protein tyrosine phosphatase-like (proli	0.42
	407850	AW086230	Hs.244912	ESTs ESTs	0.42 0.42
	449884 436327	AI673110 AA813075	Hs.222195 Hs.120181	ESTs	0.42
15	415972	H11436	Hs.260201	ESTs	0.42
	400917				0.43
	435309	AW089050	Hs.187993	ESTs	0.43 0.43
	424410 445577	W79027 N40696	Hs.271762 Hs.146077	ESTs ESTs	0.43
20	411069	AL133092	Hs.68055	hypothetical protein DKFZp434l0428	0.43
	440286	U29589	Hs.7138	cholinergic receptor, muscerinic 3	0.43
	451123	AI927224	Hs.213480	ESTs ESTs	0.43 0.43
	457151 459185	AW206116 AI908222	Hs.253538	gb:RC-BT165-300399-020 BT165 Homo sapien	0.43
25	411607	AW853498		gb:RC1-CT0252-170200-025-h02 CT0252 Homo	0.43
	424815	AA347287	Hs.104573	ESTs	0.43
	429704 411067	AA584440 Al681006	Hs.185812 Hs.301543	ESTs ESTs	0.43 0.43
	430172	AA468591	Hs.161889	ESTs	0.43
30	435124	AA725362	Hs.120456	ESTs	0.43
	445966	L17330	Hs.280	pre-T/NK cell associated protein	0.43
	443741	AW451759	Hs.145420	ESTs głyoxylate reductase/hydroxypyruvate red	0.43 0.44
	416275 451138	H42823 W92287	Hs.155742 Hs.40268	ESTs	0.44
35	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	0.44
	426730	AL040738		gb:DKFZp434B1615_r1 434 (synonym: htes3)	0.44
	410056	AL117664	Hs.58419 Hs.183864	DKFZP586L2024 protein elastase 3B	0.44 0.44
	427965 418026	D00306 BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	0.44
40	408479	BE047329	Hs.144483	ESTs	0.44
	457994	AW136239	Hs.132922	ESTs	0.44
	435564	AF210652	Hs.16614 Hs.54650	5(3)-deoxyribonucleotidase (dNT-2); nucl vascular endothelial junction-associated	0.45 0.45
	435869 434399	AF255910 AA878845	Hs.125769	ESTs	0.45
45	415797	AI291896	Hs.72800	ESTs	0.45
	430264	AA470519		gb:nc71f10.s1 NCI_CGAP_Pr1 Homo sapiens	0.45
	409435	AJ810721	Hs.95424	ESTs	0.45 0.45
	433542 455400	AA598869 AW936342	Hs.173770	ESTs qb:QV4-DT0021-281299-070-h12 DT0021 Homo	0.45
50	412047	AA934589	Hs.49696	ESTs	0.45
	443948	T56148	Hs.9997	Homo sapiens mRNA full length insert cDN	0.45
	450307	AW450336	Hs.201783	ESTs Homo sapiens clone IMAGE:113431 mRNA seq	0.45 0.45
	434500 420460	AF143877 AA262331	Hs.215047 Hs.135503	ESTs	0.45
55	450752	AA012986	Hs.60466	ESTs	0.45
	418138	AA213626	Hs.136204	EST	0.45
	441088	AA916546	Hs.126546	ESTs gb:RC3-ST0186-250200-018-c05 ST0186 Homo	0.46 0.46
	410990 438211	AW812929 T08401		gb:EST06292 Infant Brain, Bento Soares H	0.46
60	434349	NM_015678	Hs.3821	neurobeachin	0.46
	409824	AW501063		gb:UI-HF-BP0p-aiz-c-01-0-UI.r1 NIH_MGC_5	0.46
	403279	AW974752	Hs.269497	ESTs	0.46 0.46
	434882 404629	A11314132	115.203437	L319	0.46
65	427393	A8029018	Hs.177635	KIAA1095 protein	0.46
	454651	AW812091		gb:RC4-ST0173-191099-032-b04 ST0173 Homo	0.46
	401992	AA463422	Hs.209431	ESTs	0.46 0.46
	457275 403710	MM03422	113.203431	2013	0.46
70	419728	L36861	Hs.92858	guanylate cyclase activator 1A (retina)	0.46
	401075			and the control of the second	0.46
	421387	AF059566 AA035446	Hs.103983 Hs.261224	solute carrier family 5 (sodium iodide s ESTs	0.46 0.46
	453404 407208	T10695	Hs.102948	enigma (LIM domain protein)	0.46
75	440681	AW449696	Hs.166547	ESTs	0.46
	454206	AW810279		gb:MR4-ST0125-151299-029-a09 ST0125 Homo	0.47
	402466	N90822	Hs.48969	ESTs	0.47 0.47
_	429996 403680	1130044	113.40303	2013	0.47
80	428151	AA422028		gb:zv26g06.r1 Soares_NhHMPu_S1 Homo sapi	0.47
	410495	N95428		gb:zb80d09.s1 Soares_senescent_fibroblas	0.47
	402851 438421	AA806907	Hs.194451	ESTs	0.47 0.47
	730721	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	12.101101		<b>-</b> . ~

	10.00	BE244138	11- 42420	gb:TCBAP1E1218 Pediatric pre-8 cell acut SH3 domain binding glutamic acid-rich pr	0.47 0.47
			Hs.47438 Hs.177386	ESTs	0.47
			Hs.75236	ELAV (embryonic lethal, abnormal vision,	0.47
5		M62843 A1564739	Hs.68505	ESTs	0.47
3		AI208986	Hs.143945	FCTe	0.47
		AW752597	112.140040	gb:IL3-CT0214-161299-045-B06 CT0214 Homo	0.47
		AA905097	Hs.85050	nhospholamban	0.47
		BE255083		gb:601111390F1 NIH_MGC_16 Homo sapiens c	0.47 0.47
10	448869	A1792798	Hs.12496	ESTs	0.47
	400749				0.48
	458745	AW207347	Hs.211101	ESTS	0.48
	418437	AA771738	Hs.295351	ESTs ESTs	0.48
1.5	452286	Al358570	Hs.123933	ESTs	0.48
15	430369	AA477631	Hs.119484 Hs.31848	ESTs Weakly similar to hypothetical pro	0.48
	453572	AA382590	MS.31040	gb:RC2-BN0033-180200-014-h09 BN0033 Hamo	0.48
	455175	AW993247 AV655102	Hs.117266	FSTs	0.48
	445765 400322	AF045576	Hs.247758	offactory receptor, family 5, subfamily	0.48
20	412526	M90366	Hs.73982	zona pellucida glycoprotein 2 (sperm rec	0.48
20	407986	U32659	Hs.41724	interteutrin 17 (cytotoxic T-lymphocyte-a	0.48
	455479	AW948312	12	gb:RC0-MT0015-280300-021-h04 MT0015 Homo	0.48
	450308	Al692571	Hs.201681	ESTs	0.48
	411149	N68715	Hs.269128	ESTs	0.48 0.48
25	453982	AW014252	Hs.252837	ESTs	0.48
23	410971	AW812258		gb:RC0-ST0174-191099-031-b02 ST0174 Homo	0.48
	410839	NM_006849	Hs.66581	protein disuffide isomerase	0.48
	421553	AA536080	Hs.97302	ESTs	0.48
	442376	W95588	Hs.129982	Homo sapiens cONA FLJ12228 fis, clone MA	0.48
30	454754	AW819191		gb:CM1-ST0283-071299-061-d08 ST0283 Homo	0.49
	447858	AW080339	Hs.211911	ESTs	0.49
	422639	AI929377	Hs.173724	creatine kinase, brain	0.49
	402449				0.49
	420440	NM_002407		mammaglobin 2	0.49
35	435056	AW023337	Hs.5422	gtycoprotein M6B	0.49
	419543	AA244170	Hs.188719	ESTs gb:Human teukemia Inhibitory factor rece	0.49
	407033	U78628		gb:aa89d11.r1 Stratagene fetal retina 93	0.49
	437468	AA457619		ESTs	0.49
40	412639	AW961284	Hs.296235	E918	0.49
40	406109				0.49
	404519			gb:zm63d05.r1 Stratagene fibroblast (937	0.49
	410285	AA083609		Aprillogogy and appril	0.49
	406014				0.49
45	400938	A1568801	Hs.71721	ESTs	0.49
43	414290	AW014734		ESTs	0.49
	432433 405273	AHUIAISA	113.10.000	= :	0.49
	454738	BE072139		gb:PM1-BT0533-291299-002-b05 BT0533 Homo	0.49
	414383	BE279406		ob 601157981F1 NIH MGC_21 Homo sapiens c	0.49 0.49
50	445911	AI985987	Hs.145645	ESTs, Moderately similar to ALU1_HUMAN A	0.49
-	451241	A1767545	Hs.209572	ESTs	0.49
	428336	AA503115	Hs.183752	microseminoprotein, beta-	0.49
	418310		Hs.86693	ESTs	0.49
	452152			protein phosphatase 2 (formerly 2A), reg	0.49
55	454869			gb:PM0-LT0019-170200-001-d11 LT0019 Homo	0.49
	400332		Hs.248032	FLT4	0.49
	425280		Hs.1872	phosphoenolpyruvate carboxykinase 1 (sol	0.49
	408221			ESTs	0.50
-	440179		Hs.125904	ESTs gb:601076309F1 NIH_MGC_12 Homo sapiens c	0.50
60	425360		1	ga.go:101000at 3 fatt_moo_12 fatta	0.50
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	418594			ESTs	0.50
	43212			ESTs	0.50
65	458611			solute carrier family 25 (mitochondrial	0.50
03	42649			ESTs	0.50
	44106			ESTs	0.50
	42810 40080		e 113.104031	20.0	0.50
	43999		5 Hs.221675	ESTs	0.5
70	47233	m W21030			
70		E 44B:			
	Pkey:		Unique Eas probes	et identifier number	
		number:	Gene cluster numb	er	
	Acces		Genbank ax	cession numbers	
75					
/ >	Pkey	CAT nur	nber Accession		
75	40930		1 AA126190	AA074486 AA074707 AA070059 AA084886	
/3			1 AW501063	AW503034 AW501523	
13	WUds.			AA083790 AA112048	
	4098: 4102:	85 119128	J AAUSJOUS		
	4102			3404A AM7E13EE U91097	00007 AMORAS
80	4102	95 1205826	1 N95428 W	24040 AW751366 H81987 - Awgrasso Awgrasir Awgrasso R58427 AW984332 AW7:	99807 AW9843
	41021 4104	95 1205826 32 1218556	5_1 N95428 W 5_1 AW984328 5_1 AW812258	3404A AM7E13EE U91097	99807 AW9843 W812264

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AW853498 AW853442 AW853590 AW853433 AW853592
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BE156765 BE156770 BE156767 BE156769 BE156803 BE156802 BE156807 BE156833 BE156780 BE156836 BE156792 BE156834 BE156779
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AL040738 AA383683
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AW970998 AW971004 AA574217 AA493538
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                                                   AA457619 AL390167
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 45
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                 TABLE 44C:
                                            Unique number corresponding to an Eos probeset
                 Pkey:
                                            Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA
                 Ref:
  50
                                            sequence of human chromosome 22' Dunham, et al. (1999) Nature 402:489-495.
                                            Indicates DNA strand from which exons were predicted.
                 Strand:
                                            Indicates nucleotide positions of predicted exons.
                 Nt_position:
                                                                        Nt_position
                 Pkey
                                                      Strand
  55
                 400749
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                                                      Minus
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7652890
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                                                      Minus
                                                                         31452-31649
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                                 4153858
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                                                      Plus
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69553-69702
                                                      Minus
                  402851
                                  9650753
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8072597
                  403059
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                                                                         162569-162768,163918-164168
                  403279
                                                      Plus
                  403429
                                                                         52789-52917
                                  9719566
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                                                       Plus
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                                  8152000
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                                                       Plus
                                  9796665
3213020
                                                                          55584-55798
                   404629
                                                       Plus
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                   404973
                                                       Plus
   80
                                   8096888
                                                                          118940-119100
                                                       Minus
                   405110
                                   4156137
                                                       Minus
                                                                          98141-98754
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                                   4926864
                                                       Minus
                                                                          54424-55488
                                                        Minus
                                   7283744
                   405742
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	406014	6758904	Minus	23738-24076
	406036	6758919	Plus	17942-18163
	406109	9127147	Minus	58328-58485
	406255	7417729	Plus	2959-3200
	406326	9212385	Plus	84508-84655
	406600	8248616	Minus	36296-36610

TABLE 45A: ABOUT 947 GENES UP-REGULATED IN STOMACH CANCER COMPARED TO NORMAL ADULT TISSUES

Table 45A lists about 947 genes up-regulated in stomach cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affyrmetrix/Eos Hu03

GeneChip array such that the ratio of "average" stomach cancer to "average" normal adult tissues was great that the ratio of somethic cancers. The "average" normal adult tissue level was set to the 90th percentile amongst various non-malignant tissues. In order to the 90th percentile background levels of non-specific hybridization, the 15th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkay: Unique Eos probeset identifier number

Exacon: Exemplar Accession number, Genbank accession number

UniquenelD: Uniquen equene title

Uniquene gene title 10 15

Pkey: ExAccn: Unigene1D: Unigene Title: R1:

Unigene gene title Ratio of stormach cancer compared to normal stormach 20

					R1
	Pkey			Unigene Title	66.80
	418007			matrix metalloproteinase 1 (interstitial	61.16
	411243	,	Hs.69319	CA11	42.36
25	428368		Hs.83326	matrix metalloproteinase 3 (stromelysin collagen, type X, alpha 1 (Schmid metaph	35.80
	427585		Hs.179729		28.34
	425679		Hs.159177	lipase, gastric	26.91
	409041		Hs.50081	KIAA1199 protein	26.22
••	452121	NM_004081	Hs.70936	deleted in azoospermia	25.00
30	403776			NA anillin (Drosophila Scraps homolog), act	23.90
	444783	AK001468	Hs.62180	hypothetical protein FLJ10461	23.90
	422956	BE545072	Hs.122579	carbamoyl-phosphate synthetase 1, mitoch	23.35
	409187	AF154830	Hs.50966	hypothetical protein FLJ20513	22.26
26	424252	AK000520	Hs.143811 Hs.67709	Homo sapiens mRNA full length insert cDN	21.06
35	439759	AL359055	Hs.317584	ESTs	20.72
	415989	A1267700	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	19.84
	416209	AA236776	Hs.29352	tumor necrosis factor, alpha-induced pro	15.50
	452401	NM_007115	Hs.31409	ESTs	15.16
40	438639	A1278360 M86699	Hs.169840	TTK protein kinase	14.54
40	426427	AA045573	Hs.22900	nuclear factor (erythroid-derived 2)-lik	14.26
	449032	AAU45573 AI128388	Hs.143655	ESTs	14.22
	443211	R27496	Hs.1378	ennovin A3	13.96
	421470	AA635062	Hs.50094	Homo sapiens mRNA; cDNA DKFZp43400515 (f	13.94
45	400792 424086	AI351010	Hs.102267	lvevi oxidase	13.73
43		AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	13.38
	437789 409757	NM_001898	Hs.123114	cystatin SN	13.33
	447033	Al357412	Hs.157601	FSTs	13.20
	447164	AF026941	Hs.17518	Homo saniens cio5 mRNA, partial sequence	12.80
50	420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	12.66
50	432596	AJ224741	Hs.278461	matritin 3	12.64
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	12.46
	413582	AW295647	Hs.71331	hypothetical protein MGC5350	12.32 12.18
	423020	AA383092	Hs.1608	replication protein A3 (14kD)	12.10
55	448693	AW004854	Hs.228320	hypothetical protein FLJ23537	11.73
-	442660	AW138174	Hs.130651		11.16
	441693	AA384673	Hs.7943	RPB5-mediating protein	11.08
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	10.90
	414142	AW368397	Hs.150042	Horno sapiens cDNA FLJ14438 fis, clone HE	10.48
60	424717	H03754	Hs.152213		10.44
	443715	AI583187	Hs.9700	cyclin E1	10.38
	420900		Hs.44269		10.36
	453922	AF053306	Hs.36708		10.20
	415076		Hs.77890		10.18
65	452291		Hs.28853		10.14
	410566		Hs.43047		10.12
	414422		Hs.33723 Hs.22972		10.02
	409269		Hs.77695		10.02
70	414972			ATO hinding cassette sub-family C (CFTR	9.80
70	418882 428365				9.72
	416661				9.68
	400195		113.73411	NA NA	9.66
	418738		Hs.6682	solute carrier family 7, (cationic amino	9.64
75	420170		Hs.9563	1 Human normal keratinocyte mRNA	9.60
, ,	414259		Hs.3012	96 Homo sapiens cDNA: FLJZ3131 hs, clone L	9.58
	41751			a POPA (noncession of precursor, S. cerev	9.34
	44699		Hs.1676	2 Homo sapiens mRNA; cDNA DKFZp56482062 (1)	9.26
	42948			63 hypothetical protein FLJ 10339	9.16
80	42822			small inducible cytokine subfamily B (C)	8.95
	43181		Hs.2708	As kinesin-like 5 (mitotic kinesin-like pro	8.84 8.80
	41926		Hs.8979	wingless-type MMTV integration site fami	8.78
	42592		31 Hs.1622	11 solute carrier family 6 (neurotransmitte	0.10
				47	12

	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	8.69
	413268	AL039079	Hs.75256	regulator of G-protein signalling 1	8.68 8.68
	417801 452461	AA417383 N78223	Hs.82582 Hs.108106	integrin, beta-like 1 (with EGF-like rep transcription factor	8.68
5	425916	NM_006786	Hs.162200	urotensin 2	8.64
	422805	AA436989	Hs.121017	H2A histone family, member A	8.54
	438394 441377	BE379623 BE218239	Hs.27693 Hs.202656	peptidylprolyl isomerase (cyclophilin)-l ESTs	8.52 8.41
	445891	AW391342	Hs.199460	ESTs	8.31
10	408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed	8.30
	439521	AI808955	Hs.58248	ESTs	8.30
	425087 424653	R62424 AW977534	Hs.126059 Hs.151469	ESTs calcium/calmodulin-dependent serine prot	8.28 8.22
	441795	NS8115	Hs.21137	AD024 protein	8.02
15	427878	C05766	Hs.181022	CGI-07 protein	8.00
	413583	AL120806	Hs.5888	ESTs	7.98 7.98
	407853 426269	AA336797 H15302	Hs.40499 Hs.168950	dickkopf (Xenapus laevis) homolog 1 Homo sapiens mRNA; cDNA DKFZp566A1046 (f	7.97
••	404996	1110000	14.140300	NA	7.96
20	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	7.96
	410044 417655	BE566742 AA780791	Hs.58169 Hs.14014	highly expressed in cancer, rich in leuc hypothetical protein FLJ14813	7.94 7.92
	452838	U65011	Hs.30743	preferentially expressed antigen in meta	7.91
0.5	418895	AA894638	Hs.14600	ESTs	7.90
25	446155	AI553695	Hs.159422	Homo sapiens cDNA FLJ13997 fis, done Y7	7.86 7.82
	423123 434539	NM_012247 AW748078	Hs.124027 Hs.214410	SELENOPHOSPHATE SYNTHETASE; Human selen ESTs, Weakly similar to MUC2_HUMAN MUCIN	7.80
	447505	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (fr	7.72
20	418763	AK000219	Hs.88367	hypothetical protein FLJ20212	7.70
30	447289 443354	AW247017 AW970672	Hs.36978 Hs.9247	melanoma antigen, family A, 3 protein kinase, AMP-activated, atpha 1 c	7.70 7.69
	427718	AI798680	Hs.25933	ESTs	7.66
	434032	AW009951	Hs.206892	ESTs	7.60
25	427738	NM_000318	Hs.180612	peroxisomal membrane protein 3 (35kD, Ze	7.58 7.51
35	450480 418678	X82125 NM_001327	Hs.25040 Hs.167379	zinc finger protein 239 cancer/testis antigen	7.49
	431494	AA991355	Hs.298312	hypothetical protein DKFZp434A1315	7.44
	452705	H49805	Hs.246005	ESTs	7.36
40	443646	AI085198 BE536911	Hs.164226 Hs.234545	ESTs	7.32 7.30
70	425420 420617	AK001652	Hs.99423	hypothetical protein NUFZR ATP-dependent RNA helicase	7.28
	421155	H87879	Hs.102267	lysyl oxidase	7.24
	450715	AI266484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	7.24
45	447254 435473	NM_004153 N53550	Hs.17908 Hs.260881	origin recognition complex, subunit 1 (y ESTs	7.22 7.20
•••	413293	AL047483	Hs.302498	GTP-binding protein homologous to Saccha	7.14
	449347	AV649748	Hs.295901	KIAA0493 protein	7.11
	452281	T93500	Hs.28792 Hs.250822	Homo sapiens cDNA FLJ11041 fis, clone PL serine/threonine kinase 15	7.11 7.11
50	408908 408660	BE296227 AA525775	Hs.292523	ESTs, Moderately similar to PC4259 ferri	7.10
	453688	AW381270	Hs.194110	hypothetical protein PRO2730	7.02
	426890	AA393167	Hs.41294	ESTs	6.98 6.97
	404440 426642	AW068223	Hs.171581	NA ubiquitin C-terminal hydrolase UCH37	6.96
55	431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	6.95
	413833	Z15005	Hs.75573	centromere protein E (312kD)	6.94
	426249 441421	F05422 AA356792	Hs.168352 Hs.334824	nucleoporin-like protein 1 hypothetical protein FLJ14825	6.94 6.92
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	6.85
60	423903	M57765	Hs.1721	interleukin 11	6.84
	431041	AA490987	Hs.197955	KIAA0704 protein turnor necrosis factor receptor superfami	6.74 6.74
	417256 426921	U94332 AA037145	Hs.81791 Hs.172865	cleavage stimulation factor, 3 pre-RNA,	6.70
	407771	AL138272	Hs.62713	ESTs	6.69
65	433393	AF038564	Hs.98074	itchy (mouse homolog) E3 ubiquitin prote	6.66
	407162 411343	N63855 U77949	Hs.142634 Hs.69563	zinc finger protein CDC6 (cell division cycle 6, S. cerevisi	6.64 6.64
	427920	211502	Hs.181107	annexin A13	6.59
70	450159	AI702416	Hs.200771		6.58
70	427401 447102	U20582 BE167434	Hs.2149 Hs.98471	actin like protein ESTs, Weakly similar to T18712 hypotheti	6.55 6.54
	431806	AF186114	Hs.270737	tumor necrosis factor (ligand) superfami	6.54
	435159	AA668879	Hs.116649	ESTs	6.54
75	440209	H05049	Hs.22269	neurexin 3	6.54 6.50
13	418134 451807	AA397769 W52854	Hs.86617 Hs.27099	ESTs hypothetical protein FLJ23293 similar to	6.47
	434894	AW977850	Hs.23856	hypothetical protein MGCS297	6.40
	422505	AL120862	Hs.124165		6.34
80	426010 414696	AA136563 AF002020	Hs.1975 Hs.76918	hypothetical protein FLJ21007 Niernann-Pick disease, type C1	6.32 6.31
-	408380	AF123050	Hs.44532	diubiquitin	6.31
	420218	AW958037	Hs.285	ribosomal protein L4	6.29
	405817	NA		NA	6.28

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			0.2.02		6.24
				annexin A2 KIAA1136 protein	6.24
				hypothetical protein MGC3178	6.20
	10.000		Hs.151046	hypothetical protein FLJ11193	6.17
5		N32860	Hs.24611	ESTs, Wealdy similar to 154374 gene NF2	6.17 6.16
	401644		405045	NA ribulose-5-phosphate-3-epimerase	6.13
		AA380177 AA448542	Hs.125845 Hs.251677	G antigen 7B	6.12
	427335 450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	6.07
10	422420	U03398	Hs.1524	humor necrosis factor (ligand) superfami	6.06
10	419752	AA249573	Hs.152618	ESTs, Moderately similar to ZN91_HUMAN Z	6.06 6.06
	413573	AI733859	Hs.149089	ESTs .	6.02
	408758	NM_003686	Hs.47504	exonuclease 1 peptidytprolyt isomerase B (cyclophilin	6.02
15	444188 407746	Al393165 AK001962	Hs.699 Hs.38114	hypothetical protein FLJ11100	6.00
13	446364	AB006624	Hs.14912	KIAA0286 protein	5.98
	418939	AW630803	Hs.89497	lamin B1	5.90 5.88
	424639	AI917494	Hs.9812	Homo sapiens cDNA FLJ14388 fis, clone HE Homo sapiens cDNA FLJ11382 fis, clone HE	5.86
20	434377	AW137148	Hs.306593	Homo sapiens mRNA; cDNA DKFZp761D191 (fr	5.84
20	419863	AW952691 AI940727	Hs.93485 Hs.270556	ESTs, Highly similar to AF156779 1 ASB-4	5.82
	430849 428822	W28418	Hs.30715	notassium voltage-gated channel, isk-rei	5.80
	448776	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	5.74
	442957	AI949952	Hs.49397	ESTs	5.72 5.72
25	444577	AI207721	Hs.11393	RAD51 (S. cerevisiae) homolog C guanytate cyclase 1, soluble, alpha 3	5.71
	424565	AW102723	Hs.75295 Hs.132816	hypothetical protein MGC14801	5.68
	433330 428618	AW207084 AA885360	Hs.160199	NADPH oxidase, EF hand calcium-binding d	5.68
	432867	AW016936	Hs.233364	ESTs	5.64
30	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	5.63 5.62
	433133	AB027249	Hs.104741	PDZ-binding kinase; T-cell originated pr	5.57
	418379	AA218940	Hs.137516		5.57
	434551	BE387162 BE379594	Hs.280858 Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	5.56
35	442353 427386	AW836261	Hs.337717	ESTs	5.54
33	425650	NM_001944		desmoglein 3 (pemphigus vulgaris antigen	5.52
	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	5.51 5.50
	449370	AK002114	Hs.23495	hypothetical protein FLJ11252	5.50
40	431118	BE264901	Hs.250502 Hs.1695	! carbonic anhydrase VIII matrix metalloproteinase 12 (macrophage	5.50
40	423673 453931	BE003054 AL121278	Hs.25144	ESTs	5.49
	409044	Al129586	Hs.33033	hypothetical protein FLJ14623	5.48
	436291	BE568452	Hs.5101	protein regulator of cytokinesis 1	5.45 5.44
	448336	R53848	Hs.44976		5.42
45	454018	AW016892	Hs.10085		5.42
	457030	AI301740 AI160873	Hs.17338 Hs.69233		5.40
	412246 432193	AA372264	Hs.27319	3 hynothetical protein FLJ10706	5.40
	437319	BE410958	Hs.56406	Homo saniens cDNA FLJ13549 fis, clone PL	5.40 5.40
50	427660	AI741320	Hs.11412		5.38
	452862	AW378065		ESTs collagen, type IX, atpha 3	5.36
	409327	L41162 H06382	Hs.53563 Hs.21400		5.34
	412811 448390		Hs.21068	hypothetical protein	5.32
55	428187		Hs.2855	29 G protein-coupled receptor 49	5.30 5.29
	450434	AA156950		70 hypothetical protein FLJ14991	5.28
	434265				5.27
	407811				5.26
60	446638 444743			57 mudix (nucleoside diphosphate linked moi	5.43
00	424902				5.24 5.24
	452150	W42490	Hs.2608	44 ESTs	5.24
	43286				5.22
65	45338				5.22
05	44704 42651		Hs.1701		5.22
	45388		5 Hs.3623		5.20 5.20
	42962	5 AA45556		314 ESTs	5.20 5.20
70	41347				5.19
70			21 Hs.785 Hs.116		5.18
	44405 40943		Hs.544		5.17
	41271	9 AW0166	10 Hs.129	911 ESTs	5.15
	44434	2 NM_014	398 Hs.108	87 similar to hysosome-associated membrane	5.14 5.12
75			Hs.159		5.12
	45219			K75 Homo saniens Genratein coupled receptor	5.10
	4456! 4346!			425 Homo sapiens cDNA FLJ11980 fis, clone HE	5.09
	4242		4 Hs.155	140 casein kinase 2. alpha 1 polypeptide	5.08
80	) 4416	45 AJ22227	9 Hs.201	1555 ESTs, Wealdy similar to T23406 hypotheti	5.06 5.06
	4127				5.05
	4488				5.04
	4473	42 Al19926	IO 113, 13,		

	411835	U29343	Hs.72550	hyakuronan-mediated motility receptor (R	5.04
	421373 448991	AA808229 AW771565	Hs.167771 Hs.189594	ESTs ESTs	5.04 5.02
_	429370	C19097	Hs.89709	glutamate-cysteine ligase, modifier subu	5.00
5	454036	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	4.98
	405770 421110	AJ250717	Hs.1355	NA catheosin E	4.96 4.96
	452588	AA889120	Hs.110637	homeo box A10	4.92
10	433159	AB035898	Hs.150587	kinesin-like protein 2	4.91
10	420952 408321	AA282067 AW405882	Hs.88972 Hs.44205	ESTs, Moderately similar to A46010 X-fin contistatin	4.88 4.87
	441801	AW242799	Hs.86366	ESTs	4.84
	450568	AL050078	Hs.25159	Homo sapiens cONA FLJ10784 fis, clone NT	4.83
15	452909	NM_015368	Hs.30985	pannexin 1	4.82 4.82
13	409799 451105	D11928 AI761324	Hs.76845	phosphoserina phosphatase-like gb:wi50b11.x1 NCI_CGAP_Co16 Homo sapiens	4.80
	417168	AL133117	Hs.81376	Homo sapiens mRNA; cDNA DKFZp586L1121 (f	4.80
	418203	X54942	Hs.83758	CDC28 protein kinase 2	4.80
20	418994 436982	AA296520 AB018305	Hs.89546 Hs.5378	selectin E (endothelial adhesion molecul spondin 1, (f-spondin) extracellular mat	4.78 4.78
	432874	W94322	Hs.279651	melanoma inhibitory activity	4.78
	440351	AF030933	Hs.7179	RAD1 (S. pombe) homolog	4.78
	431956 442980	AK002032 AA857025	Hs.272245 Hs.8878	Homo sapiens cDNA FLJ11170 fis, clone PL kinesin-like 1	4.77 4.76
25	432437	W07088	Hs.293685	ESTs	4.76
	414869	AA157291	Hs.21479	ubinuclein 1	4.74
	446254	BE179829 AA425473	Hs.179852 Hs.84429	Homo sapiens cDNA FLJ12832 fis, clone NT	4.74 4.74
	418380 419343	AA456245	Hs.85603	KIAA0971 protein down-regulated by Clinib1, a	4.74
30	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	4.72
	425813	AA364136	Hs.210553	hypothetical protein DKFZp7611172	4.71 4.71
	425071 412733	NM_013989 AA984472	Hs.154424 Hs.74554	deiodinase, iodothyronine, type II KIAA0080 protein	4.68
	444325	AW152618	Hs.16757	ESTs	4.66
35	407638	AJ404672	Hs.334483	hypothetical protein FLJ23571	4.66
	430345 428330	AK000282 L22524	Hs.239681 Hs.2256	hypothetical protein FLJ20275 matrix metalloproteinase 7 (matrilysin,	4.66 4.64
	449448	D60730	Hs.57471	ESTs	4.62
40	409732	NM_016122	Hs.56148	NY-REN-58 antigen	4.62
40	432415 421987	T16971 Al133161	Hs.289014 Hs.286131	ESTs, Weakly similar to A43932 mucin 2 p CGI-101 protein	4.62 4.60
	430217	N47863	Hs.336901	ribosomal protein S24	4.58
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	4.57
45	425932	M81650	Hs.1968	semenogelin I	4.57 4.56
4)	408728 428434	AL137379 AW363590	Hs.47125 Hs.65551	hypothetical protein FLJ13912  Homo sapiens, Similar to DNA segment, Ch	4.55
	451254	AI571016	Hs.172967	ESTs	4.54
	422426	W79117	Hs.58559	ESTs	4.54
50	439483 435420	T69980 Al928513	Hs.58323 Hs.59203	Homo sapiens cDNA FLJ11613 fis, clone HE ESTs	4.53 4.53
30	447519	U46258	Hs.339665	ESTs	4.52
	424176	AL137273	Hs.142307	hypothetical protein	4.52
	414812 438069	X72755 N80701	Hs.77367 Hs.33790	monokine induced by gamma interferon ESTs	4.51 4.50
55	450096	AI682088	Hs.79375	holocarboxylase synthetase (biotin-[prop	4.50
	438159	Z83947		gb:H.sapiens mRNA; clone CD 117	4.50
	433925 417866	Al183551 AW067903	Hs.26481 Hs.82772	SBB126 protein collagen, type XI, alpha 1	4.48 4.48
	433384	A1021992	Hs.124244		4.47
60	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	4.47
	453941	U39817	Hs.36820	Bloom syndrome coagulation factor II (thrombin) recepto	4.45 4.44
	423401 430510	NM_001992 AW162916	Hs.128087 Hs.241576	hypothetical protein PRO2577	4.43
	424084	AI940675	Hs.20914	hypothetical protein FLJ23056	4.42
65	459587	AA031956	11- 1001CF	gb:zk15e04.s1 Soares_pregnant_uterus_NbH	4.42
	417956 449433	AA210704 AI672096	Hs.190465 Hs.9012	ESTs ESTs, Wealdy similar to S26650 DNA-bindi	4.42 4.42
	421477	AI904743	Hs.104650		4.42
70	406687	M31126	Hs.272620		4,41
70	451813 415091	NM_016117 AL044872	Hs.27182 Hs.77910	phospholipase A2-activating protein 3-hydroxy-3-methylglutaryl-Coenzyme A sy	4.41 4.40
	425142	AW954397	Hs. 154762		4.40
	441720	A1345487	Hs.28739	ESTs	4.40
75	409683	U33317	Hs.711	defensin, alpha 6, Paneth cell-specific hypothetical protein FLJ20516	4.39 4.38
, ,	411571 430044	AA122393 AA464510	Hs.70811 Hs.152812		4.36
	436246	AW450963	Hs.119991	ESTs	4.37
	409582	R27430	Hs.271565		4.37 4.35
80	453652 425211	AW009640 M18667	Hs.28368 Hs.1867	ESTs, Moderately similar to S65657 alpha progastricsin (pepsinogen C)	4.34
- •	448692	AW013907	Hs.167531	methylcrotonoyl-Coenzyme A carboxylase 2	4.34
	409459	D86407	Hs.54481	low density lipoprotein receptor-related	4,34 4.33
	442470	AW273860	Hs.5759	ESTs	4.33

			<b>.</b> .		4.32
				Homo sapiens, clone IMAGE:3685398, mRNA, cartilage oligomeric matrix protein (pse	4.31
		L32137 A1683487	Hs.1584 Hs.152213	wingless-type MMTV integration site fami	4.31
		AW079766	He 134880	ESTs. Wealdy similar to unnamed protein	4.30
5		AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	4.29 4.29
		BE563085	Hs.833	interferon-stirnulated protein, 15 kDa	4.28
	451592	AI805416	Hs.213897	ESTs. Wealdy similar to ALU8_HUMAN ALU S	4.28
	453900 422892	AW003582 AA988176	Hs.226414 Hs.121553	hypothetical protein FLJ20641	4.26
10	431699	NM_001173	Hs.267831	Rho GTPase activating protein 5	4.26
10	428389	AW135714	Hs.283127	ESTs, Weakly similar to T19201 hypotheti	4.24 4.23
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	4.22
	409913	8E243842	Hs.283077 Hs.12844	centrosomal P4.1-associated protein; unc EGF-like-domain, multiple 6	4.21
15	445537 445640	AJ245671 AW969626	Hs.31704	ESTs, Wealty similar to KIAA0227 [H.sapi	4.20
13	422232	D43945	Hs.113274	transcription factor EC	4.18
	442655	AW027457	Hs.30323	ESTs, Wealdy similar to B34087 hypotheti	4.18 4.16
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	4.16
20	434217	AW014795	Hs.23349 Hs.75334	ESTs exostoses (multiple) 2	4.14
20	413384 407768	NM_000401 AW002841	Hs.29475	FSTs	4.14
	419168	A1336132	Hs.33718	Homo saniens cDNA FLJ12641 fis, clone NT	4.13
	408165	AL137573	Hs.43143	Homo sapiens mRNA; cDNA DKF2p564A2463 (f	4.12 4.12
0.5	443691	AI081724	Hs.17267	ESTs	4.12
25	409640	U78722 AW138970	Hs.55481 Hs.122113	zinc finger protein 165 ESTs	4.10
	438176 435532	AW291488	Hs.117305	Homo sapiens, clone IMAGE:3682908, mRNA	4.10
	419606	AW294795	Hs.198529	ESTs	4.08
	452824	W27643	Hs.73965	splicing factor, arginine/serine-rich 2	4.08 4.08
30	414152	NM_003248	Hs.75774	thrombospondin 4	4.07
	418688	T85017	Hs.1192	KIAA0074 prolein NA	4.06
	404253 421741	AK001879	Hs.107527	hypothetical protein FLJ11017	4.06
	428218	AA424266	Hs.123642	FnhA3	4.06
35	428858	AA436760		gb:zv67d11.r1 Soares_total_fetus_Nb2HF8_	4.06 4.05
	428336	AA503115	Hs.183752	microseminoprotein, beta- Homo sapiens clone TCCCTA00142 mRNA sequ	4.04
	442875	BE623003 AA908197	Hs.23625 Hs.108850		4.04
	421841 451177	A1969716	Hs.13034	ESTs	4.04
40	425188	AK002052	Hs.155071	hynothetical protein FLJ11190	4.04
	421262	AA286746	Hs.9343	Homo sapiens cDNA FLJ14265 fis, clone PL	4.03 4.02
	424634	NM_003613			4.02
	438777	AA825487 AA324643	Hs.142179 Hs.246106	===	4.02
45	423343 425788	BE466417	Hs.231899		4.02
	409928	AL137163	Hs.57549	hypothetical protein dJ47384	4.01 4.01
	406671	AA129547	Hs.285754		4.00
	442973	BE567665	Hs.288550 Hs.173544	Homo sapiens cDNA: FLJ23156 fis, clone L ATPase, Class V, type 10D	4.00
50	433225 411765	AW816515 H43346	rts. 17334	gb:yp09a04.r1 Soares breast 3NbHBst Homo	4.00
20	452022	AW072330	Hs.29387	5 ESTs	4.00
	451806	NM_00372	9 Hs.27076		3.99 3.99
	423541	AA296922	Hs.12977		3.99
55	414132 452453	AI801235 AI902519	Hs.48480	gb:QV-BT009-101198-051 BT009 Homo sapien	3.98
))	418454		Hs.19587	n hypothetical protein FLJ14991	3.98
	430134		Hs.10522		3.98 3.97
	453160		Hs.23988		3.96
60	417235				3.95
00	425398 414136				3.94
	436608			71 down syndrome critical region protein US	3.94
	431753		Hs.2841	neuromedin U	3.94 3.94
45	453161			6 ESTs gb:QV4-TT0008-091199-025-103 TT0008 Homo	
65	454821 427961				3.94
	43945				3.93
	40956			3 fracture callus 1 (rat) homolog	3.93 3.92
70	41839				3.92
70	45141				3.92
	44588 40769				3.91
	44289		Hs.2611	08 ESTs	3.90
	43336	1 AW4693	73 Hs.3001	41 ribosomal protein L39	3.90 3.89
75					3.88
	41377			R2 hypothetical protein FLJ10525	3.86
	45294 42854			929 Homo sapiens cDNA FLJ14369 fis, clone HE	3.86
	45612	O AA53524	4 Hs.783	05 RAB2, member RAS oncogene family	3.86 3.85
80	45219	34 AI69441	3 Hs.332		3.85
	42124				3.85
	41777 4188			140515	3.84
	4,00				177

	430899	BE018217	Hs.183528	hypothetical protein FLJ14906	3.84
	421246	AW582962	Hs.102897	CGI-47 protein	3.83
	407366	AF026942		gb:Homo sapiens cig33 mRNA, partial sequ	3.83
5	428698	AA852773	Hs.334838	KIAA1866 protein	3.82 3.82
3	435202 454074	AI971313 R63503	Hs.170204 Hs.28419	KIAA0551 protein ESTs	3.82
	448917	A1683598	Hs.201615	ESTs	3.82
	410507	AA355288	Hs.40834	transitional epithelia response protein	3.82 3.82
10	452571 445663	W31518 A1247343	Hs.34665 Hs.149232	ESTs ESTs	3.82
10	450701	H39960	Hs.288467	Homo sapiens cDNA FLJ12280 fis, clone MA	3.80
	423025	AA831267	Hs.12244	hypothetical protein FLI 20097	3.80
	425656	AB018284	Hs.158688 Hs.117183	KIAA0741 gene product ESTs	3.80 3.79
15	407168 403422	R45175 NA	ns.11/100	NA	3.79
	425492	AL021918	Hs.158174	zinc finger protein 184 (Kruppel-like)	3.79
	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	3.79 3.78
	457325 433800	AA744550 A1034361	Hs.136345 Hs.135150	ESTs lung type-I cell membrane-associated gly	3.77
20	428865	BE544095	Hs.164960	Barti-like homeobox 1	3.76
	424188	AW954552	Hs.142634	zinc finger protein	3.75
	424638	AI472106 RS2795	Hs.49303 Hs.25954	Homo sapiens cDNA FLJ11663 fis, clone HE interleukin 13 receptor, alpha 2	3.75 3.75
	451099 448105	AW591433	Hs.298241	Transmembrane protease, serine 3	3.74
25	452785	AL359942	Hs.296434	erythroid differentiation and denucleati	3.74
	459000	AA903705	Hs.4190	Homo sapiens cDNA: FLJ23269 fts, clone C ESTs, Wealdy similar to JC7328 amino aci	3.74 3.73
	432653 409632	N62096 W74001	Hs.293185 Hs.55279	serine (or cysteine) proteinase inhibito	3.73
••	414883	AA926960	Hs.334883	CDC28 protein kinase 1	3.73
30	415064	AA159804	Hs.149305	hypothetical protein MGC2603	3.72 3.72
	432198 458194	Al475306 AW383618	Hs.50458 Hs.265459	ESTs Moderately similar to ALU2_HUMAN A	3.72
	415263	AA948033	Hs.130853	ESTs	3.71
2.5	408296	AL117452	Hs.44155	DKFZP586G1517 protein	3.71
35	408460 437496	AA054726 AA452378	Hs.285574 Hs.170144	ESTs Homo sapiens mRNA; cDNA DKFZp547J125 (fr	3.71 3.70
	443486	NM_003428	Hs.9450	zinc finger protein 84 (HPF2)	3.68
	432021	AA524470	Hs.58753	ESTs	3.68
40	420092	AA814043	Hs.88045	ESTs	3.68 3.68
40	414923 429432	AW445008 AI678059	Hs.77637 Hs.202676	homeo box A4 synaptonemal complex protein 2	3.68
	435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-r	3.67
	430544	AA481066	Hs.105153	Homo sapiens, done IMAGE:3461987, mRNA,	3.67 3.67
45	432542 410782	AW083920 AW504860	Hs.16098 Hs.288836	claudin 2 hypothetical protein FLJ12673	3.66
43	421106	AA877124	Hs.172844	ESTs	3.64
	439107	AL046134	Hs.13944	adrenergic, beta, receptor kinase 2	3.64 3.64
	418735 411598	N48769 BE336654	Hs.44609 Hs.70937	ESTs H3 histone family, member A	3.63
50	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase 8	3.63
	436411	AW67#352		gb:ba63c07.y1 NIH_MGC_12 Homo sapiens cD	3.63
	429774	AI522215	Hs.50883 Hs.177164	KIAA1804 protein ESTs	3.62 3.61
	448844 402473	AI581519 AB033035	Hs.51965	KIAA1209 protein	3.61
55	441085	AW136551	Hs.181245	Homo sapiens cDNA FLJ12532 fis, clone NT	3.61
	429534	AW976987	Hs.163327		3.60 3.60
	414706 436211	AW340125 AK001581	Hs.76989 Hs.334828	KIAA0097 gene product hypothetical protein FLJ10719; KIAA1794	3.59
	422938	NM_001809		centromere protein A (17kD)	3.59
60	451381	BE241831	Hs.172330		3.58 3.58
	428664 424345	AK001666 AK001380	Hs.189095 Hs.145479		3.58
	440717	AA904527	Hs.42207	ESTs	3.58
45	450698	W31489	Hs.95044	ESTs, Weakly similar to I38022 hypotheti	3.58 3.58
65	423675 424882	A1990509 A1379461	Hs.131342 Hs.153636		3.57
	410784	AW803201	113.133000	gb:IL2-UM0077-070500-080-E06 UM0077 Homo	3.55
	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	3.55 3.54
70	430294 439225	AI538226 AA192669	Hs.32976 Hs.45032	guanine nucleotide binding protein 4 ESTs	3.54
70	429183	AB014604	Hs.197955		3.54
	419948	AB041035	Hs.93847	NADPH oxidase 4	3.53
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1 5-hydroxytryptamine (serotonin) receptor	3.52 3.52
75	408556 417048	U49516 AI088775	Hs.46362 Hs.55498	geranylgeranyl diphosphate synthase 1	3.52
	432101	AI918950	Hs.123647	2 EphA3	3.52
	419216	AU076718	Hs.16402		3.51 3.51
	444754 422093	T83911 AF151852	Hs.11881 Hs.11144		3.50
80	404766	NA		NA .	3.50
	441513		Hs.11242		3.50 3.50
	444301 417315		Hs.10760 Hs.33690		3.50
				•	

					3.49
			Hs.230157	ESTs Homo sapiens cDNA FLJ13103 fis, clone NT	3.49
	443204 432289		Hs.29643 Hs.55118	ESTs	3.49
	453644	AI813444	Hs.42197	FSTs	3.48
5	427986	N45214	Hs.282387	Homo sapiens cDNA: FLJ21837 fis, clone H	3.48 3.48
	405466	U64820	Hs.66521	NA Machado-Joseph disease (spinocerebellar	3.48
	410804 430357	AW976789	Hs.165607	ESTs	3.46
	418428	Y12490	Hs.85092	thyroid hormone receptor interactor 11	3.46 3.46
10	422260	AA315993	Hs.105484	regenerating gene type IV polyadenylate binding protein-interactin	3.46
	421928 451403	AF013758 AA885569	Hs.109643 Hs.40919	Horno sapiens cDNA FLJ14511 fis, clone NT	3.46
	406117	74100000		NA	3.46 3.46
	458242	BE299588	Hs.28465	Homo sapiens cDNA: FLJ21869 fis, clone H Homo sapiens mRNA for KIAA1568 protein,	3.45
15	408562	A1436323 AA694010	Hs.31141 Hs.6932	Homo saniens clone 23809 mRNA sequence	3.45
	440105 443767	BE562136	Hs.9736	proteasome (prosome, macropain) 26S subu	3.45
	426320	W47595	Hs.169300	transforming growth factor, beta 2	3.45 3.45
20	444478	W07318	Hs.240	M-phase phosphoprotein 1 POP4 (processing of precursor, S. cerev	3.44
20	425904 416702	A1805990 AA186428	Hs.82238 Hs.85591	ESTs	3.44
	448668	AI560305	Hs.199852	ESTs	3.42
	410004	AI298027	Hs.5057	carboxypeptidase D	3.42 3.42
26	428771	AB028992	Hs.193143 Hs.313	KIAA 1069 protein secreted phosphoprotein 1 (osteopontin,	3.42
25	446619 429628	AU076643 H09604	Hs.13268	ESTs	3.40
	448816	AB033052	Hs.22151	KIAA1226 protein	3.40 3.39
	456032	AW957446	Hs.301711	ESTs hypothetical protein FLJ22729	3.39
30	439635	AA477288 AW970254	Hs.94891 Hs.889	Charot-Leyden crystal protein	3.38
30	414275 447207	AA442233	Hs.17731	hypothetical protein FLJ12892	3.38
	416057	AI927382	Hs.29857	ESTs	3.38 3.38
	430704	AW813091	Hs.335799 Hs.310359		3.38
35	423600 453891	AI633559 AB037751	Hs.36353	Homo sapiens mRNA full length insert cDN	3.38
33	430178	AW449612	Hs.15247		3.37 3.37
	417791	AW965339	Hs.11147		3.37
	408867	AA437199 AW901804	Hs.656 Hs.23984	cell division cycle 25C hypothetical protein FLJ20147	3.37
40	449802 457003	S78234	Hs.17240	5 cell division cycle 27	3.36
40	458076	R80061	Hs.16447	B hypothetical protein FLJ21939 similar to	3.36 3.36
	436203	BE384982	Hs.5076 Hs.14665	Homo sapiens cDNA: FLJ22128 fis, clone H ESTs	3.34
	418782 449722	AI792648 BE280074	Hs.23960		3.34
45	447984		Hs.37244	ESTs	3.34 3.34
	451103		Hs.25956		3.34
	408812 448305		Hs.25476 Hs.2649	5 Homo saniens cDNA FLJ12908 fis, clone N1	3.34
	418849				3.33 3.32
50	450531	AW301032			3.32
	411263		Hs.6936 Hs.7936		3.31
	416530 425746				3.30
	421037	7 A1684808	Hs.1976	53 ESTs	3.30 3.30
55	430388				3.30
	433132 447078				3.30
	40240	8 NA		NA .	3.29 3.29
۷0	43704				3.28
60	42312 44622			699 hypothetical protein FLJ12969	3.27
	45191			Horno sapiens unknown mRNA	3.27 3.26
	41933				3.26
65	41107 41979		Hs.182 Hs.932		3.26
03	42711			574 ESTs	3.26 3.26
	40025	50 NA		NA SORT-	3.25
	42904				3.24
70	45105 44743			73 acylphosothatase 1, erythrocyte (common)	3.24
	4103		49 Hs.817	7 FSTs. Weakly similar to PIHUB6 salivary	3.23 3.22
	4165				3.22
	4420 4091			778 nihan omtein	3.22
75	4189	26 AA23265	8 Hs.10	5794 UDP-glucose:glycoprotein glucosyltransfe	3.22 3.21
	4083				3.20
	4454 4429			4743 ESTs	3.20
	4392		21 Hs.55	hypothetical protein MGC5347	3.20 3.20
80	) 4409	953 AI68303			3.20
	4470 4511		Hs.16 10 Hs.20	7461 ESTs	3.19
	422				3.19
	·				470

	411573	AB029000	Hs.70823	KIAA1077 protein	3.19
	424539	L02911	Hs.150402	activin A receptor, type I	3.18 3.18
	443179 452545	AI928402 N31940	Hs.6933 Hs.14434	hypothetical protein FLJ12684 ESTs, Wealdy similar to I38022 hypotheti	3.18
5	433024	AA573847	Hs.26549	KIAA1708 protein	3.18
	414737	AI160386	Hs.125087	ESTs	3.18
	444230 419741	H95537 NM_007019	Hs.146067 Hs.93002	ESTs ubiquifin carrier protein E2-C	3.18 3.17
	428945	AW192803	Hs.98974	ESTs, Wealthy similar to S65824 reverse t	3.17
10	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	3.17
	418661	NM_001949	Hs.1189	E2F transcription factor 3	3.17
	443598 413516	AW499970 BE145907	Hs.14822	ESTs, Wealty similar to 178885 serine/th gb:MR0-HT0208-221299-204-e12 HT0208 Homo	3.16 3.16
_	434389	AA971235	Hs.128098	ESTs	3.16
15	431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo	3.15
	432158	W33165	Hs.22983	UDP-glucose:glycoprotein glucosyltransfe	3.15 3.15
	453331 410286	AI240665 AI739159	Hs.8895 Hs.61898	ESTs DKFZP586N2124 protein	3.14
	408687	AL110280	Hs.301152	Homo sapiens mRNA; cDNA DKFZp434F053 (fr	3.14
20	422789	AK001113	Hs.120842	hypothetical protein FLJ10251	3.14
	419078 414080	M93119 AA135257	Hs.89584 Hs.47783	insulinoma-associated 1 B aggressive lymphoma gene	3.14 3.14
	451525	AW001757	Hs.14005	ESTs	3.13
0.0	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	3.13
25	433183	AF231338	Hs.222024	transcription factor BMAL2	3.12 3.12
	424783 413170	AA913909 BE068819	Hs.153088	TATA box binding protein (TBP)-associate gb:MR0-BT0374-220300-001-b03 BT0374 Homo	3.12
	437181	Al306615	Hs.125343	ESTs, Weakly similar to KIAA0758 protein	3.12
20	442991	BE281238	Hs.8886	hypothetical protein FLJ20424	3.11
30	453867 437641	AI929383 - AA811452	Hs.33032 Hs.291911	hypothetical protein DKFZp434N185 ESTs	3.11 3.10
	428651	AF196478	Hs.188401	annexin A10	3.09
	427927	AJ879165	Hs.2227	CCAAT/enhancer binding protein (C/EBP),	3.09
25	419196	AF110908	Hs.297660	TNF receptor-associated factor 3	3.09 3.09
35	414569 408633	AF 109298 AW963372	Hs.118258 Hs.46677	prostate cancer associated protein 1 PRO2000 protein	3.09
	403381	MIJOGOTE	143.40077	NA .	3.08
	444619	BE538082	Hs.8172	ESTs, Moderately similar to A46010 X-lin	3.08
40	422363	T55979 AA625804	Hs.115474	replication factor C (activator 1) 3 (38 gb:zu86h01.s1 Soares_testis_NHT Homo sap	3.08 3.07
40	434138 425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	3.07
	436556	Al364997	Hs.7572	ESTs	3.07
	427043	AA397679	Hs.3991	ESTs	3.06
45	443055 419229	AV653742 AI827237	Hs.15536 Hs.282884	hypothetical protein DKFZp761J139 ESTs	3.06 3.05
••5	414718	H95348	Hs.107987	ESTs	3.05
	439737	AI751438	Hs.41271	Homo sapiens mRNA full length insert cDN	3.05
	448587	AI539652	Hs.28338	KIAA1546 protein	3.04 3.04
50	448595 407201	AB014544 N31998	Hs.21572 Hs.164256	KIAA0644 gene product hypothetical protein FLJ20657	3.04
-	423065	R96158	Hs.267130	Homo sapiens, clone MGC:5406, mRNA, comp	3.04
	431980	AA523696	Hs.324507	hypothetical protein FLJ20986	3.04
	416198 429410	H27332 X98494	Hs.99598 Hs.201676	hypothetical protein MGC5338 M-phase phosphoprotein 10 (U3 small nucl	3.04 3.04
55	432140	AK000404	Hs.272688	hypothetical protein FLJ20397	3.03
	441031	Al110684	Hs.7645	fibrinogen, B beta polypeptide	3.03
	446142 402167	A1754693	Hs.145968	ESTs NA	3.02 3.02
	402299			NA NA	3.02
60	417830	AW504786	Hs.122579	hypothetical protein FLJ10461	3.02
	419910	AA662913	Hs.190173 Hs.137476		3.02 3.01
	424001 413930	W67883 M86153	Hs.75618	patamally expressed 10 RAB11A, member RAS oncogene family	3.01
	439924	AI985897	Hs.125293		3.01
65	414343	AL036166	Hs.323378		3.01 3.00
	432201 445845	AI538613 AI261870	Hs.298241 Hs.145555		3.00
	420727	H75701	Hs.99886	complement component 4-binding protein,	3.00
70	427510	Z47542	Hs.179312		3.00
70	403637	NA AK000305	Un CYNEE	NA hypothetical protein FLJ20298	3.00 3.00
	410947 413430	R22479	Hs.67055 Hs.167073		3.00
	423575	C18863	Hs.163443	Horno sapiens cDNA FLJ11576 fis, clone HE	2.99
75	426711	AA383471	Hs.180669		2.99 2.98
13	442204 429682	AI535450 NM_006306	Hs.21914 Hs.211602	ESTs SMC1 (structural maintenance of chromoso	2.98 2.98
	419227	BE537383	Hs.89739	cholinergic receptor, nicotinic, beta po	2.97
	447233	AW246333	Hs.17901	Homo sapiens, clone IMAGE:3937015, mRNA,	2.97
80	441826	AW503603	Hs,129915		2.97 2.96
90	433404 450506	T32982 NM_004460	Hs.102720 Hs.418	fibroblast activation protein, alpha	2.96
	423880	BE278111	Hs.134200	DKFZP564C186 protein	2.96
	411750	BE562298	Hs.71827	KIAA0112 protein; homolog of yeast ribos	2.96

	*****	AD044500	Un 42122	ΚΙΔΛ	0628 gene product	2.96
			Hs.43133 Hs.199665	EST:	3	2.96
	451250	AA491275	Hs.236940		thetical protein FLJ12542	2.96 2.96
-			Hs.154850	colla EST:	gen, type IX, alpha 1	2.95
5	447829 410561	AI433029 BE540255	Hs.164104 Hs.6994	Hom	o saciens cDNA: FLJ22044 fis, clone H	2.95
	417873	BE266659	Hs.293659	Horr	no sapiens, Similar to RIKEN cDNA A430	2.95 2.95
	452693	179153	Hs.48589	zinc	finger protein 228 stransferase family, cytosolic, 1C,	2.94
10	407742	AF186252 AW207555	Hs.38084 Hs.97093	Hon	no sapiens cDNA: FLJ23004 fis, done L	2.94
10	421430 407995	A1094748	Hs.100134	hyp	othetical protein FLJ12787	2.94
	413281	AA861271	Hs.222024	tran	scription factor BMAL2	2.94 2.94
	452381	H23329	Hs.290880	ES1	s, Weakly similar to ALU1_HUMAN ALU S	2.94
15	441020 425397	W79283 J04088	Hs.35962 Hs.156346	top	oisomerase (DNA) II alpha (170kD)	2.94
1.5	420005	AW271106	Hs.133294	ES.	Ts .	2.93 2.93
	412530	AA766268	Hs.266273	hyp	othetical protein FLJ13346 haracterized bone marrow protein BM03	2.93
	435602	AF217515	Hs.283532 Hs.287955	Und	mo sapiens cDNA FLJ13090 fis, clone NT	2.93
20	447247 443341	AW369351 AW631480	Hs.8688	FS	Ts	2.92
20	436481	AA379597	Hs.5199	HS	PC150 protein similar to ubiquitin-con	2.92 2.92
	410144	W07189	Hs.68185	ES	Ts, Weakly similar to ARL3_HUMAN ADP-R inoblastoma-like 1 (p107)	2.92
	434450	\$78664 BE218027	Hs.87 Hs.89969	ES	Ts.	2.92
25	450402 422026	U80736	Hs.110826	trin	nucleotide repeat containing 9	2.92 2.92
	421562	AA530994	Hs.334471		relin precursor	2.92
	410434	AF051152	Hs.63668 Hs.119018		l-like receptor 2 Inscription factor NRF	2.91
	422665 428966	AJ011812 AF059214	Hs.194687	ch	niesterol 25-hydroxylase	2.90
30	412416	AI628253	Hs.22580	ali	kylglycerone phosphate synthase	2.90 2.90
	446232	AI281848	Hs.194691	re	tinoic acid induced 3 v:MR4-ST0124-270300-005-b11 ST0124 Homo	2.90
	454600	AW810001 AK001160	Hs.5999	p.	pothetical protein FLJ10298	2.90
	438018 433252	AB040957	Hs.151343	. K	IAA1574 protein	2.90 2.90
. 35	444355	BE383686	Hs.191621	E	STs, Moderately similar to ALU6_HUMAN A	2.89
	443054	AI745185	Hs.8939		es-essociated protein 65 kDa rucine zipper protein FKSG14	2.89
	421308 411643	AA687322 AI924519	Hs.192843 Hs.192570		ypothetical protein FLJ22028	2.89
	419559	Y07828	Hs.91096	ri	ng finger protein	2.89 2.88
40	433527	AW235613	Hs.13302	) E	STs umor necrosis factor (tigand) superfami	2.88
	426274	D38122	Hs.2007		IMOR NECTOSIS FACTOR (ligarity) superiors	2.88
	406182 432731	NA R31178	Hs.28782		bronectin 1	2.88
	429274	Al379772	Hs.99206		STs	2.87 2.87
45	418216	AA662240	Hs.28309 Hs.59346		AF15q14 protein hypothetical protein FLJ10514	2.86
	410166 452665	AK001376 AW839326	Hs.33041	4 1	ESTs, Moderately similar to \$65657 alpha	2.86
	424696		Hs.15190	3 (	GrpE-like protein cochaperone	2.86 2.85
	410174		Hs.59461		DKFZP434C245 protein	2.85
50	443640		Hs.13421 Hs.2003		ESTs ESTs	2.85
	432912 431611		Hs.2644	28	tissue specific transplantation antigen	2.85
	446565		Hs.311		phosphoribosyl pyrophosphate amidotransf Homo sapiens HDCME13P mRNA, partial cds	2.85 2.84
55	424770		Hs.1106 Hs.8923		chromobox homotog 5 (Drosophila HP1 alph	2.84
55	418845 403639		F15.0323		NΔ	2.84
	451110		Hs.2653		ESTs, Wealdy similar to transformation-r	2.84 2.84
	41618				KIAA1785 protein B aggressive lymphoma gene	2.83
60	44466 42344		Hs.2783		absent in melanoma 1 like	2.83
00	45058		Hs.6037	71	ESTs CONTRACT CONTRACT	2.83 2.83
	42019				Homo sapiens mRNA for FLJ00057 protein, ESTs, Weakly similar to ALU1_HUMAN ALU S	2.83
	42559 42440				collagen, type V, alpha 1	2.83
65	44875		Hs.381		ESTs	. 2.82 2.82
0.5	44494	6 AW13920			hypothetical protein FLJ22408	2.82
	43534				ESTs hypothetical protein FLJ22649 similar to	2.82
	43843 42768				histamine receptor H1	2.82
70	4269		6 Hs.974	54	ESTS	2.82 2.82
	4279				ESTs ESTs	2.82
	4425 4410				ESTs	2.81
	4147		Hs.772		plasminogen activator, urokinase	2.81
75	4171	60 N76497	Hs.176		proteolipid protein 1 (Pelizaeus-Merzbac hypothetical protein DKFZp7620096	2.81 2.81
	4093		6 Hs.543 Hs.633		carbonic anhydrase IX	2.81
	4104 4071		113.03		gb:ye53h05.s1 Soares fetal liver spleen	2.81
	4358	49 BE30524			daudin 2	2.80 2.80
80					ESTs ESTs, Wealthy similar to 138022 hypotheti	2.80
	4283 4207		00 ns.30 Hs.12		Homo sapiens cDNA FLJ11381 fis, clone HE	2.80
	4213				deleted in malignant brain tumors 1	2.80
						401

	419423	D26488	Hs.90315	KIAA0007 protein	2.79
	452355	N54926	Hs.29202	G protein-coupled receptor 34	2.79
	425826	U97698	Hs.159593	mucin 6, gastric DNA replication factor	2.79 2.79
5	457465 426472	AW301344 BE246138	Hs.122908 Hs.30853	ESTs	2.79
•	424081	NM_006413	Hs.139120	nbonuclease P (30kD)	2.78
	425851 419236	NM_001490 AA330447	Hs.159642 Hs.135159	glucosaminyl (N-acetyl) transferase 1, c Homo sepiens cDNA FLJ11481 fis, clone HE	2.78 2.78
	423430	AF112481	Hs.128501	RAD54, S. cerevisiae, homolog of, B	2.78
10	410011	AB020641	Hs.57856	PFTAIRE protein kinase 1	2.78
	453700 431250	AB009426 BE264649	Hs.560 Hs.251377	apolipoprotein 8 mRNA editing enzyme, ca taxol resistance associated gene 3	2.78 2.77
	414043	AI521210	Hs.97977	ESTs	2.77
16	418054	NM_002318	Hs.83354	lysyl oxidase-like 2	277
15	439223 425956	AW238299 M60828	Hs.250618 Hs.164568	UL16 binding protein 2 fibroblast growth factor 7 (keratinocyte	2.76 2.76
	437612	AA827715	Hs.105153	Homo sapiens, clone IMAGE:3461987, mRNA,	2.76
	426119	W94997	Hs.189917	ESTs	2.76
20	459574 442339	AI741122 BE299668	Hs.101810 Hs.227591	Horno sapiens cDNA FLJ14232 fis, clone NT ESTs, Wealtly similar to 1901303A Leu zip	2.76 2.76
20	414334	AA824298	Hs.21331	hypothetical protein FLJ10036	2.76
	418217	AJ910647	Hs.13442	ESTs	2.76
	420022 408243	AA256253 Y00787	Hs.120817 Hs.624	ESTs interleukin 8	2.76 2.75
25	421346	Z34277	Hs.103707	apomucin	2.75
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.75 2.75
	425773 449611	N21279 A1970394	Hs.237749 Hs.197075	ESTs ESTs	274
	424827	AI057094	Hs.96867	Homo sapiens cDNA: FLJ23155 fis, clone L	2.74
30	448621	AI097144	Hs.5250	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.74 2.73
	428523 410839	AW974540 NM_006849	Hs.98626 Hs.66581	ESTs protein disutfide isomerase	2.73
	437380	AL359577	Hs.112198	Homo sapiens mRNA; cDNA DKFZp547M073 (fr	2.73
25	424641	AB001106	Hs.151413	glia maturation factor, beta	2.73
35	431708 436209	A1698136 AW850417	Hs.108873 Hs.254020	ESTs ESTs, Moderately similar to unnamed prot	2.73 2.73
	430209	AW294909	Hs.132208	ESTs	2.73
	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	2.73
40	409506 423482	NM_006153 BE280172	Hs.54589 Hs.129228	NCK adaptor protein 1 galactokinase 2	2.73 2.73
70	417015	M83772	Hs.80876	flavin containing monooxygenase 3	2.72
	448165	NM_005591	Hs.202379	meiotic recombination (S. cerevisiae) 11	2.72 2.72
	448826 447803	AI580252 BE620578	Hs.293246 Hs.30858	ESTs, Weakly similar to putative p150 (H ESTs, Weakly similar to S65657 alpha-1C-	2.72
45	429703	T93154	Hs.28705	ESTs	2.72
	448796	AA147829	Hs.301431	endothelial zinc finger protein induced	2.72 2.72
	410902 424745	AW809665 AA214618	Hs.152759	gb:MR4-ST0124-261099-015-g07 ST0124 Homo activator of S phase kinase	2.72
	454469	AW792775	10.102100	gb:CM0-UM0001-010300-258-g10 UM0001 Homo	2.72
50	458632	A1744445	Hs.167073		2.72 2.72
	452012 422109	AA307703 S73265	Hs.279766 Hs.1473	kinesin family member 4A gastrin-releasing peptide	2.72
	438008	AA775026	Hs.203802		2.72
55	420552	AK000492	Hs.98806	hypothetical protein	2.71 2.71
33	427038 409239	NM_014633 AA740875	Hs.173288 Hs.44307	KIAA0155 gene product ESTs, Moderately similar to 138022 hypot	2.71
	425371	D49441	Hs.155981	mesothelin	2.71
	439857	AA847194	Hs.232002	ESTs gb:RC4-NN0027-150400-012-g04 NN0027 Harno	2.71 2.71
60	455309 439580	AW894017 AF086401	Hs.293847		2.70
	437257	AI283085	Hs.290931	ESTs, Weakly similar to YFJ7_YEAST HYPOT	2.70
	435039	AW043921 W67821	Hs.130526 Hs.109590		2.70 2.70
	438796 407013	U35637	113.103550	gb:Human nebutin mRNA, partial cds	2.70
65	445413	AA151342	Hs.12677	CGI-147 protein	2.70
	418416 441362	U11700 BE614410	Hs.84999 Hs.23044	ATPase, Cu  transporting, beta polypept RAD51 (S. cerevisiae) homolog (E coli Re	2.70 2.69
	448045	AJ297436	Hs.20166	prostate stem cell antigen	2.69
70	441868	A1400276	Hs. 183485		2.69 2.69
70	449076 427528	AI627826 AU077143	Hs.209109 Hs.179565		2.69
	427526	D42063	Hs.199179	RAN binding protein 2	2.69
	414618	AI204600	Hs.96978		2.69 2.68
75	441350 419310	AB020690 AA236233	Hs.7782 Hs.188716	paraneoptastic antigen MA2 5 ESTs	2.68
	445279	R41900	Hs.22245	ESTs .	2.68
	439741	BE379646	Hs.6904 Hs.156829	Homo sapiens mRNA full length insert cDN Homo sapiens mRNA for KIAA1763 protein,	2.68 2.68
	445692 449300	Z44514 Al656959	Hs.22216		2.68
80	444585	AW170015	Hs.6594	ESTs	2.68
	444384 448104	BE174527 AI674818	Hs.11065 Hs.31643		2.68 2.67
	446839	BE091926	Hs.16244		2.67

PCT/US02/29560

					2.67
				transcriptional intermediary factor 1 ESTs	2.66
			Hs.87113 Hs.150028	ESTs	2.66
			Hs.121296	ESTs	2.66
5	403548			NA .	2.66 2.66
		AW295390	Hs.213062 Hs.271593	ESTs, Moderately similar to A47582 B-cel	2.66
	449532 453985	W74653 N44545	Hs.251865	ESTS	2.65
	409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	2.65 2.65
10	409446	AI561173	Hs.67688	ESTs	2.65
	422094	AF129535	Hs.272027	F-box only protein 5 hypothetical protein MGC3077	2.64
	445462 432670	AA378776 AA806536	Hs.288649 Hs.291841	FSTs	2.64
	418634	AK000064	Hs.86905	ATPase, H+ transporting, lysosomal (vacu	2.64 2.64
15	453628	AW243307	Hs.83937	hypothetical protein	2.64
	442117	AW664964	Hs.128899 Hs.23450	ESTs mitochondrial ribosomal protein S25	2.64
	416248 414631	H99169 AW970130	Hs.65406	FSTs	2.64
	423268	BE386898	Hs.131162	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.64 2.63
20	413597	AW302885	Hs.117183	ESTs Homo sapiens BAC clone RP11-505D17 from	2.63
	446031	A)271704	Hs.18987 Hs.24485	chondroitin sulfate proteoglycan 6 (barna	2.63
	450142 436304	AW207469 AA339622	Hs.108887	ESTs	2.63
	439832	T81829	Hs.14870	Horno sapiens, Similar to hect domain and	2.63
25	449207	AL044222	Hs.23255	nucleoporin 155kD	2.62 2.62
	416111	AA033813	Hs.79018 Hs.77204	chromatin assembly factor 1, subunit A ( centromere protein F (350/400kD, mitosin	2.62
	414747 423811	U30872 AW299598	Hs.77204 Hs.50895	homeo box C4	2.62
	439474	AJ824060	Hs.211501	FSTs	2.62 2.62
30	417218	AA005247	Hs.285754	met proto-oncogene (hepatocyte growth fa Homo sapiens cDNA FLJ 10366 fis, clone NT	2.62
	408031	AA081395	Hs.42173 Hs.8752	transmembrane protein 4	2.62
	<b>442</b> 821 418245	BE391929 AA088767	Hs.83883	transmembrane, prostate androgen induced	2.62
	447917	AL048037	Hs.164588	ESTs. Moderately similar to neuronal thr	2.61 2.61
35	424840	D79987	Hs.153479	extra spindle poles, S. cerevisiae, homo	2.61
	443268	AI800271	Hs.129445 Hs.2186	hypothetical protein FLJ12496 eukaryotic translation elongation factor	2.61
	403056 433037	R58624 NM_014158		N HSPC067 aratein	2.61
	410358	AW975168	Hs.13337	ESTs. Weakly similar to unnamed protein	2.60 2.60
40	426181	AA371422	Hs.334371	hypothetical protein MGC13096	2.60
	414853	U31116	Hs.77501	sarcoglycan, beta (43kD dystrophin-assoc B ESTs	2.60
	457233 416049	AI355009 AI970536	Hs.22169 Hs.16603		2.60
	418946	AI798841	Hs.16452		2.60 2.60
45	441891	AW129145	Hs.12807		2.60
	443742	AW627805	Hs.14542		2.60
	433868 442717	AA612960 R88362	Hs.33730 Hs.18059		2.59
	444542	AI161293	Hs.28038	0 aminopeptidase	2.59 2.59
50	452940	AA029722	Hs.2173	fucosyltransferase 4 (alpha (1,3) fucosy	2.59 2.59
	429170	NM_00139		dual specificity phosphatase 4 serine/threonine kinase 2	2.59
	417531 401458	NM_00315	/ NS.1907	NΔ	2.58
	436016		Hs.1215	36 Human DNA sequence from clone RP11-472E5	2.58 2.58
55	430980	AW971904			2.58
	441581		Hs.1271 Hs.1198		2.58
	435693 431814			47 delta-tubulin	2.58
	446269			9 hypothetical protein FLJ10540	2.58 2.58
60	422765	AW40970			2.56 2.58
	456999				2.58
	425234 434423			L LIM domaio only 4	2.57
	425782		Hs.1595		2.57 2.57
65	43392			79 ESTs	2.57
	41490		Hs.7755 Hs.7215		2.57
	41178 43562		Hs.118	i	2.57
	43216			805 hypothetical protein FLJ20556	2.57 2.57
70	43237				2.57
	42405				2.57
	42431 43566			273 FSTs	2.56
	43927		Hs.164	478 hypothetical protein FLJ21939 similar to	2.56
75	42774	7 AW4114		1655 corine/thrennine kinase 12	2.56 2.56
	43818	32 AW3421			2.56
	42110				2.56
	44572 44824				2.56
80	4428	81 AJ02317	5 Hs.16	7022 ESTs	2.56 2.56
	4221	65 AL04119			2.56 2.56
	4258 4485				2.55
	4463	., <u>0</u> .,020	J. 100.E1		102

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416806
                     NM 000288
                                   Hs 79993
                                                peroxisomal biogenesis factor 7
                                                                                                    2.55
                                   Hs.8882
          438113
                     AJ467908
                                                 ESTs
                                                 ribonucleotide reductase M2 polypeptide
                                                                                                    2.55
          413374
                     NM_001034
                                   Hs.75319
                                                                                                    2.55
          448275
                     BE514434
                                   Hs 20830
                                                kinesin-like 2
 5
                                                                                                    2.55
                                   Hs.94070
          419987
                     NM 005014
                                                osteomodulin
          439929
                     S73205
                                                 obinsulin activator factor (human, panc
                                   Hs.61232
                                                                                                    2.55
          452240
                     AI591147
                                                                                                    2.55
          417806
                      AI867277
                                    Hs.183733
                                                 ESTs
                                                                                                    2.55
          421482
                     At 135462
                                   Hs.104715
                                                inversin
                                                                                                    2.55
10
                                   Hs.155150
                                                 ribonuclaase P (14kD)
          456884
                     AA054679
          442961
                     BE614474
                                    Hs.289074
                                                 F-box only protein 22
          411274
                      NM_002776
                                   Hs.69423
                                                 kallikrein 10
                                                                                                    2.55
                      AL043202
                                    Hs.90073
                                                 chromosome segregation 1 (yeast homolog)
                                                                                                    2.54
          419359
                                                                                                     2.54
                     NM_014953
Z43846
                                   Hs.323346
                                                 KIAA1008 protein
          448666
          428911
                                                 Homo sapiens mRNA; cDNA DKFZp434O1572 (f
15
                                    Hs.194478
                      R71338
                                                 Homo sapiens cDNA: FLJ21592 fis, clone C
                                                                                                     2.54
          452778
                                    Hs.5921
                                                                                                     2.54
          430733
                      AW975920
                                    Hs.283361
                     NM_003616
AI168596
                                                                                                     2.54
                                                 survival of motor neuron protein interac
          421184
                                   Hs.102456
Hs.117117
                                                 ESTs
          435361
20
                                                                                                    2.54
2.54
                                                 KIAA0124 protein
          452833
                      BE559681
                                    Hs.30736
                                                 epiregulin
TRAM-like protein
           422330
                      D30783
                                    Hs.115263
                                                                                                     2.54
                      NM_012288
           424962
                                   Hs.153954
                                                                                                     2.53
                                                 gb:nc71f10.s1 NCI_CGAP_Pr1 Homo sapiens
                      AA470519
          430264
                      AW594641
                                    Hs.192417
                                                                                                     2.53
           447178
25
                                                                                                     2.53
2.53
           411773
                      NM_006799
                                    Hs.72026
                                                 protease, serine, 21 (testisin)
                                                 ESTs, Weakly similar to unnamed protein
Homo sapiens cDNA FLJ14294 fis, clone PL
           433571
                      AA765256
                                    Hs.135191
                      H18417
                                                                                                     2.53
           419449
                                    Hs.57483
           448019
                      AW947164
                                    Hs.195641
                                                 ESTs, Moderately similar to I38022 hypot
                                                                                                     2.53
           409435
                      AIB10721
                                    Hs.95424
                                                 ESTs
                                                                                                     2.52
30
                                                                                                     2.52
           417900
                      BE250127
                                    Hs.82906
                                                 CDC20 (cell division cycle 20, S. cerevi
                                                 membrane-spanning 4-domains, subfamily A
                                                                                                     2.52
                                    Hs.11090
           431385
                      BE178536
                                                                                                     2.52
                      K01900
                                    Hs.73890
                                                 interferon, alpha 8
           422314
           441343
                      AI970348
                                    Hs.132230
                                                                                                     2.52
                                                                                                     2.52
2.52
           417185
                      NM_002484
                                    Hs.81469
                                                 nucleotide binding protein 1 (E.coli Min
35
           401747
                                                 KIAA1023 protein
           448526
                      AB028946
                                    Hs.21361
                                                                                                     2.52
           419488
                      AA316241
                                    Hs.90691
                                                 nucleophosmin/nucleoplasmin 3
                      BE182082
                                     Hs.246973
                                                                                                     2.51
           413627
                                                                                                     2.51
           441285
                      NM_002374
                                     Hs.167
                                                  microtubule-associated protein 2
                                                  small inducible cytokine subfamily A (Cy
                                                                                                     2.51
40
                                     Hs.16530
                      AB012113
           446921
                                     Hs.164589
                      AA779725
           429357
                                                  ESTs
                                     Hs.9030
                                                                                                     2.50
           443171
                      BE281128
           446636
                      AC002563
                                     Hs.15767
                                                  citron (rho-interacting, serine/threonin
                                                                                                     2.50
                                                                                                     2.50
                      AA323037
AI538880
           420795
                                     Hs.128645
                                                  sorting nexin 16
45
                                     Hs.94812
           448582
                                                  ESTs
                                                                                                     2.50
                      AI478629
                                     Hs.158465
                                                  likely ortholog of mouse putative IKK re
           445459
           423909
                                     Hs.135194
                                                  immunoglobulin superfamily, member 6
                                                                                                     2.50
                      AJ223183
                                                  gb:HSB650052 STRATAGENE Human skeletal m
                                                                                                     2.50
           414315
                      Z24878
                                     Hs.62699
                                                                                                     2.50
            407568
                      AA740964
                                                  FST<sub>8</sub>
50
                      AW503857
                                                  Sarcolemmal-associated protein
            453911
                                     Hs.4007
                                                  splicing factor proline/glutamine rich (
                                                                                                     2.50
            431571
                      AW500486
                                     Hs.180610
            433843
                       AW021423
                                     Hs.112819
                                                  ESTs
                                                                                                     250
                                                  gb:B711F Heart Homo sapiens cDNA clone B
                                                                                                     2.50
            456254
                       T19844
                                                                                                      2.50
            403137
                                                  NA
 55
                                     Hs.161427 zinc finger protein 215
                                                                                                     2.50
            425895
                       AI269484
            418612
                      AB037788
                                     Hs.224961 cleavage and polyadenylation specific fa
                                                                                                     250
            TARIF 45R
                               Unique Eos probeset identifier number
 60
            CAT number.
                               Gene cluster number
                               Genbank accession numbers
            Accession:
                       CAT Number
            410784
                                     AW803201 BE079700 BE062940
                       1221005_1
 65
                                     AW809665 AW810108 AW809781 AW809844
H43346 AA248302 AA095182
                       1226078_1
            410902
            411765
                       125700_1
                                     BE068819 BE068821 BE068825
                       1351880 1
            413170
                       1374595_1
                                     BE145907 BE145796 BE145803 BE145851 BE145923 BE145812 BE145809 BE145852 BE145856
            413516
                                     Z24878 AA494098 F13654 AA494040 AA143127
AA436760 AW237453 BE327496 N47347 N56967
AA470519 BE303010 BE302954 BE384120
            414315
                       143512_1
 70
                       296453_1
315008_1
            428858
            430264
            431322
                       331543_1
                                     AW970622 AA503009 AA502998 AA502989 AA502805 T92188
            434138
                       380572_1
                                     AA625804 AW418787 AW074833 AI675642 AI393368
            435411
                       419334_1
                                     AW674352 AA715374 Z25205
 75
                       45106_-2
48059_-1
            438159
                                     Z83947
            439929
                                     S73205
                       859083_1
                                      AJ761324 AW880941 AW880937
            451105
                                     AI902519 AI902518 AI902516
AW792775 BE072509 AW792958
            452453
                       918300_1
            454469
                        1213727 1
 80
                                      AW810001 AW810092 AW810170 AW809884 AW809664 AW810353 AW810428 AW810099 AW810429 AW810154 AW810168 AW809785 AW810006
            454600
                        1226077 1
                                      AW809672 AW809694 AW810552 AW810345 AW810432 AW809960
AW833504 AW833751 AW833493 AW833341
            454821
                        1236365_1
                                      AW894017 AW893956 AW894032
            455309
                        1278153 1
```

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1699246_1 T19844 T11755 T11830 T20136 T11957 R45834 R45828 R15595
         456254
         TABLE 45C:
                             Unique number corresponding to an Eos probeset
          Pkey:
                             Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA
 5
          Ref:
                             sequence of human chromosome 22' Dunham, et al. (1999) Nature 402:489-495. Indicates DNA strand from which exons were predicted.
          Strand:
                             Indicates nucleotide positions of predicted exons
          Nt_position:
10
                                    Strand
                                                 Nt position
                     9187886
                                                 76485-77597
          401458
                                    Plus
                                                 82655-83959
          401644
                      8576138
                                    Ptus
                                                 118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866-
          401747
                      9789672
                                    Minus
                                                  131932 132451-132575 133580-134011
                                                  109122-110357
15
                      8571795
          402167
                                    Plus
                                    Plus
                                                  23367-25175
                      6693370
          402299
          402408
                      9796239
                                    Minus
                                                  110326-110491
                                                  92349-92572,92958-93084,93579-93712,93949-94072,94591-94748,95214-95337
          403137
                      9211494
                                    Minus
                                                  26009-26178
                      9438267
                                    Minus
          403381
20
          403422
                      9665041
                                     Minus
                                                  151169-151561
                                                  38760.39352
           403548
                      8081591
                                    Minus
                                                  142647-142771,145531-145762
          403637
403639
                      8671936
                                     Minus
                      8671948
                                     Plus
                                                  113234-113326,115186-115287,119649-119786
           403776
                      7770611
                                     Minus
                                                  1414-1513,1624-1756
25
           404253
                      9367202
                                     Minus
                                                  55675-56055
                                                  80430-81581
           404440
                      7528051
                                     Ptus
                                                  158681-158882,160838-160973
           404766
                      7882612
                                     Minus
                                                  37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
           404996
                      6007890
           405466
                      7767904
                                     Minus
                                                  64498-64675
30
                                                  61057-62075
           405770
                      2735037
                                     Pkis
                                                  19914-20112,25655-25810
                      4071056
                                     Plus
           405817
                                                  54304-54584
           406117
                      9142932
                                     Plus
                                                  28256-28935
                      5923650
           406182
35
           TABLE 46A: ABOUT 1303 GENES UP-REGULATED IN STOMACH CANCER COMPARED TO NORMAL STOMACH
           Table 46A lists about 1303 genes up-regulated in stomach cancer compared to normal stomach. These were selected as for Table 45A except using non-malignant stomach
           specimens in determining the denominator value and the ratio was equal to or greater than 5.0.
                               Unique Eos probesel identifier number
           Pkey:
                               Exemplar Accession number, Genbank accession number
40
           ExAcon:
           UnigenelD:
                               Unigene number
           Unigene Title:
                               Unigene gene title
                               Ratio of turnor to normal body tissue
45
                                     UnigenelD
Hs.313
Hs.75774
                                                  Unigene Title
            Pkey
                       ExAcon
                                                                                                             80.50
                                                  secreted phosphoprotein 1 (asteopontin,
            446619
                       AU076643
                                                                                                             70.52
                       NM_003248
                                                  thrombospondin 4
            414152
                                                   secreted frizzled-related protein 4
                                                                                                             65.30
            421552
                       AF026692
                                      Hs.105700
                                                                                                             61.90
                       AA852773
                                      Hs.334838
                                                   KIAA1866 protein
            428698
 50
                                                                                                             50.60
                                                   matrix metalloproteinase 3 (stromelysin
            428368
                       BE440042
                                      Hs.83326
                                                                                                             44.50
                       AB033025
                                                   KIAA1199 protein
            409041
                                      Hs 50081
                                                   Homo sapiens cDNA FLJ11041 fis, clone PL
                                      Hs.28792
                                                                                                             41.10
            452281
                       T93500
                                                                                                             33.50
                                                   ESTs
            452862
                       AW378065
                                      Hs.8687
                                                  collagen, type X, alpha 1 (Schmid metaph
Homo sapiens cDNA FLJ10570 fis, clone NY
                                                                                                             32.10
                                      Hs.179729
            427585
424834
                       D31152
                       AK001432
                                                                                                             26.90
 55
                                      Hs.153408
                                                                                                             26.40
            428398
                       A1249368
                                      Hs.98558
                                                   ESTs
                                                                                                              25.48
                                                   cystatin SN
            409757
                       NM_001898
                                      Hs.123114
                                                                                                             24.90
            403776
                                                   H2B histone family, member Q
                                                                                                             23.80
                       NM_003528
                                      Hs.2178
            427674
                                                                                                              23.10
 60
                        X04430
                                      Hs.93913
                                                    interleukin 6 (interferon, beta 2)
            419968
                                                                                                              21.76
            427108
                        AB028976
                                      Hs 173571
                                                   KIAA1053 protein
                                                                                                              20.70
                                                   tumor necrosis factor, alpha-induced pro
                                      Hs.29352
                        NM 007115
            452401
                                                                                                              20.40
            400419
                       AF084545
                                                                                                              19.80
             415989
                        AI267700
                                      Hs.317584
                                                   ESTs
  65
                                                                                                              19.70
             432101
                        At918950
                                      Hs.123642
                                                    EphA3
                                                    selectin E (endothelial adhesion molecul
                                                                                                              19.00
                                      Hs.89546
            418994
                        AA296520
                                                    Homo sapiens cDNA FLJ11309 fis, clone PL
                                                                                                              18.40
             452110
                                       Hs.28005
                        T47667
                                                                                                              18.20
                        AJ801777
                                       Hs.6774
             412652
                                                                                                              17.71
                                                    ubiquitin carboxyl-terminal esterase L1 S100 calclum-binding protein A7 (psorias
             414430
                        AI346201
                                       Hs.76118
  70
            422168
448988
                        AA586894
                                       Hs.112408
                                       Hs.22785
                                                    gamma-aminobutyric acid (GABA) A recepto
                                                                                                               17.36
                        Y09763
                                                                                                              17.00
                        AA788946
             437446
                                       Hs.16869
                                                    ESTs, Moderately similar to CA1C RAT COL
                                                                                                               17.00
             440594
                        AW445167
AA464510
                                       Hs.126036
                                                    ESTs
                                       Hs.152812
                                                                                                               17.00
                                                    ESTs
             430044
                                                    pre-B-cell leukemia transcription factor
  75
                                       Hs.294101
                                                                                                               16 90
                        AA243464
             426647
                                                                                                               16.50
                        AJ160386
                                       Hs.125087
                                                    ESTs
             414737
                        AA448542
                                                                                                               16.30
             427335
                                       Hs.251677
                                                    G antigen 7B
                                                                                                               15.50
                        AW450737
                                       Hs.128791
                                                    CGI-09 protein
             423453
                                                    prostate cancer associated protein 1
             414569
                                                                                                               15 40
                         AF109298
                                       Hs.118258
  80
                                                                                                               15.40
                                                     NΑ
             401961
                                                                                                               15.40
                         RF387162
                                       Hs 280858
                                                    ESTs, Highly similar to A35661 DNA excis
             434551
                         AW975868
                                       Hs.294100
                                                                                                               15.30
                                                    ESTs
             432069
                         AA643687
                                       Hs.149425
                                                    Homo sapiens cDNA FLJ11980 fis, clone HE
                                                                                                               15.30
             434699
```

	409062	AL157488	Hs.50150	Homo sapiens mRNA; cDNA DKFZp564B182 (fr	15.30 15.20
	400289 415138	X07820 C18356	Hs.2258 Hs.295944	matrix metalloproteinase 10 (stromelysin tissue factor pathway inhibitor 2	15.20
	428820	AA436187	Hs.172631	integrin, elpha M (complement component	15.19
5	410763	AF279145	Hs.8966	hypothetical protein FLJ21776	15.10
	438639	A1278360	Hs.31409	ESTs ESTs	15.10 15.00
	458997 432731	AW937420 R31178	Hs.69662 Hs.287820	fibranectin 1	14.90
	459247	N46243	Hs.110373	ESTs, Highly similar to T42626 secreted	14.70
10	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	14.70
	452242 426427	R50956 M86699	Hs.159993 Hs.169840	gycosyftransferase TTK protein kinase	14.70 14.50
	439924	M00033 AI985897	Hs.125293	ESTs	14.45
	414869	AA157291	Hs.21479	ubinuclain 1	14.40
15	411573	AB029000	Hs.70823	KIAA1077 protein	14.40 14.37
	418693 421823	AI750878 N40850	Hs.87409 Hs.28625	thrombospondin 1 ESTs	14.30
	423903	M57765	Hs.1721	interleukin 11	14.20
20	419227	BE537383	Hs.89739	chofinergic receptor, nicotinic, beta po	14.10
20	447417 416406	AW732858 D86961	Hs.143067 Hs.79299	KIAA1602 protein lipoma HMGIC fusion partner-like 2	13.96 13.90
	446392	AF142419	Hs.15020	homolog of mouse quaking QKI (KH domain	13.90
	412863	AA121673	Hs.59757	zinc finger protein 281	13.90
25	449509	AA001615	Hs.84561	ESTS	13.80 13.80
25	440953 432415	AI683036 T16971	Hs.124135 Hs.289014	Homo sapiens cDNA FLJ13051 fis, clone NT ESTs, Wealdy similar to A43932 mucin 2 p	13.60
	428769	AW207175	Hs.106771	ESTs	13.60
	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	13.41
30	424580	AA446539 T49300	Hs.339024 Hs.35304	ESTs, Wealdy similar to A46010 X-linked Homo sapiens cONA FLJ13655 fis, clone PL	13.40 13.30
30	438459 431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	13.26
	406972	M32053		gb:Human H19 RNA gene, complete cds.	13.19
	432368	AW970244	Hs.162188	ESTs	13.16 13.08
35	424806 440351	AA382523 AF030933	Hs.105689 Hs.7179	MSTP031 protein RAD1 (S. pombe) homolog	12.98
75	437789	AI581344	Hs.127812	ESTs, Wealthy similar to T17330 hypotheti	12.90
	447164	AF026941	Hs.17518	Homo saplens cig5 mRNA, partial sequence	12.80
	417412	X16896 NA	Hs.82112	interleutiin 1 receptor, type I NA	12.80 12.78
40	402363 444301	AK000136	Hs.10760	asporin (LRR class 1)	12.76
. •	416783	AA206186	Hs.79889	monocyte to macrophage differentiation-a	12.60
	435706	W31254	Hs.7045	GL004 protein	12.50 12.50
	414618 439737	AI204600 AI751438	Hs.96978 Hs.41271	hypothetical protein MGC10764  Homo sapiens mRNA full length insert cDN	12.49
45	405770	74101400	1.0.712.1	NA	12.46
	418678	NM_001327	Hs.167379	cancer/testis antigen	12.45
	414132	AI801235 AF051152	Hs.48480 Hs.63668	ESTs tall-like receptor 2	12.40 12.30
	410434 451092	AP031132 AJ207256	Hs.13766	Homo sapiens mRNA for FLJ00074 protein,	12.26
50	407891	AA486620	Hs.41135	endomucin-2	12.20
	450506	NM_004460	Hs.418	fibroblast activation protein, alpha	12.01 12.00
	411213 436476	AA676939 · AA326108	Hs.69285 Hs.33829	neuropilin 1 bHLH protein DEC2	12.00
	413582	AW295647	Hs.71331	hypothetical protein MGC5350	11.90
55	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	11.90 11.88
	401747 409619	AK001015	Hs.55220	NA BCL2-associated athanogene 2	11.84
	432596	AJ224741	Hs.278461	matrilin 3	11.80
60	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	11.73
60	425688 407938	U48361 AA905097	Hs.159223 Hs.85050	NGFI-A binding protein 2 (ERG1 binding p phospholamban	11.72 11.70
	419948	AB041035	Hs.93847	NADPH oxidase 4	11.70
	459645	AA074346	Hs.250715		11.51
65	438462	AI624122	Hs.89578	general transcription factor IIH, polype	11.50 11.50
UJ	434851 418699	AA806164 BE539639	Hs.116502 Hs.173030		11.47
	413453	AA129640	Hs.128065		11.40
	442028	AI239437	Hs.48945	ESTs	11.40
70	428479 453313	Y00272 BE005771	Hs.184572 Hs.153746		11.39 11.20
70	421633	AF121860	Hs.106260		11.20
	410339	Al916499	Hs.298258	ESTS	11.20
	448111	AA053486	Hs.20315	Interferon-induced protein with tetratri DKFZP586E1621 protein	11.15 11.15
75	453857 430217	AL080235 N47863	Hs.35861 Hs.336901		11.10
,,	452823	AB012124	Hs.30696	transcription factor-like 5 (basic helix	11.10
	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	11.06 10.90
	416854	H40164 D61594	Hs.80296 Hs.17279	Purkinje cell protein 4 tyrosytorotein sulfotransferase 1	10.90
80	447072 424882	AI379461	Hs.153636		10.80
	448593	AW004854	Hs.228320	hypothetical protein FLJ23537	10.80
	408750		Hs.93581	hypothetical protein FLJ 10512 cytoskeleton associated protein 2	10.80 10.80
	450221	AA328102	Hs.24641	cheveren essenten house e	10.00

PCT/US02/29560

					40.00
	436411	AW674352		gb:ba63c07.y1 NIH_MGC_12 Homo sapiens cD	10.80 10.80
	441693	AA384673		RPB5-mediating protein glycine cleavage system protein H (amino	10.80
	414922 441801	D00723 AW242799		ESTs	10.80
5	417173	U61397	Hs 81424	ubiquitin-like 1 (sentrin)	10.80
•	415727	BE501389	Hs.20848	ESTs. Weakly similar to APAF_HUMAN APOPT	10.80
	414142	AW368397		Homo sapiens cDNA FLJ14438 fis, clone HE	10.80 10.80
	421650	AA781795		ESTs	10.70
10	439999	AA115811		ras homolog gene family, member E thrombospondin 2	10.69
10	421814 415060	L12350 AJ223810	Hs.108623 Hs.43213	ESTs, Weakly similar to IEFS_HUMAN TRANS	10.67
	421462	AF016495	Hs.104624	aguaporin 9	10.66
	410444	W73484	-	gb:zd54e04.s1 Soares_fetal_heart_NbHH19W	10.61
	409743	N48721	Hs.183506	hypothetical protein FLJ14213	10.60 10.60
15	446142	AI754693	Hs.145968	ESTs	10.60
	444114	T58003	Hs.10323	Homo sapiens mRNA from chromosome 5q31-3 replication protein A3 (14kD)	10.55
	423020 453891	AA383092 AB037751	Hs.1608 Hs.36353	Homo sapiens mRNA full length insert cDN	10.50
	417352	AA195919	113.50000	gb:zp95h09.r1 Stratagene muscle 937209 H	10.46
20	417866	AW067903	Hs.82772	collagen, type XI, alpha 1	10.42
	427718	AI798680	Hs.25933	ESTs	10.40 10.40
	412589	R28660	Hs.24305	ESTs Homo sapiens clone TCCCTA00151 mRNA sequ	10.40
	433332	A1367347	Hs.44898 Hs.152213	wingless-type MMTV integration site fami	10.30
25	424717 450434	H03754 AA166950	Hs.195870	hypothetical protein FLJ14991	10.30
23	409044	Al129586	Hs.33033	hypothetical protein FLJ14623	10.30
	423600	AI633559	Hs.310359	ESTs	10.30
	433819	AW511097	Hs.112765	ESTs	10.18 10.10
20	415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	10.10
30	410503	AW975746	Hs.188662	KIAA1702 protein lung type-I cell membrane-associated gly	10.10
	433800 429357	AI034361 AA779725	Hs.135150 Hs.164589	ESTs	10.00
	425337 452838	U65011	Hs.30743	preferentially expressed antigen in meta	10.00
	414117	W88559	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	10.00
35	416198	H27332	Hs.99598	hypothetical protein MGC5338	10.00 10.00
	413918	AW015898	Hs.71245	ESTs	10.00
	400570	NA NATIONALIZADO	11- 425250	NA Homo sapiens cDNA FLJ13795 fis, clone TH	9.97
	439333	AW384710 AW384082	Hs.125258 Hs.104879	serine (or cysteine) proteinase inhibito	9.93
40	444863 450101	AVV364062 AV649989	Hs.24385	Human hbc647 mRNA sequence	9.90
40	434352	AF129505	Hs.86492	small muscle protein, X-linked	9.90
	453160	AI263307	Hs.239884	H2B histone family, member L	9.90
	433929	Al375499	Hs.27379	ESTs	9.89 9.81
45	413273	U75679	Hs.75257	stem-loop (histone) binding protein	9.80
45	437536	X91221	Hs.144465	ESTs paraneoplastic antigen MA2	9.80
	441350 452291	AB020690 AF015592	Hs.7782 Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	9.80
	432291	AI380429	Hs.172445		9.80
	417849	AW291587	Hs.82733	nidogen 2	9.78
50	424086	AI351010	Hs.102267	tysyl oxidase	9.72
	428186	AW504300	Hs.295605		9.70 9.70
	414422	AA147224	Hs.337232	ESTs KIAA1615 protein	9.70
	419197	N48921 Al741320	Hs.27441 Hs.114121		9.70
55	427660 449347	AV649748	Hs.295901		9.70
	409643		Hs.257359	ESTs .	9.70
	436209	AW850417			9.70 9.60
	439508				9.60
60	430290		Hs.136355	6 ESTs RBP1-like protein	9.60
00	447124 413879		Hs.17428 Hs.212533		9.60
	408101			·	9.58
	418067		Hs.83393		9.54
	424001		Hs.13747		9.50 9.50
65	443037				9.50 9.50
	428493				9.50
	420170		Hs.95631 Hs.22972		9.50
	409269 443162		Hs.9029	DKFZP434G032 protein	9.45
70	444381			3 ESTs, Wealdy similar to \$64054 hypotheti	9.43
	424026		Hs.13757		9.40
	440052		Hs.19564		9.40 9.37
	403137			NA SOT	9.35
75	418051				9.30
13	41870° 43029°				9.30
	42613				9.30
	40019	5 NA		NA .	9.30
	41152	9 AA43034	Hs.31759		9.20 9.20
80	42393	6 U77629	Hs.13563		9.20
	41425		Hs.30129 3 Hs.7944		9.20
	41666 40554		- ns./344	NA	9.20
	40534	·		•	

	420900	AL045633	Hs.44269	ESTs	9.11
	450757	BE081050	Hs.31570	ESTs. Weakly similar to KIAA1324 protein	9.10
	410929	H47233	Hs.30643	ESTs	9.10
_	427319	AW631495	Hs.27135	B-cell receptor-associated protein BAP29	9.10
5	443745	AB039670	Hs.9728	ALEX1 protein	9.10 9.10
	436574 407192	AW293527 AA609200	Hs.126465	eSTs gb:af12e02.s1 Soares_testis_NHT Homo sap	9.08
	426075	AW513691	Hs.270149	ESTs, Weakly similar to 2109260A B cell	9.07
	408778	AI500519	Hs.63382	hypothetical protein PRO2714	9.03
10	434542	AA769310	Hs.61260	hypothetical protein FLJ13164	9.00
	404440	045435	Un 447402	NA ESTs	9.00 9.00
	407168 451678	R45175 AA374181	Hs.117183 Hs.26799	DKFZP564D0764 protein	9.00
	431946	AI018336	Hs.131730	ESTs	8.92
15	408875	NM_015434	Hs.48604	OKFZP4348168 protein	8.90
	409928	AL137163	Hs.57549	hypothetical protein dJ473B4	8.90
	430294	AI538226	Hs.32976	guarine nucleotide binding protein 4	8.89 8.86
	445029 442717	AF196481 R88362	Hs.12256 Hs.180591	midline 2 ESTs, Wealdy similar to T23976 hypotheti	8.80
20	409089	NM_014781	Hs.50421	KIAA0203 gene product	8.80
	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	8.80
	416190	N54000		gb:yy99d02.r1 Sozres_multiple_sclerosis_	8.80
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act Homo sapiens, Similar to SWI/SNF related	8.77 8.76
25	416440 421262	AI823912 AA286746	Hs.79335 Hs.9343	Homo sapiens cDNA FLJ14265 fis, clone PL	8.70
2,5	441031	Al110684	Hs.7645	fibrinogen, B beta polypeptide	8.70
	452234	AW084176	Hs.223296	ESTs. Weakly similar to 138022 hypotheti	8.70
	452822	X85689	Hs.288617	hypothetical protein FLJ22621	8.70
30	430462	AI584156	Hs.105640	Homo sapiens, ctone IMAGE:4139775, mRNA,	8.65 8.65
30	426457 412054	AW894667 W87482	Hs.169965 Hs.302209	chimerin (chimaerin) 1 ESTs	8.64
	450236	AW162998	Hs.24684	KIAA1376 protein	8.63
	418782	AI792648	Hs.14665	ESTs	8.60
0.5	452631	A1188658	Hs.87496	ESTs	8.60
35	425268	AJ807883	Hs.180059	Homo sapiens cDNA FLJ20653 fis, clone KA ESTs, Wealdy similar to ALU4_HUMAN ALU S	8.60 8.60
	432014 440270	H66741 NM_015986	Hs.38540 Hs.7120	cytokine receptor-like molecule 9	8.60
	414784	NM_000344	Hs.288986	survival of motor neuron 1, telomeric	8.60
	426809	BE313114	Hs.29706	ESTs	8.60
40	419704	AA429104	Hs.45057	ESTs	8.60 8.60
	452909	NM_015368	Hs.30985	pannexin 1 gb:EST385886 MAGE resequences, MAGM Homo	8.60
	432639 430418	AW973785 R98852	Hs.36029	heart and neural crest derivatives expre	8.58
	450480	X82125	Hs.25040	zinc finger protein 239	8.58
45	444984	H15474	Hs.132898	fatty acid desaturase 1	8.58
	419085	NM_000216	Hs.89591	Kallmann syndrome 1 sequence	8.57
	430518	AW363687	Hs.82916	chaperonin containing TCP1, subunit 6A ( short-chain alcohol dehydrogenase family	8.50 8.50
	424735 414061	U31875 NM_000699	Hs.272499 Hs.300280		8.50
50	407894	AJ278313	Hs.41143	phosphoinositide-specific phospholipase	8.50
	441079	AW150697	Hs.107418	ESTs	8.50
	419354	M62839	Hs.1252	apolipoprotein H (beta-2-glycoprotein I)	8.50 8.50
	418618	U66097	Hs.86724	GTP cyclohydrolase 1 (dopa-responsive dy endoplasmic reticulum resident protein 5	8.50
55	416565 441540	AW000960 C01367	Hs.44970 Hs.127128		8.50
55	416434	AW163045	Hs.79334	nuclear factor, interleukin 3 regulated	8.50
	417801	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like rep	8.50
	426855	AL117427	Hs.172778		8.48 8.43
60	436515 416315	AJ278111 AA179483	Hs.195292 Hs.73605	putative tumor antigen ESTs	8.42
00	408432	AW195262	113.1000	qb:xn67b05.x1 NCI_CGAP_CML1 Homo sapiens	8.40
	410094	BE147897	Hs.58593	general transcription factor IIF, polype	8.40
	419198	AA234938	Hs.87384	ESTs	8.36 8.36
65	448920	AW408009	Hs.22580 Hs.62185	alkylglycerone phosphate synthase solute carrier family 9 (sodium/hydrogen	8.31
03	410305 408687	AF030409 AL110280	Hs.301152		8.30
	427707	NM_005578			8.30
	459060	H89244	Hs.303627	heterogeneous nuclear ribonucleoprotein	8.30
70	451957	A1796320	Hs.10299	Homo sapiens cDNA FLJ13545 fis, clone PL	8.30 8.30
70	443977	AL120986 AA806616	Hs.150627 Hs.209523		8.30
	457997 451934	AI540842	Hs.61082		8.30
	404335	745-00-12	110,01002	NA .	8.30
~~	445073	AW291389	Hs.13056	hypothetical protein FLJ13920	8.30
75	431566	AF176012	Hs.260720		8.29 8.28
	445307	T50083 AA332680	Hs.9094	ESTs gb:EST36768 Embryo, 8 week I Homo sapien	8.26
	423928 436420		Hs.31595	ESTs	8.25
	426110			replication factor C (activator 1) 1 (14	8.25
80	442988	AI026130	Hs.13168	3 ESTs	8.25 8.24
	402408		Hs.5326	NA amino acid system N transporter 2; porcu	8.23
	438707 425770				8.22
				• •	

			u. 040247	heterogeneous nuclear protein similar to	8.21
	448704 452682		Hs.249247   Hs.9071	progesterone membrane binding protein	8.20
	411984		He 72988	sional transducer and activator of trans	8.20
_	420018	U56387		proprotein convertase subtilisin/kexin t	8.20 8.20
5	437048		Hs.91582 Hs.151469	ESTs calcium/calmodulin-dependent serine prot	8.20
	424653 447066	AW977534 BE167667		ESTs	8.20
	425932	M81650	Hs.1968	semenogelin I	8.20 8.20
••	431819	AA515995	Hs.152334	ESTS	8.20 8.20
10	431810	X67155	Hs.270845	kinesin-like 5 (mitotic kinesin-like pro gb:an03c03.x1 Stratagene schizo brain S1	8.20
	459702 406687	A1204995 M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	8.18
	413109	AW389845	Hs.110855	ESTs	8.17 8.16
	424720	M89907	Hs.152292	SWI/SNF related, matrix associated, acti	8.10
15	424335	AW021508	Hs.28170 Hs.11325	ESTs ESTs	8.10
	453096 427738	AW294631 NM_000318	Hs.180612	peroxisornal membrane protein 3 (35kD, Ze	8.10
	457796	AA913389	Hs.126691	FSTs	8.10 8.10
	429340	N35938	Hs.199429	Homo sapiens mRNA; cDNA DKFZp434M2216 (f gb:AV652831 GLC Homo sapiens cDNA clone	8.08
20	445165	AV652831	Hs.56044	ESTs	8.06
	418046 426269	W49670 H15302	Hs. 168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	8.04
	439451	AF086270	Hs.278554	heterochromatin-like protein 1	8.02 8.02
0.5	419559	Y07828	Hs.91096	ring finger protein	8.00
25	409268	AA625304	Hs.188554 Hs.17731	ESTs hypothetical protein FLJ12892	8.00
	447207 446977	AA442233 AW863613	Hs.156798	ESTs	8.00
	424565	AW102723	Hs.75295	quanviate cyclase 1, soluble, alpha 3	8.00 7.99
	407013	U35637		gb:Human nebulin mRNA, partial cds serine (or cysteine) proteinase inhibito	7.98
30	414523	AU076633	Hs.76353 Hs.7309	Homo sapiens clone 23741 mRNA sequence	7.96
	440637 417076	AW900115 AW973454	Hs.238442	ESTs, Moderately similar to ALU7_HUMAN A	7.95
	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitte	7.94 7.92
	415585	R59946	Hs.184852	KIAA1553 protein	7.92
35	453331	AI240665	Hs.8895 Hs.83286	ESTs ESTs, Weakly similar to S14747 sphingorny	7.90
	445527 417318	W39694 AW953937	Hs.12891	ESTe	7.90
	429393	AA383024	Hs.201603		7.90 7.90
	444769	Al191650	Hs.221436		7.90 7.90
40	444272	AI138596	Hs.154619	ESTs ESTs, Wealdy similar to gonadotropin ind	7.90
	425264 412642	AA353953 BE244598	Hs.20369 Hs.809	hepatocyte growth factor (hepapoietin A:	7.90
	453765	BE279901	Hs.35091	hypothetical protein FLJ10775	7.90
	421558	AB011125	Hs.105749		7.90 7.90
45	446444	AJ743737	Hs.24370	ESTs p53-inducible ribonucleotide reductase s	7.86
	420000	AB036063 8E513073	Hs.94262	gb:601171435F1 NIH_MGC_15 Homo sapiens c	7.86
	437237 409582	R27430	Hs.271565		7.84
	419235	AW470411	Hs.288433	neurotrimin	7.83 7.82
50	439620	AA838727	Hs.124400		7.80
	441690 417735		Hs.33106 Hs.82506		7.80
	441795		Hs.21137		7.80 7.80
	442992	AI914699	Hs.13297		7.80
55	422554		Hs.29633 7 Hs.12402		7.80
	423123 428627		Hs.18766		7.80
	429228		Hs.33713	9 ESTs	7.80 7.80
	429399	AA452244	Hs.16727	ESTs	7.77
60	436396 455510		Hs.15221 Hs.14364	n FSTs. Wealdy similar to hyperpolarizatio	7.76
	429396				7.76
	453439		Hs.32976	guanine nucleotide binding protein 4	7.75 7.71
15	410561	BE540255		Homo sapiens cDNA: FLJ22044 fis, clone H Homo sapiens clone TCCCTA00142 mRNA sequ	7.71
65	442875		Hs.23625		7.70
	428655 413374				7.70
	40499			NA_	7.70 7.70
70	41894		Hs.2286		7.70
70	42740		Hs.2149 Hs.1253		7.70
	41074 42626				7.70
	44695		8 Hs.1567	47 ESTs	7.70 7.70
75	44919	9 Al990122			7.70
75	44321				7.70
	44615 42716			71 KIAA1300 protein	7.70
	45262	7 Al122843	Hs.1843	119 ESTs, Weakly similar to KIAA 1006 protein	7.70 7.70
00	45258	8 AA88912			7.10 7.67
80					7.66
	42295 45122		Hs.151	344 ESTs, Weakly similar to high-risk human	7.66
	45070		Hs.288		7.65
				400	

	432695	D63480	Hs.278634	KIAA0146 protein	7.63
	447476 447289	BE293466 AW247017	Hs.20880 Hs.36978	ESTs, Wealdy similar to 138022 hypotheti melanoma antigen, family A, 3	7.60 7.60
	447505	AL049266	Hs.18724	Homo sepiens mRNA; cDNA DKFZp564F093 (fr	7.60
5	423065	R95158	Hs.267130	Homo sapiens, clone MGC:5406, mRNA, comp	7.60
	437396	BE140396	Hs.21621	hypothetical protein DKFZp7620076	7.60
	450628 418995	AW382884 H39599	Hs.204715 Hs.294008	ESTs ESTs	7.60 7.60
	416402	NM_000715	Hs.1012	complement component 4-binding protein,	7.60
10	405545	_		NA .	7.60
	440866	AI703103	Hs.271360	hypothetical protein MGC16275	7.60 7.60
	421281 424634	AI299139 NM_003613	Hs.17517 Hs.151407	ESTs cartilage intermediate layer protein, nu	7.60
	421041	N36914	Hs.14691	ESTs, Moderately similar to 138022 hypot	7.60
15	453311	AW104911	Hs.126707	hypothetical protein FU11457	7.54 7.50
	453060 417655	AW294092 AA780791	Hs.21594 Hs.14014	hypothetical protein MGC15754 hypothetical protein FLJ14813	7.50 7.50
	417531	NM_003157	Hs.1087	serine/threonine kinase 2	7.50
20	444099	D87432	Hs.10315	solute carrier family 7 (cationic arnino	7.50
20	407853 408920	AA336797 AL120071	Hs.40499 Hs.48998	dickkopf (Xenopus laevis) homolog 1 fibronectin leucine rich transmembrane p	7.50 7.50
	447806	W03616	Hs.10432	ESTs, Wealdy similar to I38022 hypotheti	7.48
	424748	AA346257	Hs.134933	ESTs	7.48
25	421089 444856	AB037771 AI888057	Hs.101799 Hs.12097	KIAA1350 protein ESTs	7.46 7.42
23	447425	A1963747	Hs.18573	acylphosphatase 1, erythrocyte (common)	7.41
	418450	R84397	Hs.193651	ESTs, Weakly similar to atternatively sp	7.40
	434539 437036	AW748078 AI571514	Hs.214410 Hs.133022	ESTs, Wealthy similar to MUC2_HUMAN MUCIN ESTs	7.40 7.40
30	414680	AA743331	Hs.272572	hemoglobin, alpha 2	7.40
	451815	AW974911	Hs.184793	Homo sapiens cDNA: FLJ21880 fis, clone H	7.40
	433577	AW007080	Hs.8817	ESTS	7.40 7.40
	453652 422665	AW009640 AJ011812	Hs.28368 Hs.119018	ESTs, Moderately similar to \$65657 alpha transcription factor NRF	7.40
35	424188	AW954552	Hs.142634	zinc finger protein	7.40
	407300	AA102616	11- 000040	gb:zn43e07.s1 Stratagene HeLa cell s3 93	7.40 7.40
	431494 452958	AA991355 AA883929	Hs.298312 Hs.40527	hypothetical protein DKFZp434A1315 - ESTs	7.40 7.40
4.0	418763	AK000219	Hs.88367	hypothetical protein FLJ20212	7.40
40	428279	AA425310	Hs.155766	ESTs, Wealdy similar to A47582 B-cell gr	7.40
	449670 449601	F07693 AA461509	Hs.23869 Hs.293565	Homo sapiens mRNA; cDNA DKFZp434K2172 (f ESTs, Weakly similar to putative p150 (H	7.40 7.40
	438490	AW593272	Hs.301299	ESTs	7.40
15	410044	BE566742	Hs.58169	highly expressed in cancer, rich in leuc	7.40
45	429509 433393	AW614420 AF038564	Hs.204354 Hs.98074	ras hornolog gene family, member 8 itchy (mouse hornolog) E3 ubiquitin prote	7.38 7.38
	434096	AW662958	Hs.75825	pleiomorphic adenoma gene-like 1	7.37
	425773	N21279	Hs.237749	ESTs	7.36
50	422755 410566	T25365 AA373210	Hs.119687 Hs.43047	RAN binding protein 8 Homo sapiens cDNA FLJ13585 fis, clone PL	7. <b>3</b> 6 7.35
30	412851	AI826502	Hs.106149	ESTs	7.35
	418661	NM_001949	Hs.1189	E2F transcription factor 3	7.35
	436246 433159	AW450963	Hs.119991 Hs.150587	ESTs kinesin-like protein 2	7.34 7.33
55	444781	AB035898 NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	7.32
	453878	AW964440	Hs.19025	DC32	7.31
	414696	AF002020 AV655272	Hs.76918 Hs.20252	Niemann-Pick disease, type C1 novel Ras family protein	7.31 7.31
	402250 439039	A1656707	Hs.48713	ESTs	7.30
60	417976	BE565892	Hs.83077	interleukin 18 (interferon-gamma-inducin	7.30
	419436 417006	AA991639 AW673606	Hs.242413 Hs.80758	hypothetical protein DKFZp434K1421 aspartyl-tRNA synthetase	7.30 7.30
	425420	BE536911	Hs.234545	hypothetical protein NUF2R	7.30
	425889	M57414	Hs.161305	tachykinin receptor 2	7.29
65	442969	AI025499	Hs.132238	ESTs	7.26 7.25
	446360 438022	N42553 AW517524	Hs.267914 Hs.135201	homolog of mouse transient receptor pote NOD2 protein	7.25
	407183	AA358015		gb:EST66864 Fetal tung III Homo sapiens	7.24
70	429882	AA278898	Hs.225979	hypothetical protein similar to small G	7.24 7.22
70	420120 400212	AL049610 NA	Hs.95243	transcription elongation factor A (SII)- NA	7.20
	431812	AA515902	Hs.130650	ESTs	7.20
	419481	AI879195	Hs.90606	15 kDa selenoprotein	7.20
75	447078 413200	AW885727 AA127395	Hs.301570 Hs.222414		7.20 7.20
. •	411750	BE562298	Hs.71827	KIAA0112 protein; homolog of yeast ribos	7.20
	439901	N73885	Hs.124169		7.20 7.20
	411815 459279	AA156679 AW814996	Hs.125790	leucine-rich repeat-containing 2 gb:MR1-ST0206-170400-024-h09 ST0206 Homo	7.20 7.20
80	445263	H57646	Hs.42586	KIAA1560 protein	7.20
	413801	M62246	Hs.35406	ESTs, Highly similar to unnamed protein nuclear transcription factor Y, beta	7.20 7.20
	418407 452221	AL044818 C21322	Hs.84928 Hs.288057		7.20 7.20
	_				

					tate alder almites to 120022 be mother?	7.20
	425202 403764	AW962282	Hs.152049	NA	s, Weakly similar to 138022 hypotheti	7.20
	416896	AI752862	Hs.5638	KIA	1572 protein	7.20 7.20
•	416636	N32536	Hs.42645	EST	s nomologous factor	7.20
5	428071 450142	AF212848 AW207469	Hs.182339 Hs.24485	chor	ndroitin suffate proteoglycan 6 (barna	7.18
	451017	BE391847	Hs.181173	hypo	othetical protein MGC10771	7.17 7.16
	409759	N40285	Hs.81182 Hs.61389	hista	amine N-methyltransferase s, Weakly similar to unnamed protein	7.16
10	452448 427951	AW182440 AI826125	Hs.43546	FST	ře	7.16
10	407939	W05608	Hs.312679	EST	rs, Weakly similar to A49019 dynein he	7.15 7.12
	419457	AA243146	Hs.209334 Hs.27207		rs, Moderately similar to S23A_HUMAN P A0982 protein	7.11
	411769 430355	AI694575 NM 006219	Hs.239818		sphoinositide-3-kinase, catalytic, be	7.10
15	419511	AA429750	Hs.75113	gen	eral transcription factor IIIA	7.10 7.10
	409032	AW301807	Hs.297260	ES	Ts ivin A receptor, type I	7.10
	424539 439221	L02911 AA737106	Hs.150402 Hs.32250	ES	Ts. Moderately similar to 178885 serin	7.10
	430719	AA488988	Hs.293796	ES	Ts	7.10 7.10
20	408020	AA127940	Hs.62781	ES	Ts osomal protein L4	7.10
	420218 443487	AW958037 AI073491	Hs.286 Hs.269887	ES	Ts, Highly similar to KPBB_HUMAN PHOSP	7.10
	414865	AA157155	Hs.274414	hy	pothetical protein FLJ14457	7.10 7.10
0.5	428724	AL390128	Hs.191268 Hs.302498	KI/	AA1530 protein rP-binding protein homologous to Saccha	7.10
25	413293 419126	AL047483 A1810144	Hs.135276	. FS	iTe.	7.09
	437044	AL035864	Hs.69517	сC	NA for differentially expressed CO16 g	7. <b>09</b> 7.07
	433730	AK002135	Hs.3542	hy	pothetical protein FLJ11273 dute carrier family 23 (nucleobase tra	7.07
30	417381 457019	AF164142 AA421844	Hs.82042 Hs.12830		pothetical protein	7.07
30	409697	AB018348	Hs.55947	K	AA0805 protein	7.06 7.06
	400977	NA	11- 200076	N.	A STs	7.03
	436668 451684	AAB31857 AF216751	Hs.209071 Hs.26813		DA14	7.03
35	404029	74 210/31	1.0.200		A	7.02 7.02
•	448719	AA033627	Hs.21858	, t	inuclectide repeat containing 3 ytoplasmic polyadenylation element bind	7.00
	445577 419647	N40696 AA348947	Hs.137064 Hs.91816		venthetical eretein	7.00
	442075	AW136928	(13.51010	g	b:UI-H-Bi1-adp-d-08-0-UI.s1 NCI_CGAP_Su	7.00 7.00
40	429598	AA811257	Hs.26971		STs	7.00
	450832	AW970602 AA531291	Hs.10542 Hs.10106	1 E	:STs Homo sapiens cDNA FLJ12777 fis, clone NT	7.00
	421389 453931	AL121278	Hs.25144	L E	ESTs	7.00 7.00
4.5	432343	NM_00296			S100 calcium-binding protein A3	7.00
45	452979	AW167599 AA259068	Hs.23228 Hs.26781	52 I	ESTs protein phosphatase 1, regulatory (inhib	7.00
	431696 413583		Hs.5888		ESTs	7.00 7.00
	436758	AW977167		72	ESTs gb:PM1-HT0422-291299-002-f03 HT0422 Homo	6.98
50	455944 430302		Hs.2386		Rag D protein	6.96
50	437613		Hs.1026		MIL1 protein	6.95 6.95
	440524	R71264	Hs.1679	8	ESTs sema domain, immunoglobulin domain (Ig),	6.93
	451047 450377				KIAA1265 protein	6.93
55	457396		Hs.3238	117	DKFZP547E1010 protein	6.93 6.92
	417393		Hs.8207		Cop/p300-Interacting transactivator, wit KIAA1679 protein	6.92
	414417 41224				zinc finger protein	6.90
	41100		Hs.1305	56	hypothetical protein FLJ13920	6.90 6.90
60	41383		Hs.7557	73	centromere protein E (312kD) NA	6.90
	40569 43168		B Hs.2676	695	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	6.90
	41442		Hs.718	18	ESTs	6.90 6.90
	42464				glia maturation factor, beta ESTs	6.90
65	41889 44590				Homo sapiens done 24787 mRNA sequence	6.90
	44600		103 Hs.135	30	deafness, autosomal dominant 5	6.90 6.87
	43203				ESTs. Weakly similar to 138022 hypotheti	6.86
70	4466° 45121				Homo sapiens cDNA FLJ11652 fis, clone HE	6.86
70	4089				heptacellular carcinoma novel gene-3 pro	6.85 6.82
	4189	34 T83845	Hs.191		ESTs ESTs	6.82
	4351- 4426		Hs.194 74 Hs.130		ESTs	6.82
75	4327		92 Hs.271	B732	hypothetical protein FLJ20285	6.81 6.80
	4359	90 AI01586			ESTs calcium channel, voltage-dependent, alph	6.80
	4490 4536					6.80
	4214		305 Hs.21	887	ESTs	6.80 6.80
80	) 4305	10 AW1625	316 Hs.24		hypothetical protein PRO2577 Homo sapiens mRNA; cDNA DKFZp43400515	
	4090 4102					6.60
	420				ESTs	6.80
					_	

	427752	AA470687	Hs.104772	ESTs	6.80
	414080	AA135257	Hs.47783	B aggressive lymphoma gene	6.80
	422420	U03398	Hs.1524	turnor necrosis factor (ligand) superfami	6.80
5	416913 426890	AW934714 AA393167	Hs.41294	gb:RC1-DT0001-031299-011-e11 DT0001 Homo ESTs	6.80 6.80
•	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	6.80
	413328	Y15723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	6.79
	437619	AW351491	Hs.334853	hypothetical protein FLJ23544	6.79
10	434267	A1206589	Hs.116243	ESTs	6.79 6.79
10	419358 435854	T78763 AJ278120	Hs.90063 Hs.4996	neurocatcin delta putative ankyrin-repeat containing prote	6.78
	424925	NM_002432	Hs.153837	myeloid cell nuclear differentiation ant	6.77
	443184	AI638728	Hs.131973	ESTs	6.77
15	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	6.77
13	429483 425605	AA974832 BE544300	Hs.128708 Hs.7076	ESTs KIAA1705 protein	6.76 6.76
	425045	AW953186	Hs.92400	ESTs	6.76
	438776	AW245243	Hs.334368	hypothetical protein MGC11257	6.75
20	458174	AA781530	Hs.127236	hypothetical protein FLJ 12879	6.74
20	445129 435532	R39878 AW291488	Hs.21394 Hs.117305	ESTs Homo sapiens, clone IMAGE:3682908, mRNA	6.74 6.73
	444442	Al149234	Hs.298423	ESTs, Moderately similar to I54374 gene	6.73
	431240	AA496790	Hs.179481	ESTs	6.72
25	422109	S73265	Hs.1473	gastrin-releasing peptide	6.70
25	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	6.70 6.70
	423811 443695	AW299598 AW204099	Hs.50895 Hs.337720	homeo box C4 ESTs, Wealdy similar to AF126780 1 retin	6.70
	420686	AI950339	Hs.40782	ESTs	6.70
20	419574	AK001989	Hs.91165	hypothetical protein	6.70
30	418269	AA806113	Hs.189025	ESTs	6.70 6.70
	434164 408660	AW207019 AA525775	Hs.148135 Hs.292523	serine/threonine kinase 33 ESTs, Moderately similar to PC4259 ferri	6.70
	453370	AJ470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	6.70
	409506	NM_006153	Hs.54589	NCK adaptor protein 1	6.70
35	454029	W05150	Hs.37034	homeo box A5	6.70
	413365 447247	AW205188 AW369351	Hs.124304 Hs.287955	Homo sapiens cDNA FLJ14635 fts, clone NT Homo sapiens cDNA FLJ13090 fts, clone NT	6.70 6.70
	426566	AF131836	Hs.170453	tropomodulin	6.70
	446261	AA313893	Hs.306219	hypothetical protein FLJ12615 similar to	6.70
40	408547	AA574291	Hs.57837	ESTs	6.70
	430458	AA479300	Hs.225706	ESTs, Weakly similar to 138022 hypotheti	6.70 6.70
	413627 410498	BE182082 AA355749	Hs.246973	ests gb:EST64459 Jurkat T-cells VI Homo sapie	6.70
	434015	AA844518	Hs.300876	hypothetical protein FLJ13386	6.70
45	453691	H12235	Hs.226505	ESTs	6.68
	415068	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypotheti	6.68
	415885 405529	D79983 AW410458	Hs.78894 Hs.5258	KIAA0161 gene product chromosome 11 open reading frame2	6.68 6.68
	438242	AW241910	Hs.122254	ESTs, Weakly similar to JX0369 collagen	6.68
50	442643	U82756	Hs.8551	PRP4/STK/WD splicing factor	6.67
	424802	X79201	Hs.153221	synovial sarcoma, translocated to X chro	6.67
	415007 458714	BE244332 R20916	Hs.77770 Hs.202501	adaptor-related protein complex 3, mu 2 ESTs	6.67 6.66
	414591	AJ888490	Hs.55902	ESTs, Weakly similar to ALUB_HUMAN ALU S	6.65
55	433260	AB040966	Hs.83575	KIAA1533 protein	6.65
	400268	NA		NA	6.63
	453180	N46243	Hs.110373	ESTs, Highly similar to T42626 secreted NA	6.62 6.60
	403973 436862	NA A1821940	Hs.264622	ESTs, Moderately similar to ALU8_HUMAN A	6.60
60	428046	AW812795	Hs.155381	ESTs, Moderately similar to 138022 hypot	6.60
	453387	A1990741	Hs.252809	ESTs	6.60
	424084	AI940675	Hs.20914	hypothetical protein FLJ23056	6.60
	418444 448172	AI902899 N75276	Hs.85155 Hs.135904	butyrate response factor 1 (EGF-response ESTs	6.60 6.60
65	409571	AA504249	Hs.187585	ESTs	6.60
	423025	AA831267	Hs.12244	hypothetical protein FLJ20097	6.60
	430701	A1760833	Hs.293971	ESTs	6.60
	450373	AI915790	Hs.337282	ESTs ESTs	6.60 6.60
70	419384 429828	AA490866 AB019494	Hs.39429 Hs.225767	LDN3 protein	6.60
. •	441761	AJ222880		gb:qp40c06.x1 NCI_CGAP_Co8 Homo sapiens	6.60
	411048	AK001742	Hs.67991	hypothetical protein DKFZp434G0522	6.60
	421111	BE299047	Hs.43532	ESTs, Weakly similar to T20177 hypotheti	6.60 6.59
75	407424 412396	AF120493 AW947895		gb:Homo sapiens elastase 1 precursor (EL gb:PM1-MT0010-200300-001-f10 MT0010 Homo	6.57
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	6.57
	406674	AA332152	Hs.288036	tRNA isopentenylpyrophosphate transferas	6.57
	400860	4.711000		NA	6.56
80	457893 426108	AA744292 AA622037	Hs.166468	gb:ny51d05.s1 NCI_CGAP_Pr18 Homo sapiens programmed cell death 5	6.55 6.54
50	420100	AW612779	Hs.333159		6.54
	421044	AF061871	Hs.311736	Human DNA sequence from clone RP1-238D15	6.54
	414136	AA812434	Hs.119023	SMC2 (structural maintenance of chromoso	6.53

					6.52
				Homo sapiens AS11 protein mRNA, partial hypothetical protein, expressed in osteo	6.52
		AB000115	Hs.75470	protein phosphatase methylesterase-1	6.50
	410416	BE410072 AW503756	Hs.63304 Hs.286184	hypothetical protein dJ551D2.5	6.50
5	419852 419677	N77342		Homo sapiens cDNA FLJ12900 fis, clone NT	6.50
,	431806	AF186114	Hs.270737	tumor necrosis factor (ligand) superfami	6.50
	429774	AI522215		KIAA1804 protein	6.50
	428228	AA424352		ESTs	6.50
	418134	AA397769	Hs.86617	ESTs	6.50 6.50
10	403859	NA		NA_	6.50
	422704	AA972147	Hs.132275	ESTs	6.50
	416737	AF154335	Hs.79691	LIM domain protein ESTs	6.50
	429854	R55508 X12784	Hs.99472 Hs.119129	cottagen, type IV, alpha 1	6.49
15	422672 453600	BE246211	Hs.119120	F3 ubinuitin ligase SMURF1	6.48
13	454835	AW833763	113.113.11	gb:QV4-TT0008-130100-077-d10 TT0008 Homo	6.48
	434603	AF147384		gb:Homo sapiens full length insert cDNA	6.48
	408243	Y00787	Hs.624	interleukin 8	6.48
	429317	AA831552	Hs.268016	Homo sapiens cDNA: FLJ21243 fis, clone C	6.47 6.46
20	451316	AI770011	Hs.208310	ESTs	6.46
	448339	AL035920	Hs.20938	RNA binding motif, single stranded inter	6.44
	433423	BE407127	Hs.8997	heat shock 70kD protein 1A ESTs, Wealdy similar to unnamed protein	6.44
	410358	AW975168	Hs.13337 Hs.216381	Homo sapiens clone HH409 unknown mRNA	6.42
25	434025 440526	AF114264 AI832243	Hs.211471	ESTs	6.42
23	432727	AA305233	Hs.278712	eukaryotic translation initiation factor	6.41
	433009	AA761668		gb:nz24c08.s1 NCI_CGAP_GC81 Homo sapiens	6.40
	435782	N49433	Hs.285737	Homo saplens cDNA: FLJ20895 fis, clone A	6.40
	415071	AK002197	Hs.284270	Homo sapiens cDNA FLJ11335 fis, clone PL	. 6.40
30	407162	N63855	Hs.142634	zinc finger protein	6.40 6.40
	446152	A1292036	Hs.150028	ESTS	6.40
	422828	AL133396	Hs.121281	prion protein 2 (dublet) gb:yc11c07.s1 Stratagene lung (937210) H	6.40
	418866	T65754	U- FE0E0	ESTs, Weakly similar to KIAA1330 protein	6.40
35	411411	AA345241	Hs.55950 Hs.301897	ESTs. Weavy suring to report 300 protein	6.40
33	429039 447254	AI524793 NM_004153	Hs.17908	origin recognition complex, subunit 1 (y	6.40
	435159	AA668879	Hs.116649	ESTs	6.40
	429625	AA455568	Hs.193814	ESTs	6.40
	430180	AA331406	Hs.75456	A kinase (PRKA) anchor protein 10	6.40
40	408420	NM_006915	Hs.44766	retinitis pigmentosa 2 (X-linked recessi	6.40
	426572	AB037783	Hs.170623		6.40 6.40
	449911	AI262106	Hs.12653	ESTS	6.40
	440105	AA694010	Hs.6932	Homo sapiens clone 23809 mRNA sequence	6.37
45	440395	AA884412	Hs.216342		6.37
45	429500	X78565 AA804698	Hs.289114 Hs.82547	retinoic acid receptor responder (tazaro	6.36
	417771 417092	H97508	Hs.181165	eukaryotic translation elongation factor	6.36
	412227	AW902282	113.151100	gb:QV3-NN1023-260400-169-g10 NN1023 Homo	6.36
	400845			NA	6.36
50	403546	NA		NA .	6.36
	412345	AW938386		gb:PM4-DT0057-201299-002-G10 DT0057 Homo	6.35 6.34
	422186	AW962364	Hs.129051	ESTS	6.34
	426990	AL044315	Hs.173094		6.33
55	417687	AI828596	Hs.250691 Hs.130391		6.32
ככ	426223 417588	AW977812 Z44510	П\$. 13003 (	gb:HSC22D091 normalized infant brain cDN	6.32
	432629	AW860548	Hs.280658		6.31
	440495	AA887212	Hs.14161	hypothetical protein DKFZp434l1930	6.31
	407771	AL138272	Hs.62713	ESTs	6.31
60	417517	AF001176	Hs.82238	POP4 (processing of precursor, S. cerev	6.30
	431041	AA490967	Hs.19795	5 KIAA0704 protein	6.30 6.30
	445571	Al378000	Hs. 15848		6.30
	433309	AA807060	Hs.12655		6.30
65	415659		Hs.78547 Hs.42892		6.30
U.J	420271 426921				6.30
	400950		113.11200	NA .	6.30
	429692		Hs.9977	ESTs, Weakly similar to B34087 hypotheti	6.30
	439813		Hs.12450		6.30
70	449444				6.30
	453596	AA441838		hypothetical protein FLJ14834	6.30 6.30
	446847		Hs.82845		6.30
	435820		Hs.18900		6.30
75	452576			•	6.30
75	448924 424343			adenylate cyclase activating polypeptide	6.30
	41259				6.30
	42664			81 ubiquitin C-terminal hydrolase UCH37	6.30
	41908			0 integrin, beta 8	6.30
80	40142			NA .	6.30
	41218		Hs.2258		6.30 6.30
	43550				6.28
	40822	1 AA91218	3 Hs.4744	7 ESTs	J.20

	413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT	6.28
	416845	H95279		gb:yu20h02.s1 Soares fetal liver spleen	6.27 6.26
	402732 413224	NA A1732470	Hs.191157	NA ESTs, Wealdy similar to ALU7_HUMAN ALU S	6.26 6.24
5	415642	U19878	Hs.336224	transmembrane protein with EGF-like and	6.24
•	449284	BE502240	Hs.38592	hypothetical protein FLJ23342	6.24
	419548	AW978142	Hs.326248	Homo sapiens cDNA: FLJ22071 fis, clone H	6.23
	453880	AI803166	Hs.28462 Hs.119140	ESTs, Weakly similar to 138022 hypotheti eukaryotic translation initiation factor	6.22 6.22
10	422675 413384	BE018517 NM_000401	Hs.75334	exostoses (multiple) 2	6.21
10	445584	AF217518	Hs.8360	PTD012 protein	6.21
	451065	AW295132	Hs.222231	ESTs, Wealthy similar to granule cell mar	6.21
	420807	AA280627	Hs.57846	ESTs	6.20 6.20
15	421155 441421	H87879 AA356792	Hs.102267 Hs.334824	hysyl oxidase hypothetical protein FLJ14825	6.20
13	440209	H05049	Hs.22269	neurexin 3	6.20
	408170	AW204516	Hs.31835	ESTs	6.20
	433590	N98410	Hs.48364	Homo sapiens regulator of G-protein sign	6.20 6.20
20	442008 420617	AI457814 AK001652	Hs.270272 Hs.99423	ESTs ATP-dependent RNA heficase	6.20
20	402343	721001004	16.55125	NA .	6.20
	432682	AI376400	Hs.159588	ESTs	6.20
	452109	AI525873	Hs.61164	hypothetical protein FLJ14909	6.20 6.20
25	429954 417256	A1918130 U94332	Hs.21374 Hs.81791	ESTs tumor necrosis factor receptor superfami	6.20
23	435525	AI831297	Hs.123310	ESTs	6.20
	413604	R51767		gb:yg73g11.r1 Soares infant brain 1NIB H	6.20
	425305	AA363025	Hs.155572	Human clone 23801 mRNA sequence	6.20 6.20
30	443285	AI301918 D13757	Hs.334264 Hs.311	ESTs phosphoribosyl pyrophosphate amidotransf	6.20
30	446565 451027	AW519204	Hs.40808	ESTs	6.20
	452243	AL355715	Hs.28555	programmed cell death 9	6.19
	429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain	6.17
35	424060	X92108 AA551060	Hs.138629	H.sapiens mRNA for subtelomeric repeat s gb:nk74f02.s1 NOI_CGAP_Sch1 Homo sapiens	6.17 6.16
33	432494 448186	AA262105	Hs.4094	Homo sapiens cONA FLJ14208 fis, clone NT	6.14
	419638	N46504	Hs.91747	profilin 2	6.13
	445595	W25950	Hs.14512	DIPB protein	6.13
40	433036	AA574091	Hs.105964	ESTs	6.13 6.13
40	457155 443715	AL110243 AI583187	Hs.187991 Hs.9700	DKFZP564A122 protein cyclin E1	6.13
	422867	L32137	Hs.1584	cartilage diigomeric matrix protein (pse	6.12
	453286	AA034319	Hs.29041	Homo sapiens cDNA FLJ14177 fis, clone NT	6.11
45	424897	D63216	Hs.153684	frizzled-related protein	6.11 6.11
45	429188 434894	AB011171 AW977850	Hs.198037 Hs.23856	KIAA0599 protein hypothetical protein MGC5297	6.10
	413339	AI818080	Hs.194290	ESTs	6.10
	453685	AL110309		gb:DKFZp564L0278_r1 564 (synonym: hfbr2)	6.10
50	421195	BE464560	Hs.133017	ESTs ESTs	6.10 6.10
50	453296 444985	AA034413 AI677737	Hs.62560 Hs.28329	hypothetical protein FLJ14005	6.10
	423492	AF020761	Hs.129683	ubiquitin-conjugating enzyme E2D 1 (homo	6.10
	419841	BE005848	Hs.7326	ESTs	6.10
55	429190	H18650	Hs.92602	ESTs	6.10 6.10
23	426116 451441	AA868729 AA017601	Hs.144694 Hs.84529	ESTs ESTs, Weakly similar to Z202_HUMAN ZINC	6.10
	401740	70011001	10.045£3	NA	6.10
	441953	H11695	Hs.322901	disrupter of silencing 10	6.10
۲۸	401464	AF039241	Hs.9028	histone deacetylase 5	6.10 6.10
60	405033 410743	AA089474	Hs.272153	NA ESTs	6.10
	454758	AW845266	113.272133	gb:IL2-CT0031-160999-003-B08 CT0031 Homo	6.10
	417728	AW138437	Hs.24790	KIAA1573 protein	6.10
65	418553	TB8964		gb:yd97a07.r1 Soares fetal fiver spleen	6.09 6.08
65	431617	AK000738 BE011437	Hs.264636	hypothetical protein FLJ20731 gb:CM4-BN0220-080500-170-f03 BN0220 Homo	6.08
	455608 450755	AA010984	Hs.159464		6.07
	455217	AW867534		gb:MR0-SN0037-160400-004-e05 SN0037 Homo	6.07
70	437179	AA393508	Hs.300642		6.06 6.06
70	408622	AA056060 F05251	Hs.202577	Homo sapiens cDNA FLJ12166 fis, clone MA gb:HSC04H101 normalized infant brain cDN	6.06
	415308 428417	AK001699	Hs.184227		6.05
	426501	AW043782	Hs.293616		6.03
75	431077	AI669133	Hs.115660		6.03
75	403040	A1403743	LL 105310	NA ESTs, Moderately similar to 138022 hypot	6.02 6.02
	445704 415637	AJ493742 R25517	Hs.165210	gb:yg44f01.r1 Soares infant brain 1NIB H	6.02
	427925	N51323	Hs.255935		6.02
٥٨	404702	NA + COO+ 200		NA	6.02 6.01
80	433183	AF231338 178028	Hs.222024 Hs.154679		6.01
	437762 443833	A1654108	Hs.135125		6.01
	422263	AA307639	Hs.129908		6.00
				40.4	,

				U	6.00
				Homo sapiens cDNA: FLJ23536 fis, clone L ephrin-A5	. 6.00
				ESTs, Weakly similar to KIAA 1324 protein	6.00
	453853			ESTs	6.00
5	444188	Al393165	Hs.699	peptidytprotyt isomerase B (cyclophilin	6.00
	451813	NM_016117		phospholipase A2-activating protein	6.00 6.00
	422505	AL120862		ESTs	6.00
	420734	AW972872	Hs.293736	ESTs gb:RC0-HT0232-211099-011-e04 HT0232 Homo	6.00
10	455082 - 444200	BE148180 AA327113	Hs.149057	ESTs	6.00
10	447432	AW958473	Hs.301957	nudix (nucleoside diphosphate linked moi	6.00
	419752	AA249573	Hs.152618	ESTs, Moderately similar to ZN91_HUMAN Z	6.00
	428412	AA428240	Hs.126083	ESTs	6.00
	407790	AI027274	Hs.288941	Horno sapiens cDNA FLJ14866 fis, clone PL	6.00 6.00
15	428945	AW192803	Hs.98974	ESTs, Weakly similar to S65824 reverse t ESTs, Weakly similar to ALU4_HUMAN ALU S	6.00
	431878	AA521207 AW163518	Hs.270202 Hs.155485	huntingtin interacting prolein 2	6.00
	425282 401093	W44 1022 10	15.135.05	NA	6.00
	411861	AW867875		gb:MR0-SN0040-050500-003-f11 SN0040 Homo	6.00
20	411800	N39342	Hs.103042	microtubule-associated protein 18	5.99
	446925	AW974605	Hs.176669	ESTs	5.98 5.98
	401708	NA		NA CMAT amazin	5.97
	449894	AK001578	Hs.24129	CLLL7 protein NA	5.96
25	403278 455212	NA AW866330		gb:QV4-SN0024-080400-167-e01 SN0024 Homo	5.96
23	410116	AW630671	Hs.58636	squamous cell carcinoma antigen recogniz	5.96
	441271	AA927290	Hs.130462	ESTs	5.95
	404072			NA	5.95
••	431596	T34708	Hs.272927	Sec23 (S. cerevisiae) homolog A	5.94 5.93
30	421622	AB037748	Hs.106204	KIAA1327 protein ESTs	5.92
	441300	R35063 AF208855	Hs.181536 Hs.12830	hypothetical protein	5.91
	445517 429559	AI985345	Hs.26425	ESTs	5.91
	443767	BE562136	Hs.9736	proteasome (prosome, macropain) 26S subu	5.91
35	440510	H08427	Hs.309165	ESTs, Weakly similar to ISHUSS protein d	5.90
	414727	BE466904		gb:hz28f03.x1 NCI_CGAP_GC6 Homo sapiens	5.90 5.90
	451686	AA059246	Hs.110293	ESTs	5.90
	438032	BE045624	Hs.152992 Hs.286148	ESTs stromal antigen 1	5.90
40	450470 430533	Z75330 AA480895	Hs.201552	ESTs, Weakly similar to T17288 hypotheti	5.90
40	432662	AL049314	Hs.280700	ESTs	5.90
	451742	T77609	Hs.117970	ankyrin 2, neuronal	5.90
	431217	NM_013427	Hs.250830	Rho GTPase activating protein 6	5.90
	412537	AL031778	Hs.797	nuclear transcription factor Y, alpha	5.90 5.90
45	447233	AW246333	Hs.17901	Homo sapiens, clone IMAGE:3937015, mRNA, Machado-Joseph disease (spinocerebellar	5.90
	410804	U64820 AW298597	Hs.66521 Hs.61884	Homo sapiens, clone IMAGE:4298026, mRNA,	5.90
	452619 433865	N29862	Hs.44104	ESTs	5.90
	453403	BE466639	Hs.61779	Homo sapiens cDNA FLJ13591 fis, clone PL	5.90
50	448743	AB032962	Hs.21896	KIAA1136 protein	5.90
	447153	AA805202	Hs.315562		5.90 5.90
	425793	AA363946	Hs.20969	ESTs	5.90
•	404632	40000034	Hs.14912	NA KIAA0286 protein	5.90
55	446364 452240	AB006624 AI591147	Hs.61232	ESTs	5.90
))	410424	AA084984	10.01202	gb:zn11a08.r1 Stratagene hNT neuron (937	5.90
	404170			ŇA	5.89
	458390	A1792585	Hs.133272		5.89
<b>60</b>	408296	AL117452	Hs.44155	DKFZP586G1517 protein	5.88 5.87
60	444406	AI147237	Hs.300697	immunoglobulin heavy constant gamma 3 (G gb:RC3-HT0600-230300-021-g10 HT0600 Homo	5.B7
	413894 453922	BE177983 AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	5.86
	446700	AW206257	Hs.156320		5.86
	443377	A1792547	Hs.13329		5.86
65	419162		Hs.30412	3 ESTs	5.85
	436608		Hs. 19237		5.84
	428650		Hs.10731		5.84 5.84
	437410				5.84
70	428303 401004		ns.10300	NA	5.83
70	414504		Hs.11517	5 sterile-atpha motif and leucine zipper c	5.83
	410979			gb:RC0-HT0295-071199-011-a01 HT0295 Homo	5.82
	424576		Hs.96833		5.82
	439352	BE614347		5 hypothetical protein FLJ20989	5.81 6.80
75	423057				5.80 5.80
	429250		Hs.19830 Hs.75182		5.80
	413048 451367				5.80
	431367			gb:nc26a07.s1 NCI_CGAP_Pr1 Homo sapiens	5.80
80	421589		7 Hs.82919	cuttin 2	5.60
	427969	NM_00196	3 Hs.2230	epidermal growth factor (beta-urogastron	5.80
	451406		Hs.6295	ESTs, Weakly similar to T17248 hypotheti	5.80 5.80
	436096	5 H55931	Hs.2695	32 ESTs	3.00

	443353	At052659	Hs.133255	ESTs	5.80
	457244	AA581385	Hs.162473	ESTs, Wealdy similar to 138022 hypotheti	5.80
	407746	AK001962	Hs.38114	hypothetical protein FLJ11100	5.80
5	440688 445745	AW404591 AB007924	Hs.147440 Hs.13245	ESTs, Weakly similar to 2192_HUMAN ZINC KIAA0455 gene product	5.80 5.80
7	405637	NA	10.10210	NA	5.80
	415293	R49462	Hs.106541	ESTs	5.80
	440404 44 <b>2</b> 227	AI015881 AW771958	Hs.324527 Hs.175437	mitochondrial ribosomal protein S5 ESTs, Moderately similar to PC4259 ferri	5.80 5.80
10	423395	AA326613	10,113431	gb:EST29922 Cerebellum II Homo sapiens c	5.80
. •	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	5.80
	416000	R82342	Hs.79856	ESTs, Weakly similar to S65657 alpha-1C	5.80 5.80
	422108 430818	AA297914 AI311928	Hs.111749	postmeiotic segregation increased (S. ce gb:qo89h04.x1 NCI_CGAP_Kid5 Homo sapiens	5.80
15	444749	Al190672	Hs.65926	ESTs	5.80
	417515	L24203	Hs.82237	ataxia-tetangiectasia group D-associated	5.79
	456192	D84109	Hs.80248	RNA-binding protein gene with multiple s ab:QV0-TT0009-111199-055-b07 TT0009 Homo	5.78 5.78
	411253 417219	AW833897 AW973473	Hs.220936	ESTs	5.78
20	409450	AW628650	Hs.61260	hypothetical protein FLJ13164	5.76
	412013	AA400753	Hs.43761	ESTs, Weakly similar to A46010 X-linked	5.76 5.76
	425566 417877	AW162943 AI025829	Hs.250618 Hs.86320	UL16 binding protein 2 ESTs	5.75 5.75
	437114	AA836641	Hs.163085	ESTs	5.75
25	421238	AB033101	Hs.102796	Homo sapiens cDNA FLJ10708 fis, clone NT	5.74
	428959	AF100779 F00183	Hs.194680 Hs.172004	WNT1 inducible signating pathway protein titin	5.73 5.73
	415209 429922	Z97630	Hs.226117	H1 histone family, member 0	5.72
	420022	AA256253	Hs.120817	ESTS	5.71
30	431485	BE621320	Hs.257486	hypothetical protein FLJ20062	5.71 5.71
	424304 434276	NM_001395 AF123659	Hs.144879 Hs.93605	dual specificity phosphatese 9 leucine zipper, putative tumor suppresso	5.71
	438085	R52518	Hs.7967	ESTs	5.70
3.5	444379	N99035	Hs.222657	ESTs	5.70
35	401348	NA AAASCOSA	Un 4000C	NA ESTo	5.70 5.70
	428878 422564	AA436884 A1148006	Hs.48926 Hs.222120	ESTs ESTs	5.70
	452560	BE077084	Hs.336432	ESTs	5.70
40	408384	BE144344	Hs.7589	ESTs, Weakly similar to A46010 X-linked	5.70 6.70
40	409948 421166	AA078643 AA305407	Hs.102308	gb:7P08B01 Chromosome 7 Placental cDNA L potassium inwardly-rectifying channel, s	5.70 5.70
	439231	AW581935	Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	5.70
	439203	AA448930	Hs.8453	KIAA1587 protein	5.70
45	442029	AW956698	Hs.14456	neural precursor cell expressed, develop	5.70 5.70
4)	451922 407808	BE463995 AA663559	Hs.211033 Hs.279789	ESTs histone deacetylase 3	5.70
	428161	M96954	Hs.182741	TIA1 cytotoxic granule-associated RNA-bi	5.70
	413430	R22479	Hs.167073	Homo sapiens cDNA FLJ13047 fis, clone NT	5.70
50	428223 427972	AA424313 AA864870	Hs.98402 Hs.181304	ESTs putative gene product	5.70 5.70
50	416283	NM_005429	Hs.79141	vascutar endothelial growth factor C	5.70
	416319	AI815601	Hs.79197	CD83 antigen (activated B lymphocytes, I	5.70
	458044	AW979114	Hs.326135	ESTs	5.70 5.70
55	432911 411643	AW807634 AI924519	Hs.279799 Hs.192570	putative zinc finger protein NY-REN-34 a hypothetical protein FLJ22028	5.70
-	408867	AA437199	Hs.656	cell division cycle 25C	5.70
	428679	AA431765		gb:zw80c03.s1 Soares_testis_NHT Homo sap	5.70 5.70
	428822 409570	W28418 AW418720	Hs.30715 Hs.167583	potassium voltage-gated channel, lsk-rel ESTs	5.70 5.70
60	457441	BE467737	Hs.146125	ESTs	5.70
-	409101	NM_004297	Hs.50612	guanine nucleotide binding protein (G pr	5.70
	420192	AA256281	Hs.105040	ESTs Horno sapiens cDNA FLJ11812 fis, clone HE	5.69 5.69
	423582 454511	BE000831 AW948146	Hs.23837	gb:RC0-MT0013-280300-031-e02 MT0013 Homo	5.68
65	419586	AI088485	Hs.144759		5.67
	416777	AF146760	Hs.79844	DKFZP564M1416 protein	5.67 5.67
	435849 457892	BE305242 AA744389	Hs.16098	claudin 2 gb:ny51e10.s1 NCI_CGAP_Pr18 Homo sapiens	5.66
	450191	AW137243	Hs.222446		5.66
70	438653	AW188099	Hs.131813		5.66
	422910 453694	AJ269508 AW504918	Hs.121591 Hs.258208		5.66 5.66
	445302	AW304916 AK001537	Hs.12488	hypothetical protein FLJ10675	5.66
20	446080	AJ221741	Hs.117777		5.65
75	425474	Z48054	Hs.158084	peroxisome receptor 1 claudin 2	5.65 5.65
	432542 446983	AW083920 AA157484	Hs.16098 Hs.97199	complement component C1q receptor	5.65
	420898	AB002379	Hs.100113	KIAA0381 protein	5.65
80	401372	AIDCOFTA	U. 0000	NA Home serieur done IMACE: 2877795 mENA	5.64 5.63
οU	428541 426249	AJ862570 F05422	Hs.299214 Hs.168352		5.63
	459705	BE082764	Hs.270252	ESTs, Weakly similar to androgen recepto	5.63
	451863	AL120634	Hs.305923	ATPase, Ca++ transporting, plasma membra	5.62

	426316	NM_002430 1		meningioma (disrupted in balanced transl	5.62 5.62
	401183			NA FOT-	5.62 5.61
				ESTs	5.61
5			Hs.171176   Hs.98471	ESTs ESTs, Wealdy similar to T18712 hypotheti	5.60
5	447102 419150		Hs.89640	TEK tyrosine kinase, endothelial (venous	5.60
	444577		Hs.11393	RAD51 (S. cerevisiae) homolog C	5.60
•	423605		He 120887	cadherin 19, tyne 2	5.60
	413447			Homo sapiens cDNA: FLJ22063 fis, clone H	5.60 5.60
10	442957			ESTs	5.60
	424296	AJ631874		casein kinase 2, alpha 1 polypeptide ESTs	5.60
	430679 449358	R44428 AA001229		ESTs	5.60
	418348	AI537167	Hs.96322	hypothetical protein FLJ23560	5.60
15	433133	AB027249	Hs.104741	PDZ-binding kinase; T-cell originated pr	5.60
	444059	R69743	Hs.116774	integrin, alpha 1	5.60 5.60
	438157	AW137011	Hs.49576	ESTs ESTs	5.60
	428233	AI358831 AA846811	Hs.20578 Hs.130554	Homo sapiens cDNA: FLJ23089 fis, clone L	5.60
20	434265 451652	AA018968	Hs.133536	ESTs	5.59
20	422762	AL031320	Hs.119976	Human DNA sequence from clone RP1-20N2 o	5.59
	447591	AI675417	Hs.282855	ESTs	5.58 5.57
	417958	AA767382	Hs.193417	ESTs	5.57
25	438146	Z36842	Hs.57548 Hs.16145	ESTs ESTs	5.57
25	413595 422406	AW235215 AF025441	Hs.116206	Opa-interacting protein 5	5.56
	420529	D25259	Hs.319844	ESTs. Moderately similar to 154374 gene	5.56
	439582	W79161	Hs.118327	Homo sapiens cDNA FLJ11522 fis, clone HE	5.56
	408744	AW806177		gb:MR1-UM0108-130400-003-d04 UM0108 Homo	5.56 5.54
30	447230	AW972147	Hs.101395	hypothetical protein MGC11352	5.54
	428856	AA436735 AA971436	Hs.183171 Hs.16218	hypothetical protein FLJ22002 KIAA0903 protein	5.53
	446813 451424	A1862026	Hs.302810	Novel human gene mapping to chomosome 20	5.53
	410516	BE537917	Hs.90034	hypothetical protein FLJ21916	5.53
35	453994	BE180964	Hs.165590	ribosomal protein S13	5.53 5.52
	435583	AA767714	Hs.291627	ESTs	5.51
	431585	BE242803 AB011084	Hs.262823 Hs.48924	hypothetical protein FLJ10326 KIAA0512 gene product; ALEX2	5.51
	408912 427966	R97130	Hs.189699	ESTs	5.51
40	433611	AW327692	Hs.3446	mitogen-activated protein kinase kinase	5.51
	401244			NA .	5.50 5.50
	410784	AW803201		gb:IL2-UM0077-070500-080-E06 UM0077 Homo	5.50 5.50
	434006	AF113688	11- 1005	gb:Homo sapiens clone FLB4630 desmoglein 3 (pemphigus vulgaris antigen	5.50
45	425650	NM_001944 AF240467	Hs.1925 Hs.179152	toll-like receptor 7	5.50
43	427507 423268	BE386898	Hs.131162	ESTs, Weakly similar to ALU5_HUMAN ALU S	5.50
	405065	NA		NA	5.50
	444302	A1140115	Hs.225130		5.50 5.50
50	418183	NM_001772		CD33 antigen (gp67)	5.50
50	435586	AI279137 AA805166	Hs.151498 Hs.154762		5.50
	438279 427189	H82453	Hs.5635	ESTs	5.50
	415263	AA948033	Hs.130853		5.50
	441818	AI630451	Hs.7976	KIAA0332 protein	5.50 5.50
55	407834	AW084991	Hs.26100	ESTs	5.50
	404012	NA A1675444	Hs.263024	NA ESTs	5.50
	449932 423760	AA775891	Hs.191980		5.50
	431576	M76665	Hs.275215	hydroxysteroid (11-beta) dehydrogenase 1	5.50
60	423172	R15652		gb:HH503-F Adult heart, Clontech Homo sa	5.50 5.50
	422295	AF051151	Hs.114408		5.50 5.50
	429044	Al261490	Hs.145527 Hs.289037		5.50
	433280 414323	AA581404 NM_014759			5.50
65	405511	NA	,	NA	5.49
	444665		Hs.47783		5.49 5.48
	434434		Hs.15720		5.47
	421997		Hs.11061 Hs.68301		5.47
70	410276 435867		Hs.11405		5.47
70	453837		Hs.25612	6 haculoviral IAP repeat-containing 7 (fiv	5.47
	409617			Homo sapiens mRNA; cDNA DKFZp434K0514 (f	5.47 6.47
	430387	AW372884	Hs.24077		5.47 5.46
75	401629		Un 2015	NA 4 retinal outer segment membrane protein 1	5.46
75	433071		Hs.28156 Hs.20919		5.46
	458247 418049			8 Homo sapiens, Similar to nuclear localiz	5.45
	418247			gb:yg87h04.r1 Soares infant brain 1NIB H	5.45
~~	453711	5 AA037675			5.44 5.44
80	43115		Hs.1326		5.43
	426873		Hs.13109	92 ESTs gb:ny51d05.s1 NCI_CGAP_Pr18 Homo sapiens	5.42
	43709 44578				5.42
	-40.0	_ ,			

	447393	AI377458		EST	5.42 5.42
	425283 401208	AA354338 NA	Hs.131100	ESTS NA	5.42
	430536	AI809163	Hs.9908	nitrogen fixation cluster-like	5.42
5	405523			NA .	5.42
	409012	AL117435	Hs.49725	DKFZP434I216 protein	5.41
	429803	W81489	Hs.223025	RAB31, member RAS oncogene family	5.41 5.40
	436982 422892	AB018305 AA988176	Hs.5378 Hs.121553	spondin 1, (Fspondin) extracellular mat hypothetical protein FLJ20641	5.40
10	456027	BE327387	Hs.13913	KIAA1577 protein	5.40
••	411897	AW875066	Hs.326876	Homo sapiens SOX6 mRNA, complete cds	5.40
	449689	AF228421	Hs.23889	DKFZP564A032 protein	5.40
	432865	AI753709	Hs.152484	ESTs, Weakly similar to 138022 hypotheti	5.40 5.40
15	408248	AW854832	Hs.85701	gb:QV2-CT0261-201099-011-f05 CT0261 Homo phosphoinositide-3-kinase, catalytic, al	5.40 5.40
IJ	418516 423289	NM_006218 N77774	15.03701	gb;yz83e01.r1 Soares_multiple_scierosis_	5.40
	453365	AA035211	Hs.17404	ESTs	5.40
	406465			NA .	5.40
20	441858	AW173339	Hs.135665	ESTs	5.40 5.40
20	432507	8E391093 AI205712	Hs.324667 Hs.125998	ESTs ESTs	5.40 5.40
	440570 445062	AI339915	Hs.44324	ESTs	5.40
	421639	NM_012082	Hs.106309	Friend of GATA2	5.40
0.5	410406	AI969703	Hs.1466	glycerol kinase	5.40
25	418939	AW630803	Hs.89497	tamin B1	5.40 5.40
	426010 400250	AA 136563 NA	Hs.1975	hypothetical protein FLJ21007 NA	5.40
	424650	AW576156	Hs.250824	Homo sapiens cDNA: FLJ23435 fis, clone H	5.40
	414998	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin	5.39
30	433384	AI021992	Hs.124244	ESTs	5.38
	428781	AF164799	Hs.193384	putatative 28 kDa protein	5.38 5.38
	438150	AA037534	Hs.79059	transforming growth factor, beta recepto NA	5.38
	400639 426485	NM 006207	Hs.170040	platelet-derived growth factor receptor-	5.37
35	424205	AA336825	1.0.11.00.10	gb:EST41732 Endometrial tumor Homo sapie	5.36
	459596	H29554	Hs.113871	ESTs	5.36
	408234	AW993356	Hs.285814	sprouty (Drosophila) homolog 4	5.36 5.36
	414547	T47770	Hs.191463	ESTs ESTs, Wealtly similar to 1207289A reverse	5.35 5.35
40	419851 411945	AA287987 AL033527	Hs.13477 Hs.92137	v-myc avian myelocytomatosis viral oncog	5.34
40	425764	AW996009	Hs.112572	Homo sapiens cONA FLJ14130 fis, clone MA	5.34
	405352	***************************************		NA .	5.33
	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	5.32
45	424284	BE541008	Hs.6193	hypothetical protein FLJ14590	5.32 5.31
43	427741 426021	AW753185 AW770897	Hs.180628 Hs.34392	dynamin 1-like ESTs, Weakly similar to I38022 hypotheti	5.31
	442186	AA984083	Hs.269746	ESTs, Weakly similar to T03306 PSD-95/SA	5.30
	437319	BE410958	Hs.56406	Homo sapiens cDNA FLJ13549 fis, clone PL	5.30
50	405287	NA		NA .	5.30
50	427032	AF012023	Hs.173274	integrin cytoplasmic domain-associated p gb:yf89b02.r1 Soares infant brain 1NIB H	5.30 5.30
	415371 420024	R15239 AA252905	Hs.194477	E3 ublquitin ligase SMURF2	5.30
	434408	AI031771	Hs.132586	ESTs	5.30
	434739	AA804487	Hs.144130	ESTs	5.30
55	421327	AA837295	Hs.188802	ESTs	5.30 5.30
	453058	AW612293	Hs.288684	Horno sapiens cDNA FLJ11750 fis, clone HE MRS2 (S. cerevisiae)-like, magneslum hom	5.30 5.30
	448776 417845	BE302464 AL117461	Hs.30057 Hs.82719	Homo sapiens mRNA; cDNA DKFZp586F1822 (f	5.30
	430264	AA470519		gb:nc71f10.s1 NCI_CGAP_Pr1 Homo sapiens	5.30
60	411402	BE297855	Hs.69855	NRAS-related gene	5.30
	419220	AA811938	Hs.291759	ESTs	5.30 5.30
	407995 459256	AJ094748 AW967468	Hs.100134 Hs.99821	hypothetical protein FLJ12787 hypothetical protein FLJ14547	5.30
	452449	AW068658	Hs.20943	ESTs	5.30
65	430366	AI057368	Hs.105575		5.30
	434360	AW015415	Hs.127780		5.30
	422560	F11469	Hs.118281	zinc finger protein 266	5.29 5.29
	441704	AI458766	Hs.201988 Hs.134214		5.29 5.29
70	443635 434342	AI080230 AI791138	Hs.116768		5.29
	423409	NM_006466			5.29
	449000	U69560	Hs.3826	kelch-like protein C3IP1	5.29
	452381	H23329	Hs.290880		5.29 5.29
75	409058	AW236991	Hs.102495		5.28
13	434860 408096	AA932386 BE250162	Hs.292667 Hs.83765	ES15 dihydrofolate reductase	5.28
	418036	237976	Hs.83337	latent transforming growth factor beta b	5.28
	435443	AJ248674	Hs.14295	ESTs	5.26
90	414269	AA298489	Hs.303171		5.26 5.26
80	408371 401205	AF161545 NA	Hs.279883	hypothetical protein NA	5.26
	450904	R07118	Hs.189924		5.26
	416351	H49704	Hs.173522		5.26

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					5.06
		AA380611		ESTs heat shock 90kD protein 1, alpha	5.25 5.25
		A1127359 AW207659	Hs.289088 Hs.6630	Homo sapiens cDNA FLJ13329 fis, clone OV	5.24
_		AW167613	Hs.248	mitogen-activated protein kinase kinase	5.24
5		Z45794	Hs.238809	ESTs	5.24 5.22
	404117 427956	NA AL046175	Hs.108169	NA Homo sapiens mRNA; cDNA DKFZp586C1619 (f	5.22
	421787	AA227068	Hs.108301	nuclear receptor subfamily 2, group C, m	5.22
• •	437255	R58970	Hs.9887	ESTs	5.22 5.20
10	424697	AL136169	Hs.250708 Hs.54976	CAAX box 1 ESTs	5.20
	449771 432193	AI668702 AA372264	Hs.273193	hypothetical protein FLJ10706	5.20
	438885	AI885558	Hs.184987	ESTs	5.20 5.20
1.5	407182	AA312551	Hs.230157	ESTs	5.20 5.20
15	452150 419680	W42490 AA249720	Hs.260844 Hs.59335	ESTs	5.20
	438940	AF075045	Hs.271609	ESTs	5.20
	405362	NA		NA	5.20 5.20
20	449370	AK002114	Hs.23495 Hs.49136	hypothetical protein FLJ11252 ESTs, Moderately similar to ALU7_HUMAN A	5.20
20	442353 409331	BE379594 M36634	Hs.53973	vasoactive intestinal peptide	5.20
	415397	H10818		gb:ym04f10.r1 Soares infant brain 1NIB H	5.20 5.20
	406735	AA603092	U- 05303	gb:np37a01.s1 NCI_CGAP_Lu1 Horno sapiens adenosine dearninase, RNA-specific, B1 (h	5.20
25	418489 431480	U76421 AA837274	Hs.85302 Hs.257005	hypothetical protein FLJ20837	5.20
LJ	425523	AB007948	Hs.158244	KIAA0479 protein	5.20 5.20
	425673	R70318	Hs.339730	ESTs, Weakly similar to A46010 X-linked	5.20
	439267 457030	AA287747 AI301740	Hs.173012 Hs.173381	dihydronyrimidinase-like 2	5.20
30	424638	AI472106	Hs.49303	Homo sapiens cDNA FLJ11663 fis, clone HE	5.20
20	454434	AA083558	Hs.261286	ESTs	5.20 5.20
	448336	R53848	Hs.44976 Hs.163327	ESTs ESTs, Weakly similar to 2109260A B cell	5.20
	429534 434803	AW976987 AW974640	Hs.303413		5.20
35	403199	NA		NA	5.20 5.20
	435225	AJ021912	Hs.187983 Hs.153952		5.20
	451664 440385	AA889081 AA884283	Hs.192136	FSTs	5.20
	432328	AI572739	Hs.195471		5.20 5.20
40	400484			NA gb:EST72986 Ovary II Horno sapiens cDNA 5	5.20 5.19
	425757	AA363171 Al671602	Hs.199602		5.19
	449841 420303	AA258282	Hs.278436		5.19
	429687	AI675749	Hs.211608		5.19 5.18
45	453345	AA302862	Hs.90063 Hs.147674		5.18
	447499 404913	AW262580	113.14707	NA NA	5.18
	405114	NA		NA	5.18 5.18
50	431117	AF003522	Hs.250500 Hs.29667		5.17
30	411995 401736	W49701 NA	115.25007	NA	5.17
	425250	AA353495	Hs.26976		5.16 5.16
	454388	AA630905 AA045573	Hs.33330 Hs.22900		5.16
55	449032 443646	AI085198	Hs.16422		5.15
00	436032	AA150797	Hs.10927	6 latexin protein	5.15 5.15
	456896	M97639	Hs.15558 Hs.28803		5.15
	433672 432826	BE281165 X75363	Hs.25077		5.14
60	439441	W67993	Hs.32313	35 ESTs	5.14 5.14
	400205		11- 4700	NA S ESTS	5.14
	430854 408771				5.14
	456804		Hs.1398	51 caveolin 2	5.14
65	424690				5.13 5.12
	449210 419013		Hs.1976 Hs.1448		5.12
	425843			27 death associated protein 3	5.12
70	422545	X02761	Hs.2878		5.12 5.11
70	424789		Hs.6126 Hs.8820		5.10
	442833 422411			1 ESTs	5.10
	45756	BE29402	Hs.2799	03 Ras homolog enriched in brain 2	5.10 5.10
75	43772				5.10
13	44689 40158		75.7110	NA	5.10
	41751	1 AL04917		23 chordin-like	5.10 5.10
	42233	6 A1761322			5.10 5.10
80	43766 42952				5.10
	44733		12 Hs.1609	918 ESTs	5.10 5.10
	43620				5.10 5.10
	42815	5 H17012	Hs.146	33 ESTs	

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	420185	AL044056	Hs.158047	ESTs Homo sapiens G-protein coupled receptor	5.10 5.10
	445657 440913	AW612141 AI267491	Hs.279575 Hs.160593	ESTs	5.10
_	452943	BE247449	Hs.31082	hypothetical protein FU10525	5.10
5	428603	BE241619	Hs.24641	cytoskeleton associated protein 2	5.10 6.10
	436577 400241	W84774 NA	Hs.17643	ESTs NA	5.10 5.10
	437205	AL110232	Hs.279243	Homo sapiens mRNA; cDNA DKFZp564D2071 (f	5.10
	423654	AI674253	Hs.35828	ESTs	5.10
10	417637	AA204969	Hs.234863	Homo sapiens cDNA FLJ12082 fis, clone HE	5.10 5.10
	430849 452605	A1940727 AW968557	Hs.270556 Hs.90012	ESTs, Highly similar to AF156779 1 ASB-4 hypothetical protein FLJ23441	5.10
	440381	AA917808	Hs.190495	ESTs	5.10
	441033	BE562555		gb:601335867F1 NIH_MGC_44 Homo sapiens c	5.10
15	450229	R18717	Hs.8929	hypothetical protein FLJ11362	5.10 5.10
	447197 442150	R36075 AJ368158	Hs.70983	gb:yh88b01.s1 Soares placenta Nb2HP Homo PTPL1-associated RhoGAP 1	5.10
	415651	AI207162	Hs.3815	stathmin-like-protein RB3	5.10
	453655	AW960427	Hs.79059	transforming growth factor, beta recepto	5.09
20	434442	AA737415	Hs.152826	ESTs Homo sapiens cDNA FLJ11079 fis, clone PL	5.09 5.09
	429389 435419	AA454779 AI281068	Hs.201441 Hs.152835	ESTs	5.09
	427620	NM_003705	Hs.179866	solute carrier family 25 (mitochondrial	5.09
0.5	445706	AA305520	Hs.108812	hypothetical protein FLJ22004	5.08
25	424071	R71340	Hs.12876	ESTs small inducible cytokine subfamily B (Cy	5.08 5.08
	428227 426400	AA321649 M78361	Hs.2248 Hs.169743	Homo sapiens clone 25121 neuronal offact	5.08
	429026	AA443385	Hs.221993	ESTs	5.08
	455847	BE146775		gb:QV4-HT0222-181099-013-e04 HT0222 Homo	5.08
30	416110	Z42262	Hs.322844	hypothetical protein DKFZp564A176	5.08 5.08
	436854 421799	AA749167 AW972292	Hs.173911 Hs.292998	ESTs ESTs	5.08
	452154	AW953265	Hs.302746	MSTP028 protein	5.06
0.5	444946	AW139205	Hs.156457	hypothetical protein FLJ22408	5.06
35	445950	AI267957	Hs.145706	ESTs ESTs	5.06 5.06
	443124 440698	A1033500 A1348455	Hs.132895 Hs.147492	Homo sapiens cDNA FLJ11777 fis, clone HE	5.06
	444713	AW812074	Hs.28631	Homo sepiens cDNA: FLJ22141 fis, clone H	5.06
40	447970	AW086109	Hs.20136	chromosome X open reading frame 6	5.06
40	419307	AW953190	Hs.23180	ESTs BUB3 (budding uninhibited by benzimidazo	5.06 5.06
	421954 451807	AA410245 W52854	Hs.40323 Hs.27099	hypothetical protein FLJ23293 similar to	5.05
	421782	AB029290	Hs.108258	actin binding protein; macrophin (microf	5.05
	407976	AI633875	Hs.77823	hypothetical protein FLJ21343	5.05
45	400869	040004		NA	5.04 5.04
	416153 428242	R13894 H55709	Hs.2250	gb:yf62a06.r1 Soares infant brain 1NIB H leukemia inhibitory factor (cholinergic	5.04
	406038	Y14443	Hs.88219	zinc finger protein 200	5.03
50	440659	AF134160	Hs.7327	claudin 1	5.03
50	425188	AK002052	Hs.155071	hypothetical protein FLJ11190	5.02 5.02
	446051 443387	BE048061 BE139135	Hs.37054 Hs.254629	ephrin-A3 ESTs	5.02
	414407	AA147026	Hs.76704	ESTs	5.02
<i>E E</i>	408349	BE546947	Hs.44276	homeo box C10	5.01 5.01
55	452510	Z33566 AK001713	Hs.301491 Hs.17860	ESTs hypothetical protein FLJ10851	5.00
	447245 413472	BE242870	Hs.75379	solute carrier family 1 (gliaf high affi	5.00
	447857	AA081218	Hs.58608	Homo sapiens cDNA FLJ14206 fis, clone NT	5.00
60	423648	AK000456	Hs.130546	hypothetical protein FLJ20449	5.00 5.00
60	412997 408964	BE046600 AF201468	Hs.49349	gb:hn41d08.x1 NCI_CGAP_RDF2 Homo sapiens beta-site APP-cleaving enzyme	5.00
	411636	AW855001	113.750	gb:PM3-CT0263-091299-007-f05 CT0263 Homo	5.00
	418111	R42003	Hs.106513		5.00
45	402709	NA HOTOGO	11. 40004	NA	5.00 5.00
65	408677	AI279892 AW877011	Hs.46801	sorting nexin 14 ab:QV2-PT0010-250300-096-b05 PT0010 Homo	5.00
	411350 453382	AA709285	Hs.5997	hypothetical protein FLJ13078	5.00
	458090	AI282149	Hs.56213	ESTs, Highly similar to FXD3_HUMAN FORKH	5.00
70	408512	AW902013	Hs.255937 Hs.16625		5.00 5.00
70	453240 440491	Al969564 R35252	Hs.24944		5.00
	423896	AA332216	Hs.13058	ESTs .	5.00
	429091	AA935658	Hs.18793		5.00 5.00
75	410968		Hs.67397 Hs.27005		5.00 5.00
13	436859 452198		Hs.61210		5.00
	424511			7 ESTs, Moderately similar to ALU7_HUMAN A	5.00
	414631	AW970130	Hs.65406		5.00
80	405481		Hs.25050	NA 2 carbonic anhydrase VIII	5.00
30	431118 421373				5.00
	424916	AW867440	Hs.23096	ESTs	5.00
	433106	AB002443	Hs.18441		5.00
				500	

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5.00
                                                       Hs.337717
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                                                        Hs.128312
                                 A1733236
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                                                                                                                                                                     5.00
                420161
                                 AI683069
                                                        Hs.175319
                                                                           ESTs
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                                                                           hypothetical protein FLJ 14906
                                                        Hs 183528
                                 BE018217
                                                                                                                                                                     5.00
                                                        Hs.258791
  5
                415188
                                 BE007531
AW293291
                                                                                                                                                                      5.00
                                                        Hs.255180
                                                                            ESTs
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                                                                                                                                                                      5.00
                                  AV655045
                                                        Hs.8366
                                                                            ESTs
                439038
                                                                                                                                                                      5.00
                                                                            ESTs, Weakly similar to KIAA0944 protein
                                                         Hs.304802
                                 A1497955
A1073424
                457031
                                                                                                                                                                      5.00
                                                         Hs.5232
                                                                            HSPC125 protein
                430865
                                                                                                                                                                      5.00
10
                                  H77859
                                                         Hs.65450
                                                                            reticulon 4
                420583
                                                                                                                                                                      5.00
                                                                            ESTs
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                                                         Hs.143587
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                                                                                                                                                                      5.00
                                                                            gb:RC3-HT0622-130400-022-a02 HT0622 Homo
                 455208
                                  BE180276
                                                                                                                                                                      5.00
5.00
                                                         Hs.89832
                 419263
                                   AWS83874
                                                                            hypothetical protein FLJ13164
                                   AA286844
                                                         Hs.61260
                 452279
                                                                                                                                                                       5.00
                                                                             hypothetical protein PP1665
                                   AA464362
                                                         Hs.6748
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                 419100
                                                                                                                                                                       5.00
                                                         Hs.123362
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                                   AA811371
                  438585
                                                                             Homo sapiens cDNA FLJ13097 fis, clone NT
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                  436953
                                                                                                                                                                       5.00
                                                         Hs.143691
                                                                            ESTs
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                 428775
                                                                             ESTs, Weakly similar to I38022 hypotheti
                 422471
                                   AA311027
                                                         Hs.271894
                                                                                                                                                                       5.00
 20
                  402524
                 TARIF 468:
                                                 Unique Eos probeset identifier number
                  Pkey:
CAT number:
                                                 Gene cluster number
                                                 Genbank accession numbers
  25
                   Accession:
                                     CAT number
                   Pkey
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AA355749 AA085520 AW966333 AA340319 BE170936
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R51767 BE152515 Z44834 H23397
BE177983 BE178322
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                                                              R15239 Z45189 F06836
H10818 F07B31 Z43072
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N54000 H26494 T83818
H95279 H95331 H95933
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                                         226804 1
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                                           38944 1
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AV552831 AA191140 AA329706 AI267893 AI796986 AW675672 AW195369 BE002835 BE003284 AA190592 AA769594 AW275548 R56781 AA807313
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                     1385569 1
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                                   AA744292 AA745577 AW748517 AW748564 AW748511 AW748513 AW748530 AW748574 BE062923
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          TABLE 46C:
20
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          Pkey:
                             Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA
          Ref:
                             sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
                             Indicates DNA strand from which exons were predicted.
          Strand:
                             Indicates nucleotide positions of predicted exons.
          Nt_position:
25
          Pkey
400484
                     Ref
                                    Strand
                                                Nt position
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                                    Minus
           400639
                      9887597
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                                                23150-23580
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                                                 34428-34612
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400860
                      9188505
                                    Plus
                                                 151830-152104,152649-152744
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                                    Minus
                      9838306
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           400869
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                                                157920-158564
73950-74364
           400950
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           400977
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                                    Plus
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                                                 127056-127196
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                                                 25693-25991
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          405770
          406465
                     9795550
                                   Plus
10
          TABLE 47A: ABOUT 370 GENES SIGNIFICANTLY DOWN-REGULATED IN STOMACH CANCER COMPARED TO NORMAL STOMACH
          Table 47A lists about 370 genes significantly down-regulated in stomach cancer compared to normal stomach. These were selected as for Table 46A, except that the numerator and
          denominator were switched and the ratio was equal to or less than 0.33.
                             Unique Eos probeset identifier number
15
          Pkey:
                             Exemplar Accession number, Genbank accession number
          ExAcon:
          UnigenelD:
                             Unigene number
                             Unigene gene title
           Unigene Title:
                              Ratio of tumor to normal body tissue
          R1:
20
                                                       Unigene Title
                                    UnigenelD
                     ExAcon
NM 000705
                                                       ATPase, H+/K+ exchanging, beta polypepti solute carrier family 26, member 3
                                    Hs.813
           412859
                                                                                                          0.02
                      AU076819
                                    Hs.1650
           423371
                                                       protease, serine, 7 (enterokinase)
                                                                                                          0.04
                      U09860
                                    Hs.158333
           425607
                                                                                                          0.04
                                                       meprin A, beta
25
                                    Hs. 194777
                      X81333
           429050
                                                                                                          0.05
                                    Hs.1460
                                                       glucagon
                      AW583807
            421996
                                                                                                          0.05
                                                       cytosolic beta-glucosidase
                                    Hs.146182
                      AW242447
           441212
                                                                                                          0.06
                                                        microsomal triglyceride transfer protein
            429093
                       NM_000253
                                    Hs.195799
                                                                                                          0.07
                      NA
            403697
                                                                                                          0.08
 30
            402760
                       NA
                                                                                                          ስ በጸ
                       AW340797
                                     Hs.98434
                                                        FSTs
            428285
                                                                                                          0.08
                       AA235900
                                     Hs.87500
                                                        ESTs
            419279
                                                                                                          0.09
                                                        omithine carbamoyltransferase
                                     Hs.117050
                       K02100
            422459
                                                        maltase-glucoamylase (alpha-glucosidase)
                                                                                                          0.09
                       AF016833
                                     Hs.122785
            422992
                                                        cholinergic receptor, muscarinic 2
                                                                                                          0.09
                                     Hs.248099
 35
                       M16404
            430867
                                                        ATPase, H+fK+ exchanging, alpha polypept
                                                                                                           0.10
            453989
                       M63962
                                     Hs.36992
                                                                                                           0.10
                                     Hs. 207604
            443022
                       AL046485
                                                        gb:RC1-BT0720-280300-011-f08 BT0720 Homo
                                                                                                           0.10
            413382
                       RE090689
                                                                                                           0.10
                                     Hs.33654
                                                         ESTs
                       AA057418
            450769
                                                                                                           0.10
                                                         retinol-binding protein 2, cellular
  40
                       T63918
                                      Hs.182313
            428070
                                                         myocilin, trabecular meshwork inducible
                                                                                                           0.11
                                      Hs 78454
            415447
                       Z97171
                                                                                                           0.11
                                                         telomerase-associated protein 1
                                      Hs.232070
                       U86136
            430073
                                                                                                           0.12
                                                         fatty-acid-Coenzyme A ligase, long-chain
                                      Hs.268012
                       D89053
            431716
                                                         mal. T-cell differentiation protein
                                                                                                           0.12
                        AW250318
                                      Hs.80395
            416889
                                                                                                           0.12
  45
                                                         NA
                        NA
             405650
                                                         carboxypeptidase A2 (pancreatic)
                        AW583139
                                      Hs.89717
             419219
                                                                                                           0.12
                        NA
             401623
                                                         KIAA0154 protein; ADP-ribosylation facto
                                                                                                           0.13
                        AF219139
                                      Hs.87726
             400811
                                                         gb:MR0-HT0165-140200-009-d04 HT0165 Homo
                                                                                                            0.13
             455826
                        BE144228
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                                                          gb:hSCG-3=stomach cancer gene-3 (oncogen
                                                                                                            0.13
                        S69741
             407486
                                                          ab:Human forkhead family (AFX1) mRNA, pa
                                                                                                            0 13
             407494
                        U10072
                                                                                                            0.13
                                                          ŇA
             401015
                                                                                                            0.14
                                                          nuclear receptor subfamily 1, group H, m
ESTs, Weakly similar to T46608 zinc fing
                        AU076646
                                      Hs.171683
             426651
                                                                                                            0.14
                                       Hs.205591
   55
                        AI744361
             450926
                                                                                                            0.14
             443564
                        AI921685
                                       Hs.199713
                                                          ESTs
                                                                                                            0.14
                                                          ESTs
                                       Hs 143945
              457955
                        AI208986
                                                          ESTs
                                       Hs.192175
              457345
                        AI699933
                                                                                                            0.14
                                                          RAB27A, member RAS oncogene family
                                       Hs.50477
                         U38654
              417118
                                                          FSTs
   60
                         BE162203
                                       Hs.314758
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                                                                                                             0.15
                                       Hs.148814
                                                          ESTs
              444938
                         AW470690
                                                                                                             0.15
                                                          NA
              403670
                         NA
                                                                                                             0.15
                                                          sucrase-isomaltase
                         X63597
                                       Hs.2996
              432440
                                                                                                             0.15
                         AW662740
                                       Hs.259391
                                                          ESTs
              428492
                                                                                                             0.15
                                       Hs.134069
   65
              443607
                         AI452512
                                                          FAT tumor suppressor (Drosophila) homolo
                                                                                                             0.15
                                       Hs.166994
                         BE044496
              446914
                                                          estrogen-related receptor gamma
gb:PM1-HT0527-280200-005-a05 HT0527 Homo
                                                                                                             0.15
                         AB020639
                                        Hs.151017
              424596
                                                                                                             0.16
              430350
                          BE169639
                                                                                                             0.16
                                       Hs.116195
                                                           ÉSTs
              431094
                          AW972276
                                                                                                             0.16
    70
                                                           NA
              401683
                          NA
                                                                                                             0.16
                                                           apolipoprotein A-IV
                          AU076799
                                        Hs.1247
              419278
                                                                                                             0.16
                                                           gb:MR0-HT0208-101299-202-e12 HT0208 Homo
              455071
                          BE145826
                                                           gb:UI-H-BWO-aio-h-05-0-UI.s1 NCI_CGAP_Su
                                                                                                             0.16
                          AW296422
              454282
                                                                                                             0.16
                                        Hs.194236
                                                            leptin (murine obesity homolog)
                          NM_000230
              428848
                                                                                                             0.16
    75
                          AW160725
                                        Hs.312469
                                                           FSTs
              451729
                                                                                                             0.16
                                                           DKFZP564D206 protein
                          R52804
                                        Hs 25956
               451103
                                                           Homo sapiens mRNA; cDNA DKFZp434M0223 (I
                                                                                                             0.16
                          AI 137479
                                        Hs.186655
               428602
                                                                                                              0.17
```

503

0 17

0.17

0.17

0.17

gb:DKFZp434A1229_r1 434 (synonym: htes3)

pregnancy specific beta-1-glycoprotein 3 gb:RC1-BN0056-230200-021-e11 BN0056 Homo

Hs.120655

Hs.282847

Hs.122082

**ESTs** 

BE048860

AL138411

AW997986

AW292520

NA H82022

437157

422731

402015

414758

412793

438152

80

	401685	NA		MA	0.17
		AA972740	Lin 127002	NA COT-	0.17
	441519		Hs.127092	ESTs	0.17
	438327	H87407	Hs.172944	chorionic gonadotropin, beta polypeptide	0.17
•	402761	BE387621	Hs.108809	chaperonin containing TCP1, subunit 7 (e	0.17
5	424268	AA397653	Hs.307438	Human DNA sequence from clone 495O10 on	0.18
	414507	AW102637	Hs.13349	Homo sapiens cDNA FLJ14647 fis, clone NT	0.18
	413808	J00287	Hs.182183	Homo sapiens mRNA for caldesmon, 3' UTR	0.18
	401132	NA		NA	0.18
	412374	X01388	Hs.73849	apolipoprotein C-III	0.18
10	423417	AP000365	Hs.128342	potassium large conductance calcium-acti	0.18
	447677	AJ419235		gb:tf21d02.x1 NCI_CGAP_Bm23 Homo sapien	0.18
	448828	AI580296	Hs.174782		0.18
	424122	AA335593		ESTs, Weakly similar to KIAA1437 protein	
			Hs.116147	ESTs	0.18
15	417332	AW972717	Hs.288462	hypothetical protein FLJ21511	0.18
15	434597	AW974668		gb:EST386757 MAGE resequences, MAGM Horno	0.19
	428804	AK000713	Hs.193736	hypothetical protein FLJ20706	0.19
	410280	AA083558	Hs.261286	ESTs	0.19
	409382	AA071244		gb:zm73g03.r1 Stratagene neuroepithelium	0.19
	428062	AA420683	Hs.98321	hypothetical protein FLJ14103	0.19
20	426069	H10807	Hs.281434	Homo sapiens cDNA FLJ14028 fis, clone HE	0.19
	430135	NM_000035	Hs.234234	eldolase B, fructose-bisphosphate	0.19
	414802	AJ793107	Hs.27018	Ris	0.19
	457432	NM_005136	Hs.268538	polassium voltage-gated channel, lsk-rel	0.19
	446909	AA004895	Hs.30082	ESTs	0.19
25	435447		ns.30062		
23		AI872932	11- 10100	gb:wm72e03.x1 NCI_CGAP_Ut2 Homo sapiens	0.20
	408611	NM_004367	Hs.46468	chemokine (C-C motif) receptor 6	0.20
	423577	AW810107	Hs.58633	Homo sapiens cDNA: FLJ22145 fis, clone H	0.20
	439328	W07411	Hs.118212	ESTs, Moderately similar to ALU3_HUMAN A	0.20
20	436741	AA860163	Hs.291319	ESTs	0.20
30	426635	BE395109	Hs.129327	hypothetical protein MGC13057	0.20
	418277	AW135221	Hs.130812	ESTs	0.20
	448871	BE616709	Hs.159265	kruppel-related zinc finger protein hcKr	0.20
	459370	AA889982	Hs.271826	ESTs. Weakly similar to 138022 hypotheti	0.21
	427469	AA403084	Hs.269347	ESTs, Weakly similar to 2109260A 8 cell	0.21
35	432887	AI926047	Hs.162859	ESTs	
55					0.21
	421296	NM_002666	Hs.103253	perilipin	0.21
	449216	AW295417	Hs.224616	ESTs	0.21
	414835	AA156720	Hs.185342	ESTs	0.21
40	459233	A1939966		gb:MR0-CT0015-160799-002-b06 CT0015 Hamo	0.21
40	439756	AL359651	Hs.283852	Homo sapiens mRNA full length insert cDN	0.21
	427167	AI239607	Hs.99196	hypothetical protein MGC11324	0.21
	400410	AF154915	Hs.283958	homeo box D12	0.21
	409828	AW501137		gb:UI-HF-BP0p-sit-e-12-0-UI,r1 NIH_MGC_5	0.22
	428470	AC002301	Hs.184507	Homo sapiens Chromosome 15 BAC clone CIT	0.22
45	455968	BE168828	113.104001	gb:QV1-HT0517-020400-145-f04 HT0517 Homo	0.22
1.5	404145	NA		NA	
			11- 22000		0.22
	454011	M31008	Hs.37009	alkaline phosphatase, intestinal	0.22
	430588	AI741461	Hs.161904	ESTs	0.22
50	403652	NA		NA	0.22
50	440410	AW204436	Hs.128715	ESTs	0.22
	453871	BE300380	Hs.69476	Homo sapiens cDNA FLJ12758 fis, clone NT	0.22
	458567	A1222075	Hs.147831	ESTs	0.22
	436004	AA703332	Hs.196270	tolate transporter/carrier	0.22
	417408	F17211	Hs.86092	Horno sapiens skeletal myosin light chain	0.22
55	448643	AI557531		gb:pt2.1-06.006,r tumor2 Homo sapiens cO	0.22
-	404401	NA		NA	0.22
	428088	AA421130	Hs.112640	EST	0.22
	427074	AA527435	Hs.178589	hepatocellular carcinoma antigen gene 52	0.22
	421972	M18185	Hs.1454		0.22
60				gastric inhibitory polypeptide	
JJ	429001	AF098951	Hs.194720	ATP-binding cassette, sub-family G (WHIT	0.22
	441155	AW161008	Hs.7719	GABA(A) receptor-associated protein	0.22
	402750	NA		NA .	0.22
	438587	AA811450	Hs.136984	ESTs	0.22
	404848	NA		NA	0.22
65	427833	AA416615	Hs.98242	ESTs	0.23
	439907	AA853978	Hs.124577	ESTs	0.23
	414373	AW162907	Hs.75969	proline-rich protein with nuclear target	0.23
	446817	AI700684	Hs. 134166	ESTs	0.23
_	437333	AA748898		gb:ny76h10.s1 NCI_CGAP_GCB1 Homo sapiens	0.23
70	404097	NA .		NA	0.23
	446393	AW014174	Hs.301956		0.23
		T41368	113.30 1330	zinc finger protein	
	456328			gb:ph1d1_19/1TV Outward Alu-primed hncDN	0.23
	401042	NA NA	11- 70000	NA	0.23
75	458441	AW842283	Hs.79933	cyclin I	0.23
75	435547	AW117431	Hs.191906	ESTs	0.23
	429060	AW139155	Hs.194995	hypothetical protein DKFZp434O0320	0.23
	425158	AW954631	Hs.266940	1-complex-associated-testis-expressed 1-	0.23
	448758	AB018311	Hs.21917	KIAA0768 protein	0.23
	441240	AA923749	Hs.132442	ESTs	0.23
80	436562	H71937	Hs.322904	ESTs, Weakly similar to 138022 hypotheti	0.23
	424104	AA669515	Hs.144950	ESTs	0.23
	447452	BE618258	Hs.102480	Homo sapiens, clone IMAGE:3869590, mRNA,	0.23
		AW204908		ESTs	
	444515	A11204300	Hs.169979	22.4	0.24

	433084	M18079	Hs.282265	fatty acid binding protein 2, intestinal	0.24
	406560	NA.	19.202230	NA	0.24
	432408	N39127	Hs.332557	ESTs, Weakly similar to A46010 X-linked	0.24
_	455699	BE068121		gb:CM1-BT0368-061299-060-a02 BT0368 Homo	0.24 0.24
5	453979	M68895	Hs.76800	alcohol dehydrogenase 6 (class V) gb:zd95g05.s1 Soares_fetal_heart_NbHH19W	0.24
	439657	W93589		gb:Human pTR5 mRNA for repetitive sequen	0.24
	407512	X15674 AW138036	Hs.201788	ESTs	0.24
	440875 404753	NA	113.201700	NA .	0.24
10	411119	M60627	Hs.753	formyl peptide receptor 1	0.24 0.24
	418692	AK000268	Hs.87383	hypothetical protein	0.24
	415327	H22769		gb:ym54c02.r1 Soares infant brain 1NIB H gb:PN2.1_A01_G12.r mynorm Homo sapiens c	0.24
	429446	AI547111		gb:QV0-HT0367-310100-102-c11 HT0367 Homo	0.25
15	455391	BE156230	Hs.97848	ESTs	0.25
13	422818 435338	AA404290 AA678071	Hs.194300	ESTs. Weakly similar to 138022 hypotheti	0.25
	414203	BE262170	Hs.78629	ATPase, Na+/K+ transporting, beta 1 poly	0.25
	403941	NA		NA	0.25 0.25
	414383	BE279406		gb:601157981F1 NIH_MGC_21 Homo sapiens c cannabinoid receptor 2 (macrophage)	0.25
20	412008	NM_001841	Hs.73037	Homo sapiens cDNA FLJ11780 fis, clone HE	0.25
	424985	A1907236 AW970060	Hs.279935	gb:EST382140 MAGE resequences, MAGK Homo	0.25
	450736 431185	H02767	Hs.28944	ESTs	0.25
	455308	AW893949	, m. 200	ab:RC4-NN0027-060400-011-a09 NN0027 Homo	0.25
25	435464	BE548300	Hs.192999	ESTs, Moderately similar to KIAA0961 pro	0.25 0.25
	418525	AW450369	Hs.86937	ESTs	0.25
	402790		11- 02/20	NA ESTs	0.25
	411869	W20027	Hs.23439 Hs.248032	FLT4	0.25
30	400332 424884	S66407 AW299437	Hs.225717	ESTs	0.25
30	414376	BE393856	Hs.66915	ESTs. Weakly similar to 16.7Kd protein [	0.25
	439780	AL109688		ob Homo saciens mRNA full length insert	0.25 0.25
	408947	AL080093	Hs.49117	Homo sapiens mRNA; cDNA DKFZp564N1662 (f	0.25
~-	404900	NA		NA FOTo	0.25
35	441918	A1733373	Hs.128119 Hs.303953	ESTs ESTs	0.25
	441639	A1133287 A1907536	Hs.103869	FSTs	0.25
	459396 452755	AW138937	Hs.213436	FSTs. Weakly similar to A34087 hypotheti	0.25
	422183	AA431698	Hs.112794	Human DNA sequence from clone 1068E13 on	0.25
40	415186	AA160945	Hs.14479	Homo sapiens cDNA FLJ14199 fis, clone NT	0.26 0.26
	429450	AA824451	Hs.94292	hypothetical protein FLJ23311	0.26
	455615	BE045344	Hs.274923	ESTs, Moderately similar to unnamed prot gb:IL3-ST0143-290999-019-D05 ST0143 Homo	0.26
	454633	AW811380	Hs.132967	Human EST clone 122887 mariner transposo	0.26
45	424853	BE549737 BE141491	FIS. 132301	gb:MR0-HT0080-011099-002-h06 HT0080 Homo	0.26
43	455802 414003	AA134472		gb:zo13c01.s1 Stratagene colon (937204)	0.26
	436363	AA843926	Hs.124434	ESTs	0.26
	456074	BE409525	Hs.902	neurofibromin 2 (bilateral acoustic neur	0.26 0.26
	430569	AF241254	Hs.178098	angiotensin I converting enzyme (peptidy ESTs, Weakly similar to ALU1_HUMAN ALU S	0.26
50	445635	AJ769774	Hs.209831	NA	0.26
	405953	NA F00055	Hs.172004	tión	0.26
	411021 428443		Hs. 184326	CDC10 (cell division cycle 10, S. cerevi	0.26
	434345			on Homo sapiens cell-line E8CASS clone E	0.26 0.26
55	455743			gb:RC0-BT0561-210100-032-d07 BT0561 Homo	0.26
	451138		Hs.40268	ESTs hypothetical protein FLJ23468	0.26
	449528		Hs.38178 Hs.178803	ESTs	0.26
	441040 458830			Homo saniens cDNA: FLJ23435 fis, clone H	0.26
60	428861			ESTs, Weakly similar to ALU8_HUMAN ALU S	0.26
•	435469			ESTs	0.27 0.27
	427562		Hs.26534	ESTs potassium inwardly-rectifying channel, s	0.27
	434779			KIAA0565 gene product	0.27
65	423520		ns.300330	NA	0.27
05	406589 450059		Hs.279626	ESTs	0.27
	41729		Hs.81884	suttotransferase family, cytosolic, 2A,	0.27
	45400			ESTs	0.27 0.27
	42606		Hs.75874	pregnancy-associated plasma protein A	0.27
70	44166		Hs.151285	ESTs NA	0.27
	40503 44682		7 Hs.254986	ESTs	0.27
	44682 44848			FSTs	0.27
	44756			ESTs, Weakly similar to 138931 Wiskoti-A	0.27
75	40854	0 L13220	Hs.639	calbindin 3, (vitamin D-dependent calciu	0.27 0.27
. •	40760	1 AC00230		sodium channel, nonvoltage-gated 1, beta	0.27
	43250		2 Hs.25682	Homo sapiens mRNA for KIAA1863 protein, NA	0.27
	40135		Hs.144651	ESTs	0.27
80	41756 44354			ESTs	0.27
30	4371			ESTs	0.27
	4321	19 T80289	Hs.302041	Homo sapiens clone 24762 mRNA sequence	0.27 0.28
	4190		Hs.89575	CD79B antigen (immunoglobulin-associated	U.20

	493049	4.4770404	11 00.00	FOT.	
	427812	AA770424	Hs.98162	ESTs	0.28
	423557 445311	AB011176	Hs.129801	KIAA0604 gene product	0.28
	402758	AW027556 NA	Hs.156286	ESTs	0.28
5	448240	AJ478345	U- 101024	NA SST-	0.28
,	401333	NA NA	Hs.191034	ESTs NA	0.28
	444107	T46839	Hs.10319	UDP glycosyttransferase 2 family, polype	0.28 0.28
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	442896	R37725	Hs.261108	gb:PM1-BT0533-291299-002-b05 BT0533 Homo ESTs	0.28
10	447949	AI446820	Hs.165839	EST	0.28
	435625	H50654	Hs.113999	EST8	0.28
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	0.28
	438380	T06430	Hs.6194	chondroitin suffate proteoglycan BEHAB/b	0.28
	442967	AI025460	Hs.220977	ESTs	0.28
15	448062	AW295923	Hs.255472	KIAA1843 protein	0.28
	425860	L29339	Hs.1964	solute carrier family 5 (sodium/glucose	0.28
	451839	AJ820516	Hs.16857	ESTs .	0.28
	446000	AV656052	Hs. 1504	hemopexin	0.28
	443506	H10661	Hs.192124	ESTs, Weakly similar to 138022 hypotheti	0.28
20	418345	AJ001696	Hs.241407	serine (or cysteine) proteinase inhibito	0.28
	445481	AW661846	Hs.148836	ESTs	0.28
	409337	H71289	Hs.220535	ESTs	0.28
	411414	AW897236		gb:CMO-NN0057-150400-335-c06 NN0057 Homo	0.28
	427642	R40761	Hs.9834	ESTs .	0.28
25	456392	W28766		gb:51d3 Human retina cDNA randomly prime	0.28
	409920	BE169746	Hs.12504	likely ortholog of mouse Arkadia	0.28
	410285	AA083609		gb:zm63d05,r1 Stratagene fibroblast (937	0.28
	442496	R55073	Hs.124130	ESTs	0.28
20	423770	AW976766	Hs.132776	Homo sapiens cDNA FLJ10077 fis, clone HE	0.28
30	423467	AK000214	Hs.129014	hypothetical protein FLJ20207	0.29
	458716	N99013	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	0.29
	423235	AW410698	Hs.169917	neurabin II	0.29
	431087	H12723	Hs.290791	ESTs	0.29
35	459106	AW589793	Hs.224713	ESTs	0.29
33	414870	N72264	Hs.300670	KIAA1204 protein	0.29
	402243	000004	11- 000490	NA	0.29
	432628	R02394	Hs.269436	ESTs, Moderately similar to PC4259 ferri	0.29
	404364	NA		NA NA	0.29
40	400480	1146000	L 77757	NA	0.29
70	456083	U46922	Hs.77252	fragile histidine triad gene	0.29
	446598	AW250546	Lt. 112207	gb:2821774.5prime NIH_MGC_7 Homo sapiens	0.29
	422201 443919	NM_001505 Al091284	Hs.113207 Hs.135224	G protein-coupled receptor 30	0.29
	453948	AI091204 AI970797	Hs.135224 Hs.64859	ESTs, Weakly similar to A47582 8-cell gr ESTs	0.29
45	403792	NA	HS.04009	NA	0.29 0.29
73	418957	AI792615	Hs.188712	ESTs	0.29
	457960	AA771881	Hs.298149	ESTs	0.29
	404269	AA771001	15.230143	NA	0.29
	439309	AF090097	Hs.6524	Homo sapiens clone IMAGE 25997	0.29
50	458239	BE439877	Hs.283389	ESTs	0.30
٠,	414941	C14865	Hs.332341	ESTs	0.30
	404954	•••••	12.002077	NA .	0.30
	441609	AA946764	Hs.133460	ESTs	0.30
	426895	AA416880	Hs.225738	ESTs	0.30
55	403182	NA		NA .	0.30
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<b>~</b>	459312	AF 107457	Hs.37035	homeo box HB9	0.30
60	431853	AA521034	Hs.70834	EST ₈	0.30
	449768	AI972746	Hs.102945	ESTs, Weakly similar to 178885 serine/th	0.30
	443609	AV650231	Hs.282941	ESTs, Highty similar to A Chain A, Human	0.30
	454293	H49739	Hs.134013	ESTs, Moderately similar to HK61_HUMAN H	0.30
65	447569	Al393202	Hs.147554	hypothetical protein FLJ23392	0.30
65	400128	NA		NA	0.30
	423208	AA323191	Hs.137064	cytoplasmic polyadenylation element bind	0.30
	434227	AF119893	Hs.63382	hypothetical protein PRO2714	0.30
	424208	AW583123	Hs.143113	pancreatic lipase-related protein 2	0.30
70	401165	NA D10010		NA	0.30
, 0	415394	R19249	Hs.22654	sodium channel, voltage-gated, type I, a	0.30
	443110	AW352243	Hs.132665	ESTs EST-	0.30
	426724	AA383523 H42314	Hs.293616	ESTs  obvio00002 at Sagree adult busin N2b5HB5	0.30
	416035	AA234847		gb:yo09e02.s1 Soares adult brain N2b5HB5	0.30 0.31
75	409753 459221	BE246522	Hs.306121	gb:zs37b10.r1 Soares_NhHMPu_S1 Homo sapi	0.31
	408895	AA058730	Hs.191464	leukocyte receptor cluster (LRC) encoded ESTs	0.31
	405110	NA NA	16,151404	NA NA	0.31
	432430	AW079984	Hs.262480	ESTs, Weakly similar to PIHUB6 salivary	0.31
	426442	AA378656	Hs.106510	ESTs, Moderately similar to ALU2_HUMAN A	0.31
80	411765	H43346	100010	gb:yp09a04.r1 Soares breast 3NbH8st Homo	0.31
	431854	AA383550	Hs.271699	polymerase (DNA directed) iota	0.31
	457553	AI861895	Hs.304505	ESTs	0.31
	412301	AW936328		gb:QV4-DT0021-281299-070-07 DT0021 Homo	0.31

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ESTs, Weakly similar to T COMPLEX TESTIS
gb:EST31752 Embryo, 12 week I Homo sapie
                                                                                                            0.32
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                                                                                                               0.33
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                                                           ESTs
                        AW173270
              451636
                                                                                                               0.33
                                        Hs.19155
                                                           ESTs
              424226
                         N94153
   60
              TARLE 478
                                 Unique Eas probeset identifier number
              Pkey:
                                  Gene cluster number
              CAT number.
                                 Genbank accession numbers
              Accession:
   65
                         CAT Number
              Pkey
408316
                                        AW807771 AW179260 AW807851 AW179240 AW845961 AW807693 BE141176 AW807594 AW807772 AW846003 AW845963 AW179239
                          1051210_1
                                         AA071244 AA071477
               409382
                         112508_1
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                          1149033 1
               409699
                                        AA234847 AA077472
AW501137 AW501295 AW501212
    70
                          115305_1
               409753
                          1155571_1
               409828
                                         AA083609 AA083790 AA112048
               410285
                          119128_1
1245024_1
                                         AW897236 AW845406
               411414
                                         H43346 AA248302 AA095182
                          125700_1
               411765
                                         AW936328 AW936539
    75
               412301
                          1288123_1
                                         AW997986
               412793
                          1327636_-1
                                         BE090689 BE090685 BE090697 BE090680 BE090691 BE090696 BE090698 BE090686
                          1365954_1
               413382
                                         AA134472 R76288 AW750262
BE279406 BE280100
                          140888_1
               414003
               414383
                           1440279_1
                                         H22769 R35182 Z43545 F05783 N92089 H71928
    80
               415327
                          1534137 1
                                         H42314 H43080 H45217 H15384
               416035
                          1567254_1
                           1573980_1
                                         Z41922 H23072 T77322
               416156
                                         T11958 T11756 T11816 T20135 T19729 R45874
               418162
                           1725383_1
```

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W28781 W26588 W26377
          419372
                      1842942_1
                      220507_1
                                     AL138411 AL138412 AA315860
           422731
                                     AA328144 AW962385 N30457
D61524 AA347654 AW961758
           423593
                      229955_1
           424844
                      244291 1
  5
           429446
                       304683_1
                                     AI547111 AW973749 AA558007
           430350
                       316401_1
                                     BE169639 AA476976
                                     AF127772 AF062358 AF060217 AA652270 F23288
AW974668 AA661959 AA649572 AA640401 AA640402
W91884 W95119 AA676941
           434345
                       38411_1
           434597
                      389383_1
403478_1
           435253
10
                                     AI872932 AA682306 BE220163 W88695 T81307 H91447
           435447
                       405400_1
           437333
                       436167_1
                                      AA748898 AW997701 AW997703
           439657
                       47499_1
                                     W93589 W93487 AF086493
AL109688 R23665 R26578
                      47673_1
68463_1
           4397R0
                                     AW250546 BE257108 BE251006 BE255957 BE250926 BE513012 AV659318
           446598
15
                       732252_1
                                      AJ419235 AW055016 BE007490 BE550241
           447677
           448643
                       773566_-1
                                      AI557531
                                      AW970060 AI732366 AI792313 AW839644
                      B44652 1
           450736
                                     AW296422 H72616 H63825
                       1091035 1
           454282
           454633
                       1227504_1
                                      AW811380 AW811385
20
                                      BE072139 BE157977 BE157974 AW857974 AW817778
           454738
                       1232449_1
                                     AW820852 AW820773 AW821088
BE145826 BE145815 BE145822 AW854707 BE145912
           454790
                       1234752_1
                       1252281_1
1278147_1
           455071
                                      AW893949 AW893960 AW893966
           455308
           455350
                       1283853_1
                                      AW901809 AW901787 AW901795 AW901792 AW901744 AW901753 AW901807 AW901798
25
                       1288067_1
1351258_1
1354978_1
                                      BE156230 BE156239 AW936260
           455391
                                      BE068121 BE068090 BE068153 BE068128 BE068197 BE068136 BE068140 BE068185 BE068105
           455699
                                      BE073754 BE073753 BE073755 BE073756 BE073752 BE073795 BE073796 BE073704 BE073791 BE073733 BE073695
           455743
           455802
                       1370828_1
                                      BE141491 BE141016 BE141479
           455826
                       1373392_1
1391117_1
                                     BE144228 BE144291
BE168828 BE168830 BE168823 BE168928 BE168820 BE168826
30
           455968
                                      T41368 T41369 T41294
           456328
                       1789791_1
                       1843059_1
                                      W28766 W26500
           456392
                                      AW752597 AW848781 AW849062 AW848490 AW752699 AW752604 AW752700
AI939966 AI939988 AI939951 AI939981 AI939976 AI939959
           458147
                       488021_1
                       944881_1
           459233
35
           TABLE 47C:
                                Unique number corresponding to an Eos probeset
           Pkey:
                                Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
           Ref:
40
                                Indicates DNA strand from which exons were predicted.
            Strand:
                                Indicates nucleotide positions of predicted exons.
            Nt_position:
                                                    Nt_position
110553-111119
            Pkey
                       Rof
                                      Strand
                       8439796
            400480
                                       Minus
45
                                                    72260-72369
            401015
                       B117441
                                      Ptus
                       8117611
                                                    151364-151606
            401042
                                       Plus
                       8705350
9438376
                                       Minus
                                                    85679-85795
            401132
                                                    168244-168423
                                       Minus
            401165
            401333
                       9884881
                                       Plus
                                                     13852-14861
 50
            401350
                        9931226
                                       Plus
                                                     14471-14623
            401623
                        8575907
                                       Plus
                                                     163249-163623
            401683
                        7689961
                                       Phr
                                                    2934-3446
                                                    8038-8319
                        7689961
            401685
                                       Minus
                                                     48791-49043,50038-50205,51530-51672,54448-54565,55933-56073
            402015
                        7417802
                                       Minus
 55
            402243
                        7690137
                                       Minus
                                                     196521-196721
                                                     116589-117549
            402319
                        7582559
                                       Plus
                                                     69466-69678,71139-71284,71572-71865
                        7210067
            402750
                                       Plus
                                                     87638-87924
            402758
                        9213869
                                       Plus
                                                    136829-136952,137336-137521
147744-147861
            402760
                        9213869
 60
                                       Minus
                       4835258
9838273
            402790
                                                     102163-102345, 102545-102725
            403182
                                       Phrs
                                                     76723-77027,79317-79484
            403214
                        7630945
                                       Minus
            403652
                        8705848
                                                     49991-50129
                                       Minus
            403670
                        7259739
                                       Minus
                                                     88377-88537
 65
                                                     102965-103174
             403697
                        3962501
                                       Minus
                        7230192
                                                     149707-149873
                                       Minus
            403792
                        7708844
                                                     317240-317391,317913-318032
             403847
                                       Ptus
                                                    114876-115342
55512-55781
             403941
                        7454203
             404097
                        7770701
                                       Plus
 70
             404145
                        9863643
                                                     30607-31266
                                       Plus
             404187
                         4481839
                                                     7644-7991
                                        Plus
                                                     70261-70404,72944-73063
             404269
                        9711443
                                                     32986-33202
             404364
404401
                        9964977
7259738
                                        Minus
                                                     71066-71326
                                       Plus
 75
                                                     14770-14931
             404753
                         7637341
                                        Ptus
                                                     23955-24034,25143-25264
22032-22219
             404848
                         8248647
                                        Minus
             404900
                         7331453
                                        Plus
                                                     131720-132042
                         7387327
             404954
                                        Phrs
             405037
                         7543748
                                                     127374-127578
                                        Minus
  80
                         8096888
                                                     118940-119100
             405110
                                        Minus
                                       Minus
                                                     71743-72291
             405650
                         4926905
                                                     14130-14270
                         4508140
             405669
                                        Plus
                         7960374
                                                     65101-65574
             405953
                                        Minus
```

```
406242
                     7417725
                                    Minus
                                                 36736-36951
                                    Ptus
                                                 9562-9867
          406291
                      5686274
                                                 17646-17953
          406293
                      5686274
                                    Minus
                      9213235
                                                 64689-64798
                                    Pfus
          406333
  5
                                    Minus
                                                 35162-35292
                      7711569
          406560
                                                 38806-38989
           406589
                      8224211
                                                 132738-132985,134266-134425,135034-135192,135471-135608,137345-137478,138768-138912
          406597
                      8248613
                                    Minus
          TABLE 48A: ABOUT 426 GENES UPREGULATED IN MELANOMA RELATIVE TO NORMAL BODY TISSUES
10
          Table 48A lists about 426 genes upregulated in melanoma relative to normal body tissues. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip
          array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA
           expression.
           Pkey:
                              Unique Eos probeset identifier number
                              Exemplar Accession number, Genbank accession number
15
           ExAcon:
           UnigenelD:
                              Unigene number
                              Unigene gene title
           Unigene Title:
                              Mean of melanoma Als divided by the mean of normal tissue Als, where the minimum value for the numerator and denominator was set to 1.0
20
                                     UnigenelO
                                                  Unigene Title
           Pkey
                      FxAccn
                                                  tyrosinase (oculocutaneous albinism IA)
Homo sapiens, clone MGC:5564, mRNA, comp
                                                                                                      376.61
                       NM 000372
                                     Hs.2053
           426555
                       H05769
                                     Hs.188757
           428655
                                                  dopachrome tautomerase (dopachrome delta
                                                                                                      231.30
                       NM 001922
                                     Hs 301865
           430377
                                     Hs.44571
                                                                                                      180 67
                                                  ESTs
                       BE349075
           453344
                                                                                                      107.36
25
                       AW139342
                                     Hs.155530
                                                  interferon, gamma-inducible protein 16
           425289
                                                                                                      97.76
           417166
                       AA431323
                                     Hs.42146
                                                  ESTs
                                                                                                      96.76
                                                  ESTs, Weakly similar to 138022 hypotheti
                                     Hs.165909
           425234
                       AW152225
                                                                                                      94.52
                                                  pyruvate dehydrogenase phosphatase
                       AF155661
                                     Hs.22265
           434826
                                                   minichromosome maintenance deficient (S.
                                                                                                      90.88
           427528
                       AU077143
                                      Hs.179565
                                                   aryl-hydrocarbon receptor nuclear transl
                                                                                                      87.91
30
            438209
                       AL120659
                                     Hs.6111
                                                                                                      85 55
                                     Hs.163724
                                                  ESTs
            443983
                       H04482
                                                  Homo sapiens clone 23785 mRNA sequence
                                                                                                      85.03
                       BE220806
                                     Hs.184697
            428513
                                                                                                      84.27
                                      Hs.40096
                                                   cadherin 19, type 2
                       AL137939
            419956
                                                                                                       80.88
                       AF047826
                                      Hs.129887
                                                   cadherin 19, type 2
            423605
                                                   Homo sapiens cDNA: FLJ22105 fis, clone H
                                                                                                       80.64
 35
            430540
                       AW245422
                                                   granzyme B (granzyme 2, cytotoxic T-lymp
                                                                                                       79.09
                       NM 004131
                                      Hs.1051
            416975
                                                                                                       71.52
                                                   sorting nextin 10
                                      Hs.106260
                       AF121860
            421633
                                                                                                       69.88
            442064
                       A1422867
                                      Hs.88594
                                                   FSTs
                                                                                                       67.94
                                      Hs 86693
                                                   FSTs
            418310
                       AA814100
                                                                                                       67,64
 40
                                      Hs.132906
                                                   19A24 protein
                       AW026300
            423799
                                                                                                       63.24
                                      Hs.279704
                                                   chromatin accessibility complex 1
ESTs, Weakly similar to AF208855 1 BM-01
            432886
                       BE159028
                                                                                                       63.18
                       AA502764
                                      Hs 123469
             456508
                                                   serum/glucocorticoid regulated kinase-li
                                                                                                       62 33
                                      Hs.279696
            432882
                       NM 013257
                                                    gb:CM0-CT0042-090899-018-f01 CT0042 Homo
                                                                                                       61.62
                       AW062425
             454088
                                                                                                       60.52
  45
                                      Hs.169395
                                                   hypothetical protein FLJ12015
             430838
                       N46664
                                                   replication factor C (activator 1) 3 (38 KIAA0606 protein; SCN Circadian Oscillat
             422363
                        T55979
                                      Hs.115474
                                                                                                       59.33
             407748
                       AL079409
                                      Hs.38176
                                      Hs.1390
                                                    proteasome (prosome, macropain) subunit,
                                                                                                       59.00
                        BE395161
             450800
                                                                                                        58.27
                                      Hs.7753
             441224
                        AU076964
  50
                                                    KIAA1435 protein
                        AW963897
                                      Hs.44743
             408418
                                                    ESTs, Moderately similar to Transforming
                                                                                                        56.45
                                       Hs 219907
             428001
                        H97428
                                                    membrane-spanning 4-domains, subfamily A
                                                                                                        56 29
                        BE247706
                                      Hs.89751
             456373
                                                                                                        56.15
                                                    butyrylcholinesterase
                        NM 000055
                                       Hs.1327
             420674
                                                    phosphoprotein associated with GEMs
                                      Hs.266175
Hs.98806
                        AA045281
             407856
                                                                                                        55.39
  55
                                                    hypothetical protein
                        AK000492
             420552
                                                                                                        54.97
                        AA456539
                                       Hs.8262
                                                    lysosomal-associated membrane protein 2
             442355
                                                                                                        52.85
             429747
                        M87507
                                       Hs.2490
                                                    caspase 1, apoptosis-related cysteine pr
DKFZP434C245 protein
                                                                                                        52.00
             410174
                        AA306007
                                       Hs.59461
                                                    hypothetical protein DKFZp7620076
                                                                                                        51.97
                                       Hs.21621
             437396
                        BE140396
                                                                                                        51.64
  60
                                       Hs.3686
                        BE182896
             409557
                                                                                                        51.42
                                                    paired box gene 5 (B-cell lineage specif
                                       Hs.22030
             420301
                         AA767526
                                                                                                         50.58
                        AW969551
AA883929
                                                    nbosomal protein L27a
             414403
                                       Hs.76064
                                                                                                         50.21
                                                    ESTs
              452958
                                       Hs.40527
                                                                                                         49.97
                         AW937420
              458997
                                                    DNA segment on chromosome X (unique) 992
KIAA0456 protein
                                                                                                         49.85
   65
                         AI796870
                                       Hs 54277
              458079
                                                                                                         48.76
                                       Hs 5003
              435905
                         AW997484
                                                                                                         48 33
                                       Hs.153203
                                                    MyoD family inhibitor
                         AI 035588
              424800
                                       Hs.172665
                                                     methylenetetrahydrofolate dehydrogenase
                                                                                                         47.91
                         AW067805
              426827
                                                     ESTs, Weakly similar to ALUC_HUMAN !!!!
                                                                                                         47.45
                         AA055449
                                       Hs.63187
              408548
                                                     p53 inducible ribonucleotide reductase s
                                                                                                         46.52
   70
                         AB036063
AA489023
              420000
                                       Hs.94262
                                       Hs.99807
                                                     ESTs, Weakly similar to unnamed protein
                                                                                                         45.79
              4194R5
                                                                                                         45.52
                         AA318315
                                        Hs.25999
                                                     hypothetical protein FLJ22195
              451134
                                                                                                         45.45
                                                     signal recognition particle 72kD interleukin 16 (lymphocyte chemoattracta
              430066
                         AI929659
                                        Hs.237825
                                                                                                         44.58
              417427
                         M90391
                                        Hs.82127
                                                     hypothetical protein P15-2
                                                                                                         43.36
   75
                         AF212223
                                        Hs.25010
              450447
                                                                                                         43.03
                                                     histone deacetylase 3
              446019
                         AI362520
                                                                                                         42.45
                         AW768399
                                                     ESTs
              430015
                                                                                                         42.36
                                                     Homo sapiens cDNA FLJ14934 fis, clone PL
                                        Hs.108646
              446880
                          AJ811807
                                                                                                         42 30
                                        Hs.53563
                                                     collagen, type IX, alpha 3
                         141162
              409327
                                                                                                         41.42
   80
                                        Hs.156114
                                                      protein tyrosine phosphatase, non-recept
                          AI092634
              425390
                                                                                                         41.21
                                                     FSTs
              411088
                          BE247593
                                        Hs.145053
                                                     Homo sapiens, clone IMAGE:3606519, mRNA,
                                                                                                          40 94
              408527
                          AL135018
                                        Hs.33074
```

40.66

Hs 190537

AI623207

441590

	457465	AW301344	Hs.122908	DNA replication factor	39.91
	430280	AA361258	Hs.237868	interleukin 7 receptor	38.91 39.70
	410700 421282	AA352335 AA286914	Hs.65641 Hs.40782	hypothetical protein FLJ20073 ESTs	38.70 38.55
5	448275	BE514434	Hs.20830	kinesin-like 2	38.00
-	453912	AL121031		SW/SNF related, matrix associated, acti	37.94
	414844	AA296874	Hs.77494	deoxyguanosine kinase	37.88 37.70
	421305 439352	BE397354 BE614347	Hs.324830 Hs.169615	diptheria toxin resistance protein requi hypothetical protein FLJ20989	37.64
10	409078	AW327515	10.105010	ESTs	37.30
	449845	AW971183	Hs.6019	OnaJ (Hsp40) homolog, subfamily C, membe	37.27
	444184 445819	T87841 AJ767472	Hs.282990 Hs.146290	Human DNA sequence from clone RP1-28H20 ESTs, Wealdy similar to putative p150 (H	37.21 37.21
	451418	BE387790	Hs.26369	hypothetical protein FLJ 20287	37.00
15	433226	AW503733	Hs.9414	KIAA1488 protein	36.88
	445784	AI253155	Hs.146065	ESTs	35.36 33.09
	454117 407756	BE410100 AA116021	Hs.40368 Hs.38260	adaptor-related protein complex 1, sigma ubiquitin specific protease 18	32.05
	447937	AL109716	Hs.20034	Homo sapiens mRNA full length insert cON	31.00
20	438549	BE386801	Hs.21858	trinucteotide repeat containing 3	30.76
	429083 444670	Y09397 H58373	Hs.227817 Hs.332938	BCL2-related protein A1 hypothetical protein MGC5370	30.73 28.45
	446839	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	27.62
0.5	433576	BE080715	Hs.161091	ESTs	27.42
25	422173	BE385828	Hs.250619	phorbolin-like protein MDS019 (CEM15)	27.36 26.66
	408962 442757	BE386436 A1739528	Hs.44317 Hs.28345	SRY (sex determining region Y)-box 10 ESTs	25.94
	414646	AA353776	Hs.901	CO48 antigen (B-cell membrane protein)	25.39
20	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	24.55
30	438461 427581	AW075485 NM 014788	Hs.286049 Hs.179703	phosphoserine arrinotransferase KIAA0129 gene product	22.48 22.15
	435256	AF193766	Hs.13872	cytokine-like protein C17	20.61
	409988	N27687	Hs.334334	transcription factor AP-2 alpha (activat	19.79
35	444863	AW384082	Hs.104879	serine (or cysteine) proteinase inhibito	19.73 19.27
33	417404 458098	NM 007350 BE550224	Hs.82101	pteckstrin homology-like domain, family metallothionein 1E (functional)	18.09
	417018	M16038	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related	16.95
	446054	AB014537	Hs.13604	KIAA0637 gene product	15.67
40	432606 414696	NM 002104 AF002020	Hs.3066 Hs.76918	granzyme K (serine protease, granzyme 3; Niemann-Pick disease, type C1	15.54 15.06
70	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	14.89
	414821	M63835	Hs.77424	Fc tragment of IgG, high affinity la, re	14.84
	422486	BE514492	Hs.117487	gene near HD on 4p16.3 with homology to minichromosome maintenance deficient (S.	14.61 14.12
45	424308 421334	AW975531 BE297729	Hs.154443	gb:601175625F1 NIH_MGC_17 Homo sapiens c	13.94
••	422423	AF283777	Hs.116481	CD72 antigen	13.77
	408996	AI979168	Hs.344096	glycoprotein (transmembrane) nmb	13.33 12.76
	416406 427536	D86961 BE277141	Hs.79299 Hs.115803	lipoma HMGIC fusion partner-like 2 gb:601178666F1 NIH_MGC_20 Homo sapiens c	12.76
50	423198	M81933	Hs.1634	cell division cycle 25A	12.66
	430770	AA765694	Hs.123296	ESTs	12.58
	407833 430822	AW955632 AJ005371	Hs.66666 Hs.248017	ESTs, Weakly similar to \$19560 proline-r glyceraldehyde-3-phosphate dehydrogenase	12.09 11.46
	424259	AK001776	Hs.143954	hypothetical protein FLJ10914	10.58
55	446950	AA305800	Hs.5672	hypothetical protein AF140225	10.04
	420956	AA351584	Hs.100543	Homo sapiens clone 24505 mRNA sequence	9.98 9.88
	448356 428799	AL120837 AJ478619	Hs.20993 Hs.104677	high-glucose-regulated protein 8 ESTs	9.56
<b>C</b> 0	437271	AL137445	Hs.28846	Homo sapiens mRNA; cDNA DKFZp566O134 (fr	9.03
60	447769	AW873704	Hs.320831	Homo sapiens cDNA FLJ14597 fis, clone NT ESTs	9.01 8.99
	408393 407966	AW015318 AA295052	Hs.23165 Hs.38516	Homo sapiens, clone MGC:15887, mRNA, com	8.99
	450534	AI570189	Hs.25132	KIAA0470 gene product	8.91
65	410101	A1338045	Hs.203559	hypothetical protein FLJ12701	8.90 8.86
65	417129 453507	AI381800 AF083217	Hs.300684 Hs.33085	calcitonin gene-related peptide-receptor WD repeat domain 3	8.68
	442739	NM 007274	Hs.8679	cytosolic acyl coenzyme A thioester hydr	8.46
	456249	AI206144	Hs.82508	HRIHFB2206 protein	8.38
70	437786 448410	BE142681 AK000227	Hs.155573 Hs.21126	polymerase (DNA directed), eta hypothetical protein FLJ20220	8.35 8.20
70	442711	AF151073	Hs.8645	hypothetical protein	8.14
	408405	AK001332	Hs.44672	hypothetical protein FLJ10470	7.96
	420208	BE276055	Hs.95972	silver (mouse homolog) like hypothetical protein FLJ 11006	7.88 7.79
75	415929 449217	AA724373 AA278536	Hs.49344 Hs.23262	ribonuclease, RNase A family, k6	7.66
. •	451239	H24302	Hs.23127	ESTs	7.50
	442426	AI373062	Hs.332938	hypothetical protein MGC5370	7.40 7.39
	447233 439574	AW246333 AI469788	Hs.17901	Homo sapiens, ctone IMAGE:3937015, mRNA, ESTs	7.13
80	431360	NM 000427	Hs.251680	loricrin	7.12
	412438	A1087928	Hs.110741		6.96 6.87
	452882 436581	AW972990 AA725726	Hs.196270 Hs.180213		6.64
	-00001				

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	404247	A A E 0.2602		b:ng23d01.s1 NCI_CGAP_Ov2 Homo sapiens	6.63
		AA502682 BE221477	Hs.132137	STs, Moderately similar to A47582 B-cel	6.58
	412490	AW803564	Hs.288850 I	lomo sapiens cDNA: FLJ22528 fis, clone H	6.53 6.52
_		AK001178		nomolog of rat orphan transporter v7-3 hypothetical protein similar to swine ac	6.50
5		R78669 AW964440		DC32	6.48
		BE242274	He 1741	integrin, beta 7	6.44
	407876	NM 004519		potassium voltage-gated channel, KQT-lik	6.44 6.39
10	409512	AW979187		melanoma differentiation associated prot ESTs	6.32
10	427951 448664	AI826125 AI879317		splicing factor 3a, subunit 1, 120kD	6.03
	416640	BE262478		neumn-specific protein	6.01
	446830	BE179030		Human DNA sequence from clone RP5-1174N9	5.98 5.93
1.5	452629	W02772	Hs.180178	Homo sapiens, clone IMAGE:3947276, mRNA, Homo sapiens cDNA: FLJ23111 fis, clone L	5.73
15	427390 427853	AI432163 AI569798	Hs.268231 Hs.98260	ESTs	5.55
	434398	AA121098	Hs.3838	serum-inducible kinase (SNK)	5.54
	450256	AA286887	Hs.24724	MFH-amplified sequences with leucine-ric	5.54 5.53
20	428524	AA429772	U- 270124	ESTs hypothetical protein FLJ20280	5.50
20	431797 418403	BE169641 D86978	Hs.270134 Hs.84790	KIAA0225 protein	5.50
	411524	AW850303	11010 11 00	ab:IL3-CT0219-191199-030-F09 CT0219 Homo	5.47
	426158	NM 001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	5.40 5.38
25	443086	AW977125	Hs.6127	sine oculis homeobox (Drosophila) homolo Homo sapiens cDNA: FLJ23020 fis, clone L	5.38
25	447735 406843	AA775268 AW196933	Hs.119598	ribosomal protein L3	5.36
	430594	AK000790	Hs.246885	hypothetical protein FLJ20783	5.35
	447674	BE270640	Hs.19192	cyclin-dependent kinase 2	5.23 5.23
20	410491	AA465131	Hs.64001	Homo sapiens clone 25218 mRNA sequence Homo sapiens, clone MGC:17339, mRNA, com	5.09
30	420338 409264	AA825595 NM 014937	Hs.88269 Hs.52463	KIAA0966 protein	5.03
	414734	AA151712	Hs.82572	ESTs	5.01
	426759	AI590401	Hs.21213	ESTs .	4.99 4.98
25	426793	X89887	Hs.172350	HIR (histone cell cycle regulation defec	4.97
35	428612	AA770001 W03011	Hs.306881	ESTs MSTP043 protein	4.92
	413550 447349	AI375546	115.000001	gb:tc23d04.x1 Soares_total_fetus_Nb2HF8_	4.86
	403328			Target Exog	4.85 4.83
40	452840	At097393	Hs.43481	hypothetical protein DKFZp564K192	4.82
40	439310	AF086120 A1768965	Hs.102793 Hs.292708	ESTs ESTs	4.82
	451281 431183	NM 006855	Hs.250696	KDFI (I vs-Asn-Glu-Leu) endoplasmic retic	4.81
	427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	4.74 4.67
	435963	AF271212	Hs.322901		4.66
45	418699	BE539639	Hs.173030	Homo sapiens, clone IMAGE:3873720, mRNA	4.66
	414770 419628	BE257224 H67546	Hs.49768	ESTs	4.64
	420258	AA477514	Hs.96247	translin-associated factor X	4.63
	446341	AL040763	Hs.310735		4.58 4.57
50	420267	N37030	Hs.173337 Hs.73792	ESTs complement component (3d/Epstein Barr vi	4.55
	412228 432888	AW503785 T86823	NS.13132	gb:yd81a08.s1 Soares fetal liver spleen	4.55
	453258	AW293134	Hs.32597	ring finger protein (C3H2C3 type) 6	4.53 4.50
	418340	NM 013286		chromosome 3p21.1 gene sequence small inducible cytokine subfamily A (Cy	4.44
55	409038		Hs.50002 Hs.29256	s Invoothetical protein FLJ14697	4.42
	447484 452036			sema domain, seven thrombospondin repeat	4.41
	406903		-	gb:Human glyceraldehyde-3-phosphate dehy	4.40 4.34
<b>C</b> 0	405451		11- 00055	dihydropyrimidinase-like 3 8 hypothetical protein PRO1855	4.33
60	434203 450088			n ESTs	4.31
	421535			R phosphoribosylformylglycinamidine syntha	4.31
	415912	H08859	Hs.20646	9 ESTs. Weakly similar to ALU6_HUMAN ALU S	4.30 4.29
15	451259				4.28
65	452548			KIAAD144 gene product	4.24
	432195 445101		Hs.12314	Homo sapiens mRNA; cDNA DKFZp586C1019 (	1 4.22
	425913	3 AA365799		SEC22, vesicle trafficking protein (S. c	4.19 4.18
70	42349			<ol> <li>Wiskott-Aldrich syndrome protein interac hypothetical protein FLJ12439</li> </ol>	4.16
70	44209 42495				4.05
	42771			26 ESTs	4.04
	41531	0 R16313		ob:yf93h09.r1 Soares infant brain 1NIB H	4.04 4.03
	41605		Hs.7899		3.93
75			Hs.9823 Hs.5858		3.92
	41007 42026			7 ESTs	3.92
	42618	31 AA37142	2 Hs.3343	71 hypothetical protein MGC13096	3.90 3.89
0.0	43163	9 AK00068			3.88
80			Hs.6179	calpastatin	3.87
	42215 42923			288 protein tyrosine phosphatase, receptor t	3.86
	4188			66 HT021	3.84
				-	

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	425050	BE391854	Hs.7970	gb:601285394F1 NIH_MGC_44 Homo sapiens c	3.82
	442271	AF000652	Hs.8180	syndecan binding protein (syntenin)	3.81
	410235	AA082977	11- 40000	gb:zn07h10.r1 Stratagene hNT neuron (937	3.79 3.78
5	408636 424624	BE294925 AB032947	Hs.46680 Hs.151301	CGI-12 protein Ca2+dependent activator protein for secr	3.76
,	411400	AA311919	Hs.69851	nucleolar protein family A, member 1 (HV	3.74
	458215	AA928160		gb:on86f10.s1 Soares_NFL_T_GBC_S1 Homo s	3.73
	452874	AK001061	Hs.30925	hypothetical protein FLJ10199	3.72
10	442643	U82756	11- 40030	PRP4/STKWD splicing factor	3.70 3.70
10	447471 447644	AF039843 AW861622	Hs.18676 Hs.108646	sprouty (Drosophila) homolog 2 Homo sapiens cDNA FLJ14934 fis, clone PL	3.67
	422616	BE300330	Hs.118725	selenophosphate synthetase 2	3.64
	433160	AW207002	Hs.134342	TASP for testis-specific adriamyoin sens	3.64
1.5	418180	BE618087	Hs.83724	hypothetical protein MGC5466	3.62
15	423032	AJ684746	Hs.119274	RAS p21 protein activator (GTPase activa Homo sapiens cONA FLJ12073 fis, clone HE	3.62 3.62
	425569 412156	AA359597 H29487	Hs.301701 Hs.17110	Homo sapiens mRNA; cDNA DKFZp434C2016 (f	3.61
	417426	NM 002291	Hs.82124	taminin, beta 1	3.61
	407188	AA457592		gb:aa92f11.s1 Stratagene fetal retina 93	3.61
20	426600	NM 003378	Hs.171014	VGF nerve growth factor inducible	3.61
	440760	AK001145 W15284	Hs.284216 Hs.74832	hypothetical protein FLJ10283 ESTs	3.60 3.59
	448481 414111	BE047679	Hs.152982	hypothetical protein FLJ13117	3.59
	437862	AW978107	Hs.5884	Homo sapiens mRNA; cDNA DKFZp586C0224 (f	3.59
25	409703	NM 006187	Hs.56009	2-5-oligoadenylate synthetase 3 (100 k	3.59
	406981	S71129	11- 002100	acetylcholinesterase (YT blood group)	3.59 3.58
	431586 415173	AW971100 AW501735	Hs.293189 Hs.180059	ESTs ESTs	3.57
	430512	AF182294	Hs.241578	U6 snRNA-associated Sm-tike protein LSm8	3.57
30	446126	AW085909		pleckstrin homology domain interacting p	3.57
	409305	AA070078		gb:zm60f05.r1 Stratagene fibroblast (937	3.57 3.56
	433867	AK000596	Hs.3618 Hs.143835	hippocalcin-like 1 gb:qn14d12.x1 NCI_CGAP_Lu5 Homo sapiens	3.56
	459721 441412	A1299050 A1393657	Hs.159750	ESTs	3.55
35	416114	AI695549	Hs.183868	glucuronidase, beta	3.55
	454870	AW836081		gb:PM0-LT0019-090300-002-e11 LT0019 Homo	3.54
	443105	X96753	Hs.9004	chondroitin sulfate proteoglycan 4 (mela	3.53 3.51
	444680 413949	AI186671 AA316077	Hs.22670 Hs.75639	ESTs Human TB1 gene mRNA, 3' end	3.51
40	437033	AW248364	Hs.5409	RNA polymerase I subunit	3.50
. •	412141	AI183838	Hs.48938	hypothetical protein FLJ21802	3.49
	437158	AW090198		KIAA1150 protein	3.48 3.47
	432642 440634	BE297635 AA921767	Hs.3069 Hs.132447	heat shock 70kD protein 9B (mortalin-2) ESTs	3.47
45	445652	AL117473	Hs.13036	DKFZP727A071 protein	3.46
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotactin)	3.43
	420460	AA262331	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	3.43 3.40
	426141 424321	C05886 W74048	Hs.293972 Hs.1765	ESTs lymphocyte-specific protein tyrosine kin	3.40
50	449209	BE616830	Hs.294145	ESTs	3.39
-	408304	AW810279		gb:MR4-ST0125-151299-029-a09 ST0125 Homo	3.37
	416561	D87328	Hs.79375	holocarboxylase synthetase (biotin-(prop	3.35
	422947	AA306782	Hs.122552 Hs.31803	G-2 and S-phase expressed 1 ESTs, Weakly similar to N-WASP (H.sapien	3.34 3.34
55	453005 409430	AW055308 R21945	Hs.346735		3.32
	417386	AL037228	Hs.82043	D123 gene product	3.32
	440999	AI951562	Hs.126370	ESTs, Weakly similar to CNE3_HUMAN COPIN	3.31
	407516	X64974	U- 04944	gb:H.sapiens mRNA HTPCRH02 for offactory transcriptional co-activator with PDZ-bl	3.31 3.31
60	450065 416902	AL050107 AA375634	Hs.24341 Hs.288974		3.28
00	432878	BE386490	Hs.279663		3.28
	443296	A1765286	Hs.313342		3.27
	429954	AI918130	Hs.21374	ESTs	3.25 3.25
65	428044 425317	AA093322 AW205118	Hs.301404 Hs.210546		3.25
03	418064	RE387287	Hs.83384	S100 calcium-binding protein, beta (neur	3.25
	432917	NM 014125			3.24
	447871	BE297946	Hs.239052		3.24
70	414829	AA321568 AW968934	Hs.77436	pteckstrin Homo sepiens cDNA: FLJ21897 fis, clone H	3.24 3.23
70	426996 416188	BE157260	Hs.173108 Hs.79070	v-myc avian myelocytomatosis viral oncog	3.22
	429530	AA454191	Hs.99362	Human DNA sequence from clone RP11-530N1	3.21
	445174	AV652850	Hs.172004		3.19
75	459227	AW167599 AI656707		ESTs ESTs	3.19 3.15
13	439039 418803	U50079	Hs.48713 Hs.88556	histone deacetylase 1	3.15
	420005	AW271106		ESTS	3.15
	422511	AU076442	Hs.117938		3.14
80	452480		Un 17171	gb:RC-BT031-090199-063 BT031 Homo sapien lymphocyte adaptor protein	3.14 3.14
OU	445701 410678	AF055581 BE540516	Hs.13131 Hs.29373		3.14
	458664	Al300427		gb:qo18h07.x1 NCI_CGAP_Lu5 Homo sapiens	3.13
	436315	BE390513	Hs.27935	hypothetical protein MGC4837	3.13

					3.12
		BE398091		desmoplakin (DPI, DPII) hypothetical protein FLJ14428	3.12
				renin-binding protein	3.11
		AF126743	Hs.279884	DNAJ domain-containing	3.11 3.10
5	452826	BE245286		peroxisomal biogenesis factor 6	3.10
	446627	Al973016 W19744	Hs.15725 Hs.180059	hypothetical protein SBBI48 Homo sapiens cDNA FLJ20653 fis, clone KA	3.09
	427647 417211	T97617		ESTs	3.08
	448140	AF146761	Hs.20450	BCM-like membrane protein precursor	3.08 3.07
10	448752	AA593867		KIAA1608 protein	3.07
	416355	H49875 AU077297	Hs.268906 Hs.155894	ESTs protein tyrosine phosphatase, non-recept	3.07
	425345 410321	Y12860	Hs.62245	solute carrier family 25 (mitochondrial	3.07
	411395	AA889673	Hs.7542	KIAA1802 protein	3.07 3.06
15	416065	BE267931	Hs.78996	proliferating cell nuclear antigen	3.06
	432343	NM 002960 BE539951	Hs.2961 Hs.306996	S100 calcium-binding protein A3 Homo sapiens, clone IMAGE:3447073, mRNA,	3.05
	457991 433201	AB040896	Hs.21104	KIAA1463 protein	3.03
	416178	AI808527	Hs.192822	serologically defined breast cancer anti	3.02 3.01
20	411975	AI916058	Hs.144583	ESTs	3.00
	448719	AA033627 AW403911	Hs.21858 Hs.266175	trinucleotide repeat containing 3 phosphoprotein associated with GEMs	3.00
	419870 409601	AF237621	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	2.94
	415668	AW957684	Hs.306814	hypothetical protein FLJ21889	2.93 · 2.81
25	453256	AI565587	Hs.32556	KIAA0379 protein	2.75
	436856	AJ469355	Hs.127310 Hs.82848	ESTs selectin L (lymphocyte adhesion molecule	2.60
	417880 408209	BE241595 NM 004454	Hs.43697	ets variant gene 5 (ets-related molecule	2.59
	440457	BE387593	Hs.21321	Homo sapiens clone FLB9213 PRO2474 mRNA,	2.55 2.51
30	415314	N88802	Hs.5422	glycoprotein M6B	2.50
	434276	AF123659	Hs.93605 Hs.139226	leucine zipper, putative tumor suppresso replication factor C (activator 1) 2 (40	2.48
	424085 410600	NM 002914 AW575742	ns. 133220	ESTs, Moderately similar to \$65657 alpha	2.48
	439180	Al393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	2.43 2.39
35	444809	BE207568	Hs.208219	oculospanin	2.39
	453837	AL138387	Hs.256126 Hs.322844	bacutoviral IAP repeat-containing 7 (liv hypothetical protein DKFZp564A176	2.37
	410290 411358	AA402307 R47479	Hs.94761	KIAA1691 protein	2.35
	427550	BE242818	Hs.311609	nuclear RNA helicase, DECD variant of DE	2.34
40	426312	AF026939	Hs.181874	interferon-induced protein with tetratri	2.29 2.27
	448569	BE382657	Hs.21486	signal transducer and activator of trans E2F transcription factor 3	2.24
	418661 459373	NM 001949 BE408266	Hs.1189 Hs.301406		2.21
	417437	U52682	Hs.82132	interferon regulatory factor 4	2.21
45	436700	AI693690	Hs.301406	hypothetical protein PP3501	2.18 2.15
	450690	AA296696	Hs.333418		2.15
	432800 421773	BE391046 W69233	Hs.278962 Hs.112457	FSTs	2.09
	409415	AA579258	Hs.6083	Homo sapiens cDNA: FLJ21028 fis, clone C	2.03
50	433364	A1075407	Hs.296083	ESTs, Moderately similar to I54374 gene	2.02 2.01
	412609	Z48804	Hs.74124 Hs.9999	ocular albinism 1 (Netlleship-Falls) epithelial membrane protein 3	2.01
	443950 451537	NM 001425 R56631	Hs.26550	retinoid X receptor, gamma	2.00
	427080	AW068287		5 ras-related C3 botulinum toxin substrate	1.96
55	413190	AA151802	Hs.40368	adaptor-related protein complex 1, sigma	1.94 1.91
	412926	A1879076	Hs.75061 Hs.43388	macrophage myristoylated atanine-rich C 28kD interferon responsive protein	1.86
	453779 453107	N35187 NM 016113		6 vanilloid receptor-like protein 1	1.86
	430637		Hs.25629	0 S100 calcium-binding protein A11 (calgiz	1.86 1.84
60	408561	Al308037	Hs.84120	hypothetical protein MGC13016	1.83
	413171		Hs.75219	tyrosinase-related protein 1 Target Exon	1.82
	406016 446644		2 Hs.15791	transmembrane 7 superfamily member 1 (up	1.81
	431836			1 heta-site APP-cleaving enzyme 2	1.77 1.77
65	439496				1.76
	447604		3 Hs.30134 Hs.32549		1.74
	438866 440672			MAD1 (mitotic arrest deficient, yeast, h	1.70
	416091			82 defensin, beta 3	1.69
70	44629	1 BE397753		3 interferon, gamma-inducible protein 30	1.67 1.67
	42253				1.67
	418918 41258		Hs.8947 Hs.1790		1.67
	44825			14 hypothetical protein FLJ20396	1.00
75	41494	5 BE07635	8 Hs.7766		1.66 1.65
	42526		Hs.1554 8 Hs.3188		1.64
	43923 42792			106 hypothetical protein PP3501	1.63
	42482		9 Hs.1533	357 procollagen-lysine, 2-oxoglutarate 5-dio	1.62
80	44185	9 AW1943	64 Hs.9481		1.60 1.58
	44598				1,58
	41293 41723		Hs.8173	and a second second second	1.56
	71124			· · · · · ·	C12

	412056	BE386745	Hs.74631	basigin (OK blood group)	1.56
	412856 447200	BE543146	Hs.281434	Homo sapiens cDNA FLJ 14028 fis, clone HE	1.54
	409614	BE297412	Hs.55189	hypothetical protein	1.53
	450663	H43540	Hs.25292	ribonuclease HI, large subunit	1.53
5	423397	NM 001838	Hs.1652	chemokine (C-C motif) receptor 7	1.49
	425535	AB007937	Hs.158287	KIAA0468 gene product	1.48
	409340	BE174629	Hs.321130	hypothetical protein MGC2771	1.46
	446755	AW451473	Hs.16134	serine/threonine kinase 10	1.46
10	454429	BE273437	Hs.301406	hypothetical protein PP3501	1.46
10	425722	AJ659076	Hs.97031	hypothetical protein MGC13047	1.45 1.44
	414509	AW161311	Hs.76294	CD63 antigen (metanoma 1 antigen) transporter 1, ATP-binding cassette, sub	1.43
	452203 436378	X57522 AJ227874	Hs.99244	ESTs	1.42
	424218	AF031824	Hs.143212	cystatin F (leukocystatin)	1.42
15	436456	AW292677	Hs.248122	G protein-coupled receptor 24	1.42
	439740	AL365512	Hs.6657	hypothetical protein bK1048E9.5	1.42
	429359	W00482	Hs.2399	matrix metalloproteinase 14 (membrane-in	1.42
	427634	A1399745	Hs.18449	hypothetical protein MGC10820	1.40
•	403409			NM_005929:Homo sapiens antigen p97 (mela	1.40
20	434262	AF121858	Hs.12169	sorting nextin 8	1.34
	413566	AW604451	Hs.285814	sprouty (Drosophila) homolog 4	1.32 1.32
	427730	AW250549	Hs.180577	granulin	1.31
	411742 450395	AW247593 BE048545	Hs.71819 Hs.161757	eukaryotic translation initiation factor ESTs	1.30
25	413291	NM 006278	Hs.75268	siatytransferase 4C (beta-galactosidase	1.26
23	442609	AL020996	Hs.8518	selenoprotein N	1.24
	416929	N20535		melastatin 1	1.21
	421975	AW961017	Hs.6459	hypothetical protein FLJ11856	1.21
	454478	AW805749		superoxide dismutase 2, mitochondrial	1.20
30	437723	AI672731	Hs.13256	ESTs	1.18
	416350	AF188625	Hs.189507	phospholipase A2, group IID	1.08
	TABLE 48		Ean amhai	set identifier number	•
35	Pkey: CAT numb		e duster numb		
55	Accession		bank accessio		
	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,				
	Pkey	CAT Number	Accession		
	430540	713_2	BC017171	BC012195 NM_007126 AF100752 AL137377 Z707	68 BM474865 BG754806 AU124376 BG757203 BG764420 BG775028 BG824418
40			BM045810	AU120387 BG770238 BG686740 BG913323 B1759	980 BG395998 BM048875 BE881070 BE313689 BE879144 BM309834 AW245847
			A1770171 E	F196861 BE856897 AA463876 AI375927 AA64881	0 AA948193 AA490916 AI459893 AI458188 AI240408 AI191843 AI131029 AW768399
			AJ365196 A	W337984 AW026150 BE466591 BE674599 AI818	138 AA772197 AI551927 AW151143 BI198825 BG819083 BM458764 BE903567 1023 BG875384 BF996406 BF988930 BM475542 AW246215 BE501897 BE903610
			BE732715	PECCOS DEDUCTOS BESUDIOS BEISTOS BESUSION BESSEL	023 BG673364 BF390406 BF3803475 BG008258 BI547991 BI459099 BE391391 BE259420
45			BE501530	8E560537 BE903762 BE732947 BIZZ7204 BG7010	AL531791 AI435581 BF793112 AL577303 AA373265 BE746965 BF743630 BE879296
43					COORDINATION AND AND AND AND AND AND AND AND AND AN
			V13ED103 (	2M018508 AIGROZGO AWDZZ450 F20201 AW15140	5 AW517572 AA773468 BG259694 BE391163 BG621529 AI421726 BG767231 BM402333
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	425913	4123_2	AV703649 AW959818 AI582119 AI523459 AI674473 AW663543 AA825476 AI335231 BF742203 AM22013 AM220
15			
	442092	22756_2	AIG27829 BG993975 AV 01723 BM449821 BM698985 BM023170 AW025563 BG152606 BM023452 AI862106 BG959957 R16313 Z46351 R14838 F05290 R14821 R16277 R16313 Z46351 R14838 F05290 R14821 R16277
	415310 422150	1869807_1 782_1	BIOSCA21 RE059136 AW003898 8F446659 AI632691 AI632607 AI703113 AI302607 AI703113 AI7031 AI
20	422130	102	AW242244 A1356530 A1492508 A1094049 A1090422 AM3507 MET 3007 A1090402 BED73984
			AI914450 AI018697 AW577591 AW577616 AA382101 AW954455 AI867766 A707995 AI337384 BF 200405 110 AW950555 AW361284 AW954458 BF224124 BE813387 BG036579 BI553906 AA304995 AW361269 AW754160 AW361276 AW361271 AI867118 AW805555 AW361284 AW954458 BF224124 BE813387 BG036579 BI553906 AA304995 AW361269 AW755296 BF399060 AW958549 BF910827 BG573750 BG168639
			AW958551 BG681507 H79011 AW205090 AW154537 AA141007 AW154505 D
25	410235	2930253_1 540112_3	AA082977 AA082955 RF176902 RF177058 RF177058 RF177058 RF176902 RF176902 RF176902 RF176902 RF177058 RF176902 RF176902 RF176902 RF177058 RF176902 RF177058 RF176902 RF177058 RF176902 RF177058 RF176902 RF177058 RF176902 RF17690000000 RF1769000000000000000000000000000000000000
23	458215 442643	2736_1	BE176902 BE177058 BC001588 BC007424 AF016369 NM_004697 B1756186 BE257019 BG500792 B1862776 AL121371 BG574833 AA703250 AA179511 AW052006 BC001588 BC007424 AF016369 NM_004697 B1756186 BE257019 BG500792 B1862776 AL121371 BG574833 AA703250 AA179511 AW052006 BC001588 BC007424 AF016369 NM_004697 B1756186 BE257019 BG500792 B1862776 AL121371 BG574833 AA703250 AA179511 AW052006 BC001588 BC007424 AF016369 NM_004697 B1756186 BE257019 BG500792 B1862776 AL121371 BG574833 AA703250 AA179511 AW052006 BC001588 BC007424 AF016369 NM_004697 B1756186 BE257019 BG500792 B1862776 AL121371 BG574833 AA703250 AA179511 AW052006 BC001588 BC007424 AF016369 NM_004697 B1756186 BE257019 BG500792 B1862776 AL121371 BG574833 AA703250 AA179511 AW052006 BC001588 BC007424 AF016369 NM_004697 B1756186 BE257019 BG500792 B1862776 AL121371 BG574833 AA703250 AA179511 AW052006 BC001588 BC007424 AF016369 NM_004697 B1756186 BE257019 BG500792 B1862776 AL121371 BG574833 AA703250 AA179511 AW052006 BC001588 BC007424 AF016369 NM_004697 B1756186 BE257019 BG500792 B1862776 AA178517 BG574833 AA703250 AA179511 AW052006 BC001588 BC007424 AF016369 NM_004697 B1756186 BE257019 BG500792 B1862776 AA178517 AW251928 AA668676 AIR7851 AW451928 AA668676 AIR7851 AWA51928 AA668676 AIR7851 AWA51928 AA668676 AIR7851 AW451928 AA66876 AIR7851 AW451928 AA66876 AIR7851 AW451928 AA66876 AIR7851 AW451928 AIR7851 AW451928 AIR7851 AW451928 AIR7851 AW45
			AAN35630 A1289987 A11848UZ A1681391 A443944 TO A133017 A133017 D
			REALGO12 A1276555 BF 196021 AA/00003 AA00900 AA77239 AA00900 AA77239 AA00900 BE3030 BE303088 BE303088 BE303081 BE303088 BE30308
30			AW195227 A1189676 BF802049 AL513632 AL554911 AL538845 BE297273 AA31527 BM931320 BC20500 AL039681 AW301265 A1141144 BM041095 BG677009 AL039691 BF995709 BE73558 BE296453 BC393609 BG824453 AL567522 A1745257 AW388641 AW301265 A1141144 BM041095 BG677009 AL039691 BF995709 BE73558 BE296453 BC393609 BG824453 AL667522 A1745257 AW388641 AW301265 A1141144 BM041095 BG677009 AL039691 BF995709 BE296458 BC296453 BC39728 BC30577 BF334914 BF109661 R44450 H13259 T47087
			AW020280 A11149362 AU152328 AA418960 AL121009 A1830030 AL320740 TTOORE
		C10.2	AW082646 BF:305834 AL577515 BM041600 BE889299 BF239768 AW3868646 BF:305834 AL577515 BM041600 BE889299 BF239768 BF946219 BF946218 BF851494 AL536879 AA457150 Al580194 AI582629 AA464515 AA916242 AA337109 AA336509 N46906 AA336322 AA336407 BF946219 BF946218 BF851494 AL536879 AA457150 Al580174 AA551730 A1701013 BM068789 AW339506 AA293021 BF891108 AI458885 AW361203
35	446126	610_2	AA717722 AA319740 BI026817 BI027030 AL330000 A1033027 7400 1100 1100 1100 1100 1100 1100 110
55			AW974652 A1761251 A1655763 AA628063 BE047125 AW085916 A1129587 N52070 AW172361 AA032931 AW052931 AW052
			AW043567 AA056762
40	409305		AW043967 AW190302 AA071475 AA112236 AA070648 AA071243 AA081725 AA085187 AA070078 AW836081 BF854404 AW578594 AW578581 BF507971 AW196760 AA779923 AA707233 AI655913 AA948295 AW089222 AW291883 AW836081 BF854404 AW578594 AW578581 BF507971 AW196760 AA779923 AA707233 AI655913 AA948295 AW089222 AW291883 BF503327 BF593552
40	454870 437158		ALDEROGRA AN 160485 AW 173544 AW 290500 AW 450000 AIDE 1505 ALTEROGRAPHICATION DEGREE AW 450602 AA 462057
	701100	, 000.02.	AA630766 A1597717 A807728 AA52312 A155522 A157522 AW000736 A1866625 AW235356 BM021837 AA911956 A1680606 W86516 103370
			AW611634 HA1653 AI468349 H19588 AW090199 AW09555 W5557
45	40830	4 646409_1	AWR10779 RF146684 AWR10193 AWR10315 AW178835 AWR10316 BETTAGET AWR10367 AWR10367 AWR10323 AWR10328
			AW810443 AW810330 AW810211 AW810328 AW810327 AW810288 AW810255 AW810257 AW610253 AW610253 AW810241 AW810441 AW846649 AW810536 AW810281 AW810321 AW178837 AW810635 BE062400 AW810198 AW810325 AW810513 BE062434 BE146679 AW810441 AW846649 AW810536 AW810289 AW178857 AW810185 BE146653 AW810636 AW810322 BE146674 AW810359 AW810293 AW810472 AW178852 AW810356 AW810514 AW810289 AW178857 AW810185 BE146653 AW810636 AW81081080 AW810636 AW81064
			AW178857 AW810185 BE146653 AW810636 AW810322 BE146674 AW616339 AW61639
50	45922	7 639802_1	AW167599 A1971 179 A1934948
50	45248	0 3144986_	4 AION3574 AION3572 AION3575 AION3571
	45866 43044		BG108218 BE560548 AW380115 BE269629 AIGHTSTO AW360115 AV36250115
			R00283 C15236 AW327776 D80759
55	41060 45220		BC014081 NM 000593 X57522 L21208 L21207 L21208 L212
	4522	,,	RITTODOS AL 554969 B1489906 AISO4693 AVV293947 BM140042 AST 32 ACCOCCA AMORTO CONTROL AND AISCOCCA AMORTO CONTROL AM
			DC000722 AAR3R610 AI539114 AI/193/5 AI029129 DO05/0/5 A725722 AU 1000727 AU 100077 AU 10007 A
60	)		AL 582801 RI256544 RF342301 BGB/55554 RAUS4430 AUSSTOL ASSOCIATION ASSOCIATION ASSOCIATION DE 271141 AL 581932 AL 541575 BIB19184
			AV660190 AL 556475 AL620U2U AWV099000 AWV07917 9 22 13 10 74 100 100 100 100 100 100 100 100 100 10
			BE874601 BF804669 AL574458 BM143502 AZGOSTA AA653084 RM009154 AA135727 H05927 H23433 R42244 N79997 AW366665 AW366601
65			
0.	4169		BC017849 BC005892 N42983 BF691Z39 N42931 N42931 N42931 N42931 N4294360 BF380449 AW794456 AW794538
	454	178 4273_10	6 AW/96921 AW/96102 AW6003/49 AW6003/2 51 55555
_	TAB	ILE 48C:	to to an Eas probacel
70	) Pke Ref:		Unique number corresponding to an Eos probeset  Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers.
	r.e.		ansurance of human chiramiscome ZZ Dullmain, et al. (1999) https://doi.org/10.1000/
	Stra	and: position:	Indicates DNA strand from which exons were predicted. Indicates nucleotide positions of predicted exons.
7	5		
	Pke	ey Ref 1328 846908	Strand NL position 35 Minus 120428-120703
	405	451 762251	7 Minus 145949-146227
Q		5016 827266 3409 94385	
0	J 40.	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	

TABLE 49A: ABOUT 1127 GENES UPREGULATED IN PRIMARY MELANOMA AND/OR MELANOMA METASTASES RELATIVE TO NORMAL BODY TISSUES

PCT/US02/29560 WO 03/025138

Table 49A lists about 1127 genes upregulated in primary melanoma and/or melanoma metastases relative to normal body tissues. These genes were selected from \$9680 probesets on the Eos/Affymetrix Hut33 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey: Unique Eos probeset identifier number

ExAcon: Exemplar Accession number, Genbank accession number

5

UnigenelD: Unigene Title: R1: R2:

Unigene gene litte
90th percentile of primary melanoma and melanoma metastasis Als divided by the 90th percentile of normal tissue Als
90th percentile of primary melanoma and melanoma metastasis Als divided by the 90th percentile of normal tissue Als
90th percentile of primary melanoma and melanoma metastasis Als divided by the 90th percentile of normal tissue Als, where the 15th percentile of normal
tissue Als was subtracted from both the numerator and denominator 10

R3: 90th percentile of primary melanoma and melanoma metastasis Als divided by the 90th percentile of heart, liver, tung, and kidney Als

			pursonad or prin	the state of the s	sour percentine or it	ear, wer, with	g, and looney /
	Pkey 452838	ExAcon U65011	UnigenetD	Unigene Title	Ri	R2	R3
15	426555	NM_000372	Hs.30743 Hs.2053	preferentially expressed antigen in meta	14.05	11.83	14.05
	430377	NM_001922	Hs.301865	tyrosinase (ocutocutaneous albinism IA) dopactyrome tautomerase (dopactyrome delta	13.15 11.77	13.27 7.43	13.15 11.77
	420208	8E276055	Hs.95972	silver (mouse homolog) like	10.53	19.95	10.27
	431360	NM_000427	Hs.251680	toricrin	9.78	7.09	0.89
20	430822 422168	AJ005371	Hs.248017	glyceraldehyde-3-phosphate dehydrogenase	9.40	7.20	8.84
20	419628	AA586894 H67546	Hs.112408 Hs.49768	S100 calcium-binding protein A7 (psorias	8.03	10.27	12.84
	438549	BE386801	Hs.21858	ESTs trinucleotide repeat containing 3	7.56 7.50	8.92	6.49
	430686	NM_001942	Hs.2633	desmoglein 1	7.52 6.06	5.47 4.13	16,47 3.31
0.5	409601	AF237621	Hs.80828	keratin 1 (epidermotytic hyperkeratosis)	5.86	9.22	0.77
25	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	5.84	3.46	5.84
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	5.82	3.94	5.82
	414812 453344	X72755 BE349075	Hs.77367 Hs.44571	monokine induced by gamma interferon ESTs	5.81	3.33	6.79
	425088	AA663372	Hs.169395	hypothetical protein FLJ12015	5.78 5.60	3.07 3.92	5.98
30	402075			ENSP00000251056*:Plasma membrane calcium	5.12	4.22	5.60 5.12
	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	5.09	3.33	4.14
	420602	AF060877	Hs.99236	regulator of G-protein signalling 20	5.06	5.78	5.06
	426600 430838	NM_003378	Hs.171014	VGF nerve growth factor inducible	5.04	6.77	9.42
35	417542	N46664 J04129	Hs.169395 Hs.82269	hypothetical protein FLJ12015	5.03	3.06	5.03
-	425234	AW152225	Hs.165909	progestagen-associated endometrial prote ESTs, Weakly similar to 138022 hypotheti	4.93 4.78	8.13 2.93	5.41
	408962	BE386436	Hs.44317	SRY (sex determining region Y)-box 10	4.75	3.28	4.78 5.30
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	4.70	3.11	4.70
40	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	4.68	2.27	4.68
40	407756 417166	AA116021	Hs.38260	ubiquitin specific protease 18	4.65	3.21	3.31
	421773	AA431323 W69233	Hs.42146 Hs.112457	ESTs ESTs	4.56	5.23	4.56
	442711	AF151073	Hs.8645	hypothetical protein	4.52 4.37	11.11 3.70	0.96 4.30
4-	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	4.37	3.08	4.30 6.75
45	428513	BE220806	Hs.184697	Homo sapiens clone 23785 mRNA sequence	4.32	2.61	4.32
	447937	AL109716	Hs.20034	Homo sapiens mRNA full length insert cDN	4.31	3.13	4.31
	451099 433658	R52795 L03678	Hs.25954	interleukin 13 receptor, alpha 2	4.28	2.89	2.17
	420301	AA767526	Hs.156110 Hs.22030	immunoglobulin kappa constant paired box gene 5 (8-cell lineage specif	4.18	2.68	5.92
50	433447	U29195	Hs.3281	neuronal pentraxin ()	4.16 4.15	2.57 2.26	4.16 6.46
	446341	AL040763	Hs.310735	ESTs, Moderately similar to ALU7_HUMAN A	4.10	4.04	4.64
	408380	AF123050	Hs.44532	diubiquitin	4.02	2.46	5.33
	421379	Y15221	Hs. 103982	small inducible cytokine subfamily B (Cy	4.02	3.48	3.19
55	421633 454117	AF121860 BE410100	Hs.106260 Hs.40368	sorting nexts 10	4.01	2.61	3.36
•	417355	D13168	Hs.82002	edaptor-related protein complex 1, sigma endothelin receptor type 8	3.96 3.95	2.68 2.46	3.96
	420267	N37030	Hs.173337	ESTs	3.88	3.87	3.66 3.88
	412228	AW503785	Hs.73792	complement component (3d/Epstein Barr vi	3.81	3.04	7.94
60	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	3.79	2.23	3.79
oo	405451 449078	AK001256	Un 22026	dihydropyrimidinase-like 3	3.78	3.74	4.06
	423799	AW026300	Hs.22975 Hs.132906	KIAA1576 protein 19A24 protein	3.76 3.75	2.83	3.76
	456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A	3.75 3.73	2.36 2.59	3.75 6.97
65	444863	AW384082	Hs.104879	serine (or cysteine) proteinase inhibito	3.72	2.15	3.92
65	427666	AI791495	Hs.180142	calmodulin-like skin protein (CLSP)	3.69	4.17	1.18
	415817 422423	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	3.64	2.08	3.64
	419956	AF283777 AL137939	Hs.115481 Hs.40096	CO72 antigen	3.64	2.94	3.64
	420338	AA825595	Hs.88269	cadherin 19, type 2 Homo sapiens, clona MGC:17339, mRNA, com	3.56	2.22 2.96	4.68
70	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	3.55 3.54	1.96	4.70 3.54
	458079	A1796870	Hs.54277	ONA segment on chromosome X (unique) 992	3.53	2.18	3.27
	444381	BE387335	Hs.283713	ESTs, Weakly similar to \$64054 hypotheti	3.48	2.83	11.00
	449722 438380	8E280074	Hs.23960	cyclin B1	3.48	2.10	4.64
75	452744	T06430 AJ267652	Hs.6194 Hs.246107	chondroitin sulfate proteoglycan BEHAB/b Homo sapiens mRNA; cDNA DKFZp434E082 (fr	3.47	3.90	4.98
	447210	AF035269	Hs.17752	phosphatidylserine-specific phosphotipas	3.45 3.44	2.38 3.83	3.45 2.09
	428804	AK000713	Hs. 193736	hypothetical protein FLJ20706	3.43	2.39	3.43
	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, will	3,41	4.33	5.41
80	423605	AF047826 NM_004833	Hs.129887	cadherin 19, type 2	3.40	1.97	4.06
55	421508 428001	H97428	Hs.105115 Hs.219907	absent in melanoma 2 ESTs, Moderately similar to Transforming	3.38	2.77	5.46
	430770	AA765694	Hs.123296	ESTs	3.36 3.36	2.41 2.08	3.36 3.63
	445784	AJ253155	Hs.146065	ESTs ·	3.32	2.02	3.63 3.80
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					3.32	1.87	3.76
	414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein) phosphoinositol 3-phosphate-binding prot	3.31	2.10	3.31
	448966 441224	AW372914 AU076964	Hs.86149 Hs.7753	calumenta prospreniosion 3-prospriate-oriental pro-	3.28	2.04	3.28
	428242	H55709	Hs.2250	teukemia inhibitory factor (cholinergic	3.26	2.43 2.94	3.56 2.85
5	413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	3.24 3.23	1.84	3.87
	416636	N32536	Hs.42645	solute carrier family 16 (monocarboxyfic hypothetical protein FLJ21889	3.22	3.10	3.13
	415668 442757	AW957684 A1739528	Hs.306814 Hs.28345	ESTs	3.22	3.41	1.45
	426317	AA312350	Hs.169294	transcription factor 7 (T-cell specific,	3.18 3.18	2.50 5.31	3.18 4.55
10	432874	W94322	Hs.279651	melanoma inhibitory activity	3.17	3.09	4.28
	412561	NM_002286	Hs.74011 Hs.163724	lymphocyte-activation gene 3 ESTs	3.16	2.21	3.16
	443983 429732	H04482 U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	3.14	1.74	3.25 3.33
	422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38	3.14 3.10	2.07 3.20	2.15
15	422424	AI186431	Hs.296638	prostate differentiation factor	3.10	2.23	3.10
	435256	AF193766	Hs.13872	cytokine-like protein C17 Homo sapiens keratin 17 (KRT17)	3.10	2.10	3.02
	401747 447674	BE270640	Hs.19192	cyclin-dependent kinase 2	3.08	3.08	4.00
	419870	AW403911	Hs.266175	phosphoprotein associated with GEMs	3.07 3.06	3.16 2.92	3.07 4.20
20	432878	BE386490	Hs.279663	Pirin	3.05	1.96	3.05
	401454	1104203	Hs.58589	NM_014226*:Homo sapiens renal tumor anti glycogenin 2	3.01	2.26	3.27
	410079 426501	U94362 AW043782	Hs.293616	ESTs	3.01	2.00	3.68
	418310	AA814100	Hs.86693	ESTs	3.00 2.96	2.35 2.31	6.76 3.78
25	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	2.96	2.49	4.74
	422309	U79745	Hs.114924	solute carrier family 16 (monocarboxyfic KIAA1435 protein	2.94	1.80	2.94
	408418 432882	AW963897 NM_013257	Hs.44743 Hs.279696	serum/glucocorticoid regulated kinase-li	2.93	1.74	2.93
	416640	BE262478	Hs.79404	neuron-specific protein	2.93	2.78 2.35	3.09 4.27
30	443264	BE221477	Hs.132137	ESTs, Moderately similar to A47582 B-cel	2.92 2.91	2.83	3.84
	410491	AA465131	Hs.64001	Homo sapiens clone 25218 mRNA sequence Target Exon	2.90	2.44	2.90
	405545 451537	R56631	Hs.26550	retinoid X receptor, gamma	2.90	4.09	3.40
	439926	AW014875	Hs.137007	ESTs	2.90	2.43 3.22	2.90 1.44
35	406673	M34996	Hs.198253	major histocompatibility complex, class	2.89 2.89	3.22	2.89
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial hypothetical protein MGC4595	2.89	4.40	3.05
	440065 442739	W03476 NM_007274	Hs.266331 Hs.8679	cytosotic acyl coenzyme A thioester hydr	2.88	2.36	4.54
	424620	AA101043	Hs.151254	kattikrein 7 (chymotryptic, stratum com	2.86	3.23	1.95 2.84
40	407856	AA045281	Hs.266175	phosphoprotein associated with GEMs	2.84 2.84	1.84 1.80	2.92
	430540	AW245422	11: 444400	Homo sapiens cDNA: FLJ22105 fis, clone H MAGE-like 2	2.84	2.26	2.84
	424153	AA451737 W93774	Hs.141496 Hs.99936	keratin 10 (epidermolytic hyperkeratosis	2.81	2.91	0.83
	420798 431317	AA502682	113.55550	gb:ng23d01.s1 NCI_CGAP_Ov2 Homo sapiens	2.81	2.17	2.96 4.10
45	424800	AL035588	Hs.153203	MyoD family inhibitor	2.80 2.79	2.06 1.85	2.42
	448111	AA053486	Hs.20315	interferon-induced protein with tetratri KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	2.78	2.34	6.53
	431183	NM_006855	5 Hs.250696 Hs.21858	trinucleotide repeat containing 3	2.78	3.75	4.01
	448719 427951	AA033627 AI826125	Hs.43546	ESTs	2.78	1.99	2.70
50	453912	AL121031		SWI/SNF related, matrix associated, acti	2.77 2.75	2.28 1.98	2.77 2.75
	426711	AA383471	Hs.343800	conserved gene amplified in osteosarcoma	2.74	3.18	3.60
	409430		Hs.346735 Hs.50081	splicing factor, arginine/serine-rich 5 Hypothetical protein, XP_051860 (KIAA119	2.72	2.24	2.72
	409041 442117			ESTs; hypothetical protein for IMAGE:447	2.72	2.31	3.59
55	420552			hypothetical protein	2.72 2.72	1.85 2.18	2.72 2.72
• -	409103		Hs.112208	XAGE-1 protein	2.71	2.20	4.48
	439963			platelet-activating factor acetyfhydrola tyrosinase-related protein 1	2.71	5.74	2.62
	413171 436700		Hs.301406	hypothetical protein PP3501	2.71	3.37	3.32
60	419098	AA234041	Hs.87271	ESTs	2.70 2.69	3.53 2.48	1.35 2.69
	436608	3 AA628980	Hs.192371	down syndrome critical region protein DS	2.68	3.04	0.56
	41806		Hs.83393	cystatin E/M thyroid hormone receptor interactor 13	2.67	2.36	3.16
	43945		Hs.6566 Hs.13256	ESTs	2.66	2.16	2.66
65	43772 41125			MD-2 protein	2.66	1.81	2.66 3.92
0,5	42432		Hs.1765	lymphocyte-specific protein tyrosine kin	2.66 2.65	2.43 3.71	2.80
	45383			baculoviral IAP repeat-containing 7 (liv pyruvate dehydrogenase phosphatase	2.64	1.85	4.72
	43482			Niemann-Pick disease, type C1	2.64	2.07	2.64
70	41469 44437			forkhead box M1	2.64	2.82	4.46
70	43629			protein regulator of cytokinesis 1	2.63	1.81 2.38	2.95 10.12
	43931		0 Hs.102793	ESTs	2.62 2.62	2.80	2.62
	42021			ribosomal prolein L4 Human melanoma-associated antigen p97 (m	2.60	3.27	2.12
75	43874			chondroitin 4-sulfotransferase	2.60	2.67	3.03
13	43282 40838			homolog of rat orphan transporter v7-3	2.59	3.22	2.59
	40852		8 Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA,	2.58	1.69 2.77	2.05 2.88
	4448	9 BE20756	8 Hs.208219	oculospanin	2.58 2.58	1.83	2.58
00	4328			chromatin accessibility complex 1 leucine zipper, putative tumor suppresso	2.55	3.70	3.28
80	4342 4123		i9 Hs.93605 Hs.73817	small inducible cytokine A3 (homologous	2.55	2.14	1.62
	4101			DKF7P434C245 grotein	2.55	2.07	2.5\$ 4.01
	4477			Homo sapiens cDNA: FLJ23020 fis, clone L	2.54	2.17	4.01

	422173	BE385828	Hs.250619	phorbolin-like protein MDS019 (CEM15)	2.53	1.68	3.16
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	2.53	2.74	3.93
	437396	BE140396	Hs.21621	hypothetical protein DKFZp7620076	2.52	1.62	3.17
	448140	AF146761	Hs.20450	BCM-like membrane protein precursor	2.51	2.67	1.88
5	442426	Al373062	Hs.332938	hypothetical protein MGC5370	2.51	2.08	4.57
•	417427	M90391	Hs.82127	interleukin 16 (lymphocyte chemoattracta	2.51	1.74	2.68
	427581	NM_014788	Hs.179703				2.24
	432800			KIAA0129 gene product	2.51	1.67	-
	408996	BE391046	Hs.278962	AIM-1 protein	2.51	5.55	2.42
10		AI979168	Hs.344096	glycoprotein (transmembrane) nmb	2.50	1.95	241
10	410326	Al368909	Hs.47650	ESTS	2.50	2.85	2.63
	452833	BE559681	Hs.30736	KIAA0124 protein	2.50	3.14	3.07
	410016	AA297977	Hs.57907	small inducible cytokine subfamily A (Cy	2.49	3.38	291
	429083	Y09397	Hs.227817	BCL2-related protein A1	2.48	1.85	2.70
16	418460	M26315	Hs.85258	CD8 antigen, atpha polypeptida (p32)	2.48	2.33	2.99
15	409142	AL136877	Hs.50758	SMC4 (structural maintenance of chromoso	2.47	1.88	4.14
	412970	AB026436	Hs.177534	dual specificity phosphatase 10	2.45	2.00	0.98
	401780			NM_005557":Homo sapiens keratin 16 (foca	2.44	2.30	1.39
	416426	AA180256	Hs.210473	Homo sapiens cDNA FLJ14872 fis, clone PL	2.44	1.57	0.88
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	2.42	1.91	2.56
20	417880	BE241595	Hs.82848	selectin L (lymphocyte adhesion molecule	2.42	2.31	4.27
	415929	AA724373	Hs.49344	hypothetical protein FLJ11006	2.41	2.73	2.41
	415752	BE314524	Hs.78776	putative transmembrane protein	2.41	2.07	3.41
	409703	NM_006187	Hs.56009	2-5-oligoadenytate synthetase 3 (100 k	2.41	2.34	3.26
	414004	AA737033	Hs.7155	ESTs, Moderately similar to 2115357A TYK	2.40	1.65	2.40
25	453857	AL080235	Hs.35861	DKFZP586E1621 protein	2.40	2.18	8.13
	410290	AA402307	Hs.322844	hypothetical protein DKFZp564A176	2.40	2.88	2.46
	403328			Target Exon	2.39	2.00	1.95
	427540	R12014	Hs.20976	ESTs	2.39	1.73	3.24
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	2.39	1.96	2.39
30	433848	AF095719	Hs.93764	carboxypeptidase A4	2.38	2.45	2.65
50	438501	Z44110	Hs.86149	phosphoinositol 3-phosphate-binding prot	2.38	1.85	2.38
	430066	Al929659	Hs.237825	signal recognition particle 72kD	2.38	1.60	2.79
	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	2.37	1.99	6.23
35	450447	AF212223	Hs.25010	hypothetical protein P15-2	2.37	1.72	3.24
22	458997	AW937420		ESTs	2.37	1.57	3.27
	451446	AI826288	Hs.171637	hypothetical protein MGC2628	2.35	1.90	2.39
	408838	A1669535	Hs.40369	ESTs	2.35	1.59	2.71
	448275	BE514434	Hs.20830	kinesin-like 2	2.35	2.19	2.35
40	424148	BE242274	Hs.1741	integrin, beta 7	2.35	1.89	3.07
40	410700	AA352335	Hs.65641	hypothetical protein FLJ20073	2.35	1.65	2.35
	409105	AW467539	Hs.255877	EST _{\$}	2.35	2.50	2.35
	452882	AW972990	Hs.196270	folate transporter/carrier	2.34	2.12	2.90
	425606	U52112	Hs.158331	renin-binding protein	2.34	2.69	1.69
	433576	BE080715	Hs.161091	ESTs	2.34	3.74	2.34
45	423494	AW504365	Hs.24143	Wiskott-Aldrich syndrome protein interac	2.34	2.08	4.48
	431620	AA126109	Hs.264981	2-5-oligoadenylate synthetase 2 (69-71	2.33	2.43	2.66
	436614	AW104388	Hs.149091	ESTs	2.33	3.37	2.33
	425289	AW139342	Hs.155530	interferon, gamma-inducible protein 16	2.33	1.67	4.28
	426827	AW067805	Hs.172665	methylenetetrahydrofolate dehydrogenase	2.33	1.58	0.40
50	430015	AW768399	***************************************	ESTs	2.33	1.76	2.33
	421282	AA286914	Hs.40782	ESTs	2.32	1.65	2.49
	447737	AK000643	Hs.19404	DKFZP564L0862 protein	2.32	2.16	1.48
	432540	AJ821517	Hs.105866	ESTs	2.32	1.58	2.35
	418064	BE387287	Hs.83384	S100 calcium-binding protein, beta (neur	2.32	2.46	9.99
55	414829	AA321568	Hs.77436	pleckstrin	2.32	1.91	2.32
	425390	AI092634	Hs.156114	protein tyrosine phosphatase, non-recept	2.31	1.63	2.31
	448569	8E382657	Hs.21486	signal transducer and activator of trans	2.31	2.79	241
	428819	AL135623	Hs.193914	KIAA0575 gene product	2.30	1.60	2.95
	409512	AW979187	Hs.293591	melanoma differentiation associated prot	2.30	1.95	3.66
60	425231	AA527161	120031	ESTs	2.28	1.96	2.36
-	416091	AF295370	Hs.283082	defensin, beta 3	2.28	2.76	2.18
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	2.27	2.88	2.46
	427719	AI393122		ESTs	2.27	1.88	2.29
			Hs.134726				
65	431830	Y16645	Hs.271387	small inducible cytokine subfamily A (Cy	2.27	2.16	4.09
05	457465	AW301344	Hs.122908	DNA replication factor	2.26	2.23	2.26
	431639	AK000680	Hs.266175	phosphoprotein associated with GEMs	2.26	2.13	3.16
	442485	BE092285	Hs.29724	hypothetical protein FLJ13187	2.26	1.75	2.84
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	2.26	3.38	2.56
70	449317	AW293413	Hs.132906	19A24 protein	2.26	2.04	2.73
70	429922	Z97630	Hs.226117	H1 histone family, member 0	2.26	1.59	2.38
	441362	8E614410	Hs.23044	RAD51 (S. cerevisiae) homotog (E coli Re	2.25	1.86	3.07
	425388	AA329384	Hs.156110	immunoglobulin kappa constant	2.25	1.91	2.25
	417282	AA195203		RAB5C, member RAS oncogene family	2.25	2.23	3.20
76	406687	M31126		matrix metalloproteinase 11 (stromelysin	2.24	2.69	2.78
75	437862	AW978107	Hs.5884	Homo sapiens mRNA; cDNA DKFZp586C0224 (f	2.23	2.20	2.51
	408015	AW136771	Hs.244349	epidermal differentiation complex protei	2.23	4.59	2.47
	442503	AF147078	Hs.150853	p53-responsive gene 5	2.23	3.62	0.85
	429747	M87507	Hs.2490	caspase 1, apoptosis-related cysteine pr	2.22	1.60	1.69
00	424825	AF207069	Hs.153357	procoffagen-lysine, 2-oxoglutarate 5-dio	2.22	5.53	2.46
80	417693	AW959741	Hs.40368	adaptor-related protein complex 1, sigma	2.21	2.40	4.37
	422947	AA306782	Hs.122552	G-2 and S-phase expressed 1	2.21	2.06	2.32
	445875	AF070524	Hs.13410	Homo sapiens clone 24453 mRNA sequence	2.20	2.69	2.91
	417366	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)	2.20	2.26	3.79
				•			

			11- 04044	terrenisticant or estimate with DD7 hi	2.20	1.96	2.44
	450065	AL050107	Hs.24341	transcriptional co-activator with PDZ-bi chemokine (C-C motif) receptor 7	2.20	3.28	2.99
	423397 427051	NM_001838 BE178110	Hs.1652 Hs.173374	Homo sapiens cDNA FLJ10500 fis, clone NT	2.20	1.98	3.40
	418203	X54942	Hs.83758	CDC28 protein kinase 2	2.20	1.44	2.31
5	409354	N68188	Hs.159472	Homo sapiens cDNA: FLJ22224 fis, clone H	2.18	244	2.70
	418941	AA452970	Hs.239527	E1B-55kDa-associated protein 5	2.18	1.75	2.70
	424723	BE409813	Hs.152337	protein arginine N-methyltransferase 3(h	2.18 2.18	1.55 1.43	2.44 2.37
	430132 452194	AA204686	Hs.234149	hypothetical protein FLJ20647 Ubiquitin-like protein FAT10??? - diubiq	2.17	3.07	1.76
10	417933	AI694413 X02308	Hs.82962	Inymidylate synthetase	217	1.86	4.15
10	420137	AA306478	Hs.95327	CD3D antigen, delta polypeptide (TiT3 co	2.17	2.38	2.91
	425317	AW205118	Hs.210546	interleukin 21 receptor	2.17	2.02	2.22
	447769	AW873704	Hs.320831	Homo sapiens cDNA FLJ14597 fis, clone NT	2.16 2.16	1.87 1.55	2.49 2.26
15	407748	AL079409	Hs.38176 Hs.40527	KIAA0606 protein; SCN Circadian Oscillat ESTs	2.15	1.56	2.84
13	452958 440325	AA883929 NM_003812	Hs.7164	a disintegrin and metalloproteinase doma	2.15	1.76	2.97
	426153	AF057169	Hs.182771	vitelliform macular dystrophy (Best dise	2.15	1.85	2.74
	430580	AA806105	Hs.300697	immunoglobulin heavy constant gamma 3 (G	2.14	1.88	4.99
20	451952	AL120173	Hs.301663	ESTs	2.13	2.08 1.67	2.13 3.41
20	450534	AI570189	Hs.25132	KIAA0470 gene product ribonuclease, RNase A family, k6	2.12 2.12	1.75	2.27
	449217 432734	AA278536 AA837396	Hs.23262 Hs.263925	LIS1-interacting protein NUDE1, rat homo	2.12	2.14	2.49
	413190	AA151802	Hs.40368	adaptor-related protein complex 1, sigma	2.12	2.46	2.67
	443991	NM_002250	Hs.10082	potassium intermediate/small conductance	2.12	2.16	2.B2
25	429624	AA458648	Hs.99476	ESTs, Weakly similar to 1313184B alpha1	2.11	201	0.68 2.10
	447178	AW594641	Hs.192417	ESTs	2.10 2.10	2.52 1.52	4.01
	423017	AW178761	Hs.227948 Hs.28005	serine (or cysteine) proteinase inhibito Horno sapiens cDNA FLJ11309 fis, clone PL	2.10	1.53	2.10
	452110 436797	T47667 AA731491	Hs.334477	hypothetical protein MGC14879	2.10	1.55	. 2.41
30	453256	AI565587	Hs.32556	KIAA0379 protein	2.09	2.13	2.89
	405547			NM_018833*:Homo sapiens transporter 2, A	2.09	2.61	2.09
	434203	BE262677	Hs.283558	hypothetical protein PRO1855	2.09	1.76 3.91	4.10 2.38
	412609	Z48804	Hs.74124	ocular albinism 1 (Nettleship-Falls) Fc fragment of IgG, high affinity Ia, re	2.09 2.09	1.62	1.28
35	414821 417576	M63835 AA339449	Hs.77424 Hs.82285	phosphoribosylglycinamide formyltransfer	2.08	1.86	2.08
55	447377	X77343	Hs.334334	transcription factor AP-2 alpha	2.08	2.83	2.08
	423198	M81933	Hs.1634	cett division cycle 25A	2.08	1.66	2.23
	433068	NM_006456	Hs.288215	sialyltransferase	2.08	1.94	2.60 3.62
40	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	2.07 2.07	1.91 3.96	0.97
40	452392 403532	1.20815	Hs.507	corneodesmosin NM_024638:Homo sapiens hypothetical prot	2.07	1.88	2.68
	439859	AW292872	Hs.124554	ESTs	2.07	1.72	2.22
	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	2.07	2.26	4.22
	442643	U82756		PRP4/STK/WD splicing factor	2.07	1.74	1.90
45	426312	AF026939	Hs.181874	interferon-induced protein with tetratri	2.06 2.06	2.08 2.12	1.43 2.06
	409988	N27687	Hs.334334 Hs.63187	transcription factor AP-2 alpha (activat ESTs, Weakly similar to ALUC_HUMAN !!!!	2.06	1.65	291
	408548 442271	AA055449 AF000652	Hs.8180	syndecan binding protein (syntenin)	2.06	1.97	2.42
	414142	AW368397	Hs.334485	hemicentin (fibulin 6)	2.05	2.44	2.05
50	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	2.05	2.37	2.05
	450325	AI935962	Hs.91973	ESTs	2.05 2.05	1.67 1.56	1.82 1.99
	424090	X99699	Hs.139262	XIAP associated factor-1 aryl-hydrocarbon receptor nuclear transl	2.04	1.52	2.07
	438209 413794	AL120659 AF234532	Hs.6111 Hs.61638	myosin X	2.04	2.02	2.11
55	414945	8E076358	Hs.77667	lymphocyte antigen 6 complex, locus E	2.04	4.57	1.64
	425580	L11144	Hs.1907	galanin	2.04	1.67	2.26
	420052	AA418850	Hs.44410	ESTs	2.03 2.03	1.90 1.53	2.21 2.31
	415947	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer, lipoma HMGIC fusion partner-like 2	2.02	1.73	2.02
60	416406 426759	D86961 AJ590401	Hs.79299 Hs.21213	ESTs	2.02	1.86	5.47
-	432435	BE218886	Hs.282070	ESTs	2.02	1.39	1.67
	444184	T87841	Hs.282990	Human DNA sequence from clone RP1-28H20	2.02	1.57	2.02
	421574	AJ000152	Hs.105924	defensin, beta 2	2.02 2.01	2.22 2.55	2.15 1.75
65	411358	R47479	Hs.94761	KIAA1691 protein ets variant gene 5 (ets-related molecule	2.01	2.55 2.58	2.39
05	408209 409262	NM_004454 AK000631	Hs.43697 Hs.52256	hypothetical protein FLJ20624	2.01	1.50	2.01
	400750	74400001	113.022.00	Target Exon	2.01	1.73	2.09
	439496	BE616501	Hs.32343	Homo sapiens, Similar to RIKEN cDNA 1110	2.01	2.42	0.78
70	420460	AA262331	Hs.48376	Homo sapiens done HB-2 mRNA sequence	2.01	1.65	1.72
70	446839	BE091926	Hs.16244	mitatic spindle coiled-coil related prot	2.01 2.00	1.61 2.11	1.03 2.33
	427647	W19744 R51386	Hs.180059 Hs.124881	Homo sapiens cDNA FLJ20653 fis, clone KA ESTs	2.00	1.89	2.24
	436200 414175		Hs.103849	hypothetical protein DKFZp761D112	1.99	1.50	1.99
	420005			ESTs	1.99	2.03	2.59
75	417848	AA206581	Hs.116586	ESTs, Wealthy similar to JC5314 CDC28/cdc	1.99	1.42	2.17
	435545		Hs.28107	ESTs	1.99 1.99	1.89 2.23	1.99 3.44
	443426		Hs.9329 8 Hs.10887	chromosome 20 open reading frame 1 similar to lysosome-associated membrane	1.99	2.23 2.05	0.32
	444342 453905			LIM domain kinase 1	1.98	2.48	2.79
80	453884		Hs.36232	KIAA0186 gene product	1.98	1.93	1.98
	459373	BE408266	Hs.301406	hypothetical protein PP3501	1.98	2.22	1.91
	422809		Hs.121028	hypothetical protein FLJ10549	1.98 1.98	1.68 1.67	1.98 2.18
	452840	A1097393	Hs.43481	hypothetical protein DKFZp564K192	1.50	1.07	4.10

	409178	BE393948	Hs.50915	kaffikrein 5	1.98	3.76	1.37
	420991		Hs.287379	Homo sapiens mRNA for FLI00111 protein.	1.98	1.90	2.63
	414020		Hs.75703	small inducible cytokine A4 (homologous	1.97	1.88	1.23
	443105		Hs.9004	chondroitin sulfate proteoglycan 4 (mela	1.97	1.95	5.55
5	413450		Hs.75372	N-acetylgatactosaminidase, alpha-	1.97	1.77	1.97
	431574		Hs.261373	hypothetical protein dJ434O14.3	1.97	1.73	3.89 2.08
	408561		Hs.84120	hypothetical protein MGC13016	1.97 1.97	2.89 1.95	2.65
	421866	M24470	Hs.1435	guanosine monophosphata reductase	1.96	1.72	2.27
10	405506	**********	000050	Target Exon Homo sapiens cDNA: FLJ22528 fis, clone H	1.96	1.74	2.35
10	412490	AW803564	Hs.288850 Hs.23765	Homo sapiens mRNA; cDNA DKFZp547M123 (fr	1.95	2.09	2.77
	437379 448356	AL359575 AL120837	Hs.20993	high-glucose-regulated protein 8	1.95	1.66	2.58
	453931	AL121278	Hs.25144	ESTs	1.95	2.38	1.95
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	1.95	1.63	2.82
15	429547	AW009166	Hs.99376	FGENESH predicted novel secreted protein	1.94	2.02	1.35
	442064	AJ422867	Hs.88594	ESTs	1.94	1.49	2.21
	400533			ENSP00000209376*:PRED65 protein (Fragmen	1.94	1.69	1.94
	448752	AA593867	Hs.300842	KIAA1608 protein	1.94	1.71	2.40 2.93
20	408636	BE294925	Hs.46680	CGI-12 protein	1.94 1.93	1.69 1.62	3.21
20	439569	AW602166	Hs.222399	CEGP1 protein	1.93	1.83	1.99
	405779	1150272	Hs.332938	NM_005367:Homo sapiens melanoma antigen, hypothetical protein MGC5370	1.93	1.97	1.93
	444670 446950	H58373 AA305800	Hs.5672	hypothetical protein AF 140225	1.93	1.56	1.61
	409185	AW961601	Hs.252406	hypothetical protein FLJ12296 similar to	1.93	2.12	2.63
25	409098	AA132672	Hs.7984	pleckstrin homology, Sec7 and coiled/coi	1.92	2.12	2.51
	413916	N49813	Hs.75615	apolipoprotein C-II	1.92	1.98	0.22
	429609	AF002246	Hs.210863	cell adhesion molecule with homology to	1.92	1.65	6.39
	402994			NM_002463°:Homo sapiens myxovirus (influ	1.92	2.45	1.89
	425722	AI659076	Hs.97031	hypothetical protein MGC13047	1.92	2.69	2.30 2.93
30	421958	AA35718S	Hs.109918	ras homotog gene family, member H	1.92	2.10 1.57	1.91
	412584	X54870	Hs.74085	DNA segment on chromosome 12 (unique) 24	1.91 1.91	1.44	1.68
	415402	AA164687	Hs.177576	mannosyl (alpha-1,3-)-glycoprotein beta-	1.90	1.52	1.14
	430280	AA361258	Hs.237868	interleukin 7 receptor intercellular adhesion molecule 1 (CD54)	1.90	2.16	1.21
35	426251	M24283 AA352702	Hs.168383 Hs.37747	Homo sapiens, Similar to RIKEN cDNA 2700	1.90	1.84	2.07
33	440773 427923	AW274357	Hs.301406	hypothetical protein PP3501	1.90	4.26	1.70
	426470	AA528794	Hs.128644	ESTs	1.90	2.69	2.04
	409557	BE182896	Hs.3686	ESTs	1.90	2.01	1.90
	429714	BE561801	Hs.2484	T-cell leukemia/lymphoma 1A	1.90	2.49	2.52
40	428125	AA393071	Hs.182579	leucine aminopeptidase	1.89	1.89	1.49
	427634	AJ399745	Hs.18449	hypothetical protein MGC10820	1.89	3.59	1,71 1.45
	452874	AK001061	Hs.30925	hypothetical protein FLJ10199	1.89	1.67 2.55	1.45
	418883	8E387036	Hs.1211	acid phosphatase 5, tartrate resistant	1.89 1.89	2.33 1.96	1.89
45	448243	AW369771		integrin, beta 8	1.89	1.70	1.10
45	416114	AI695549	Hs.183868	glucuronidase, beta	1.88	1.86	2.04
	425935	Z98200	Hs.163724 Hs.7345	HSPC019 protein MAD1 (mitolic arrest deficient, yeast, h	1.68	4.16	1.78
	440672 430171	AF083811 AF086289	Hs.234766	skin-specific protein	1.87	2.70	0.75
	407366	AF026942	Hs.17518	gb:Homo sapiens cig33 mRNA, partial sequ	1.87	2.25	1.87
50	454294	AB000734	Hs.50640	JAK binding protein	1.87	1.98	1.46
-	417370	T28651	Hs.82030	tryptophanyl-tRNA synthetase	1.87	2.73	1.71
•	409417	AA156247	Hs.104879	serine (or cysteine) proteinase inhibito	1.87	1.79	2.72
	401781			Target Exon	1.87	1.88	1.16 1.13
	440590	A1863446	Hs.266308	mosaic serine protease	1.86 1.86	1.79 1.72	4.39
55	428450	NM_014791	Hs.184339	KIAA0175 gene product	1.86	1.81	1.86
	433675	AW977653	Hs.75319	nbonucleotide reductase M2 polypeptide	1.86	1.57	1.86
	429323	NM_001649 AF217513	Hs.2391 Hs.279905	apical protein, Xenopus laevis-fike clone HQ0310 PRO0310p1	1.85	1.71	5.82
	433001 453107	NM_016113	Hs.279746	vanilloid receptor-like protein 1	1.85	2.75	1.84
60	430441	BE398091	113.413740	desmoptakin (DPI, DPII)	1.85	1.80	2.79
00	417512	X76534	Hs.82226	glycoprotein (transmembrane) nmb	1.85	1.80	1.86
	423673	BE003054	Hs. 1695	matrix metalloproteinase 12 (macrophage	1.85	1.94	1.85
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	1.85	1.72	2.52
	414737	Al160386	Hs.125087	ESTs .	1.84	1.90	1.84 1.84
65	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	1.84 1.84	1.57 1.41	0.12
	428311	NM_005651		tryptophan 2,3-dioxygenase	1.84	1.70	3.15
	412141	AI183838	Hs.48938	hypothetical protein FLJ21802	1.84	1.66	1.84
	428515	AF030339	Hs.286229	plexin C1 ESTs	1.84	2.32	2.17
70	427914		Hs.20575	hypothetical protein FLJ20989	1.84	1.55	1.84
70	439352 413278	BE614347 BE563085	Hs.169615 Hs.833	Interferon-stimulated protein, 15 kDa	1.83	3.20	1.75
	435080		Hs.155111	hypothetical protein FLJ14428	1.83	1.62	1.47
	407966		Hs.38516	Homo sapiens, clone MGC:15887, mRNA, com	1.83	1.58	2.11
_	421535		Hs.105478	phosphoribosylformylglycinamidine syntha	1.83	1.73	2.18
75	433029			opsin 3 (encephalopsin)	1.83	1.96	1.83
	426158	NM_001982		v-erb-b2 avian erythroblastic leukemia v	1.83	1.61 2.44	2.46 1.82
	426890		Hs.41294	ESTs	1,82 1,82	2.24	2.01
	411027		Hs.67846	leutocyte immunoglobulin-like receptor, ESTs, Weatdy similar to FIG1 MOUSE FIG-1	1.82	2.72	2.16
80	441859		Hs.94814	hypothetical protein DKFZp762H1311	1.82	1.50	1.82
οU	437435 448357		Hs.27027 Hs.108923	RAB38, member RAS oncogene family	1.82	2.52	1.76
	420674			butyrylcholinesterase	1.82	1.43	0.68
	439219		Hs.41322	ESTs	1.82	1.88	2.43

	432810	AA863400		ESTs	1.82	1.43	1.82
	417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	1.82	1.98	1.82
	447484	AA464839	Hs.292566	hypothetical protein FLJ14697	1.82 1.82	1.63 2.80	1.82 2.18
5	436456	AW292677	Hs.248122 Hs.89476	G protein-coupled receptor 24 CD2 antigen (p50), sheep red blood cell	1.82	2.28	2.00
,	418918 424755	X07871 AB033094	Hs.152925	KIAA1268 protein	1.82	1.85	1.62
	436315	BE390513	Hs.27935	hypothetical protein MGC4837	1.82	1.74	5.18
	420783	A1659838	Hs.99923	lectin, galactoside-binding, soluble, 7	1.81 1.81	1.87 1.88	0.80 2.03
10	417105	X60992	Hs.81226	CD6 antigen	1.81	1.73	2.45
10	423961 446019	D13666 Al362520	Hs.136348	periostin (OSF-2os) histone deacetylase 3	1.81	1.39	2.24
	412580	AA113262	Hs.17901	Homo sapiens, clone IMAGE:3937015, mRNA,	1.81	3.05	1.58
	409415	AA579258	Hs.6083	Homo sapiens cDNA: FLJ21028 fis, clone C	1.80	2.00	1.78
1.5	453684	AK001922	Hs.34578	atpha2,3-siatyltransferase	1.80 1.80	1.98 1.56	1.22 1.71
15	446921	AB012113 N35187	Hs.16530 Hs.43388	small inducible cytokine subfamily A (Cy 28kD interferon responsive protein	1.80	2.42	2.04
	453779 434706	A1656291	Hs.116394	ESTs .	1.80	1.58	1.80
	416065	BE267931	Hs.78996	proliterating cell nuclear antigen	1.80	1.79	2.51
••	453331	AI240665		ESTs	1.79	1.43	2.33 4.46
20	429412	NM_006235	Hs.2407	POU domain, class 2, associating factor	1.79 1.79	1.46 2.30	1.79
	428784 453507	Y12851 AF083217	Hs.193470 Hs.33085	purinergic receptor P2X, ligand-gated io WD repeat domain 3	1.79	1.49	1.51
	452826	BE245286	Hs.301636	peroxisomal biogenesis factor 6	1.79	1.57	2.00
	439237	AW408158	Hs.318893	ESTs, Weakly similar to A47582 B-cell gr	1.79	2.26	2.22
25	406672	M26041	Hs.198253	major histocompatibility complex, class	1.79 1.79	1.76 1.43	1.78 3.32
	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3 chemokine (C-C motif) receptor 1	1.78	1.66	1.29
	452698 424954	NM_001295 NM_000546	Hs.301921 Hs.1846	turnor protein p53 (Li-Fraumeni syndrome)	1.78	1.73	2.35
	436378	AJ227874	Hs.99244	ESTs	1.78	1.84	. 1.78
30	421778	AA428000	Hs.283072	actin related protein 2/3 complex, subun	1.78	1.66	3.67
	421948	L42583	Hs.334309	keratin 6A	1.78 1.77	1.74 2.27	3.00 2.13
	414915	NM_002462	Hs.76391	myxovirus (influenza) resistance 1, homo ESTs, Highly similar to SWI/SNF related,	1.77	1.98	2.32
	437317 427318	AA748613 AF186081	Hs.311977 Hs.175783	zinc transporter	1.77	1.61	0.92
35	418403	D86978	Hs.84790	KIAA0225 protein	1.76	1.49	2.24
	421433	AI829192	Hs.22380	ESTs	1.76	1.49 1.74	2.52 1.76
	450728	AW162923	Hs.25363	presentiin 2 (Atzheimer disease 4) Homo sapiens, clone MGC:5564, mRNA, comp	1.76 1.76	1.43	1.76
	428655 427536	H05769 BE277141	Hs.188757 Hs.115803	gb:601178666F1 NIH_MGC_20 Homo sapiens c	1.76	2.12	1.76
40	433364	AI075407	Hs.296083	ESTs, Moderately similar to 154374 gene	1.76	1.86	1.48
	401994	,		Target Exon	1.75	1.44	1.75
	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ty	1.75 1.75	1.69 1.46	1.79 1.88
	408633	AW963372	Hs.46677	PRO2000 protein ribosomal protein S6	1.75	1.60	1.92
45	429978 450690	AA249027 AA296696	Hs.333418	FXYD domain-containing ion transport reg	1.75	2.13	2.03
73	456967	AW004056	Hs.168357	T-box 2	1.74	1.95	1.42
	417866	AW067903	Hs.82772	collagen, type XI, alpha 1	1.74	2.64	2.01
	428746	AW503820	Hs.192861	Spi-B transcription factor (Spi-1/PU.1 r	1.74 1.74	2.82 1.51	2.31 1.62
50	432642	BE297635 AW820035	Hs.3069 Hs.278679	heat shock 70kD protein 98 (mortalin-2) a disintegrin and metalloproteinase doma	1.73	1.54	3.15
50	429505 412851	A1826502	Hs.97269	ESTs	1.73	1.67	1.05
	453953	AW408337	Hs.36972	CD7 antigen (p41)	1.73	2.22	2.28
	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	1.73 1.73	2.05 1.71	1.47 1.73
55	419485	AA489023	Hs.99807	ESTs, Weakly similar to unnamed protein neuropilin 2	1.73	1.62	4.70
25	447217 437673	BE465754 AW665665	Hs.17778 Hs.153034	ESTs	1.72	1.55	2.10
	437879	BE262082	Hs.5894	hypothetical protein FLJ10305	1.72	2.50	1.80
	448410	AK000227	Hs.21126	hypothetical protein FLJ20220	1.72	1.48 2.19	3.98 1.82
60	413313	NM_002047	Hs.283108	glycyl-IRNA synthetase transporter 1, ATP-binding cassette, sub	1,72 1,72	2.68	1.68
υυ	452203 443950	X57522 NM_001425	Hs.9999	epithelial membrane protein 3	1.71	2.17	2.24
	403969	1430_001424	, 10.3333	ENSP00000034663:Zinc finger protein 131	1.71	1.31	1.71
	450832	AW970602	Hs.105421	ESTs	1.71	1.33	2.38
65	453005		Hs.31803	ESTs, Weakly similar to N-WASP (H.sapien	1.71 1.71	1.67 2.10	1.95 2.20
65	439783		Hs.24835 7 Hs.167379	hypothetical protein FLJ14594 cancer/testis antigen (NY-ESO-1)	1.71	3.86	1.76
	418678 432259		Hs.274201	60S acidic ribosomal protein PO	1.71	1.85	1.94
	420340			CD3Z antigen, zeta polypeptide (TiT3 com	1,71	2.12	1.98
-	428289	M26301	Hs.2253	complement component 2	1.71	2.46	0.76 2.78
70	424006		Hs.137548	CD84 antigen (leukocyte antigen) . KIAA0472 protein	1.70 1.70	1.70 2.24	1.60
	440039 406646		Hs.6874 Hs.308026	major histocompatibility complex, class	1.70	2.27	1.33
	425367		Hs.155975	protein tyrosine phosphatase, receptor t	1.70	2.77	2.07
	420286	A1796395	Hs.111377	ESTs	1.70	1.50	3.21
75	430255			Homo sapiens mRNA for KIAA1551 protein,	1.69 1.69	1.44 2.57	1.69 1.65
	445247			ESTs gb:H.sapiens rearranged mRNA for immunog	1.69	1.52	3.13
	436965 410257		Hs.156110 Hs.61469	hypothetical protein	1.69	1.99	1.97
	424663			SH2 domain protein 1A, Duncan's disease	1.69	1.76	1.69
80	427792	M63928	Hs.180841	tumor necrosis factor receptor superfami	1.69	1.98	2.48
	458098			metallothionein 1E (functional) topoisomerase (DNA) II alpha (170kD)	1.68 1.68	1.83 1.57	1.68 4.09
	425397 421485		Hs.156346 Hs.104800	hypothetical protein FLJ10134	1.68	1.64	0.68
	72170			EQ 1			-

	421563	NM_006433	Hs.105806	ama ike ia	1.60	2.24	1.55
	448775	AB025237	Hs.388	granutysin nudix (nucleoside diphosphate linked mol	1.68 1.68	1.98	2.05
	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	1,68	1.35	1.68
_	440457	BE387593	Hs.21321	Homo sapiens clona FLB9213 PRO2474 mRNA,	1.68	1.88	1.63
5	438866	U44385	Hs.325495	tissue inhibitor of metalloproteinase 2	1.67	2.54	1.90
	401760			Target Exon	1.67	1.93	1.61
	422158 446644	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	1.67	1.85	4.25
	415701	NM_003272 NM 003878	Hs.15791 Hs.78619	transmembrane 7 superfamily member 1 (up gamma-glutamyl hydrolase (conjugase, fol	1.67 1.67	1.94 1.65	1.48 0.90
10	450293	N36754	Hs.171118	hypothetical protein FLJ00026	1.67	1.54	1.95
	412856	BE386745	Hs.74631	basigin (OK blood group)	1.67	2.71	1.47
	439318	AW837046	Hs.6527	G protein-coupled receptor 56	1.66	1.82	1.19
	424399	AI905687		AJ905687:JL-8T095-190199-019 BT095 Homo	1.66	3.65	0.44
15	432355	AA534416	Hs.162185	ESTs, Weakly similar to S42799 garp prec	1.66	1.98	1.45
13	427239 425262	BE270447	U- 165410	ubiquitin carrier protein	1.66	2.94	1.92
	413869	D87119 NM_000878	Hs.155418 Hs.75596	GS3955 protein Interleukin 2 receptor, beta	1.66 1.66	2,36 1.86	1.66 1.90
	406698	X03068	Hs.73931	major histocompatibility complex, class	1.65	2.05	1.31
	446217	AI651594	Hs.99709	ESTS	1.65	1.98	1.77
20	400222			NM_002082*:Homo sapiens G protein-couple	1.65	1.74	1.81
	432468	AW402155	Hs.3003	CD3E antigen, epsilon polypeptide (TiT3	1.65	2.50	1.77
	417237	H86385	Hs.81737	palmitoyl-protein thioesterase 2	1.65	2.89	1.57
	433012 446291	NM_004045 BE397753	Hs.279910 Hs.14623	ATX1 (antioxidant protein 1, yeast) homo	1.64 1.64	2.76 1.96	1.26 1.24
25	433867	AK000596	Hs.3618	interferon, gamma-inducible protein 30 hippocatcin-like 1	1.64	1.47	1.00
	433671	AW138797	Hs.132906	19A24 protein	1.64	2.17	1.96
	418371	M13560	Hs.84298	CD74 antigen (invariant polypeptide of m	1.64	2.18	1.43
	432336	NM_002759	Hs.274382	protein kinase, interferon-inducible dou	1.64	1.47	1.64
20	409264	NM_014937	Hs.52463	KIAA0966 protein	1.64	1.46	. 4.89
30	431836	AF178532	Hs.271411	beta-site APP-cleaving enzyme 2	1.64	2.58	1.79
	414586 418117	AA306160 AI922013	Hs.16488 Hs.83498	lymphocyte cytosolic protein 1 (L-plasti linker for activation of T cells	1.63 1.63	1.72 1.98	1.88 1.99
	448304	BE622768	Hs.290356	mesoderm development candidate 1	1.63	1.67	1.86
	425635	AB007937	Hs. 158287	KIAA0468 gene product	1.63	2.56	1.97
35	453258	AW293134	Hs.32597	ring finger protein (C3H2C3 type) 6	1.63	1.46	2.43
	420000	AB036063	Hs.94262	p53-inducible ribonucleotide reductase s	1.63	1.34	1.94
	447321	AW271217	Hs.281434	Homo sapiens cDNA FLJ14028 fis, clone HE	1.63	1.96	1.77
	422192	AA305159	Hs.113019	fis485 hypothetical protein XP_098151 (leucine-	1.62	1.45	1.62
40	450701 419381	H39960 AB023420	Hs.288467 Hs.90093	heat shock 70kD protein 4	1.62 1.62	2.23 1.57	1.53 2.38
	424779	AL046851	Hs.153053	CD37 antigen	1.62	1.92	2.10
	413283	R78669	Hs.23756	hypothetical protein similar to swine ac	1.62	1.41	1.12
	414907	X90725	Hs.77597	polo (Drosophia)-like kinase	1.62	2.03	2.13
AE	414159	AW511414	Hs.257352	apolipoprotein L, 6	1.62	1.89	1.32
45	410055	AJ250839	Hs.58241	gene for serine/threonine protein kinase	1.62	1.81	1.27
	428179 436251	AI127772 BE515065	Hs.279696	serum/glucocorticoid regulated kinase-li	1.62 1.61	1.50 1.71	2.13 2.02
	451708	AI306536	Hs.296585 Hs.60975	nucleolar protein (KKE/D repeat) ESTs	1.61	2.31	1.70
	418113	AJ272141	Hs.83484	SRY (sex determining region Y)-box 4	1.61	1.53	2.50
50	410600	AW575742		ESTs, Moderately similar to S65657 alpha	1.61	1.83	1.69
	436873	N23874	Hs.50477	RAB27A, member RAS oncogene family	1.61	1.56	1.61
	440201	AL359588	Hs.7041	hypothetical protein DKFZp762B226	1.61	1.58	1.85
	414368	W70171	Hs.75939	uridine monophosphate kinase	1.61	1.59	2.75
55	454429 422257	BE273437 NM_001716	Hs.301406 Hs.113916	hypothetical protein PP3501  Burkitt lymphoma receptor 1, GTP-binding	1.61 1.61	3.54 2.15	1.52 1.54
	426437	BE076537	Hs.169895	ubiquitin-conjugating enzyme E2L 6	1.60	2.01	1.36
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	1.60	2.00	1.60
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	1.60	1.38	2.23
۲0	429612	AF062649	Hs.252587	pituitary tumor-transforming 1	1,60	1.78	2.59
60	411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-assoc	1.60	1.78	2.07
	417324 430325	AW265494	Un 220256	ESTs	1.60	2.48	1.91
	430325	AF004562 BE169641	Hs.239356 Hs.270134	syntaxin binding protein 1 hypothetical protein FL/20280	1.60 1.60	1.74 1.46	2.53 2.46
	434449	AW953484	Hs.3849	hypothetical protein FLJ22041 similar to	1.50	1.81	3.00
65	443378	AW392550	Hs.9280	proteasome (prosome, macropain) subunit,	1.59	1.88	1.68
	417437	U52682	Hs.82132	interferon regulatory factor 4	1.59	1.90	2.26
	437949	U78519	Hs.41654	ESTs, Weakly similar to A46010 X-linked	1.59	2.14	1.59
	401797			Target Exon	1.59	1.82	1.78
70	449720	AA311152	Hs.288708	hypothetical protein FLJ21562	1.59	1.45	4.69
70	424971 415474	AA479005 NM_014252	Hs.154036 Hs.78457	tumor suppressing subtransfarable candid solute carrier family 25 (mitochondrial	1.59 1.58	1.82 1.51	1.68 0.30
	430017	AA263172	Hs.35	protein tyrosine phosphatase, non-recept	1.58	1.72	2.46
	422515	AW500470	Hs.117950	multifunctional polypeptide similar to S	1.58	1.85	1.94
	434094	AA305599	Hs.238205	hypothetical protein PRO2013	1.58	1.25	2.09
75	428844	AW972635	Hs.301904	hypothetical protein FLJ12671	1.58	1.72	1.80
	440942	AW246547	Hs.17901	Homo sapiens, clone IMAGE:3937015, mRNA,	1.58	2.60	1.58
	419596	BE379320	Hs.91448	MKP-1 like protein tyrosine phosphatase	1.58	1.84	1.22
	401151 441590	AI623207	Hs.190537	Target Exon ESTs	1.58 1.58	2.43 1.40	1.60 1.58
80	418677	S83308	Hs.87224	SRY (sex determining region Y)-box 5	1.58	1.68	1.58
	416448	L13210	Hs.79339	lectin, galactoside-binding, soluble, 3	1.58	2.28	1.60
	418739	AA310964	Hs.88012	SHP2 interacting transmembrane adaptor	1.58	214	2.10
	418216	AA662240	Hs.283099	AF15q14 protein	1.57	1.46	1.57

				And the Park American B	1.57	1.42	0.88
	427700	AA262294	Hs.180383	dual specificity phosphatase 6 immunoglobulin kappa constant	1.57	1.49	2.69
	436485 404872	X59135	Hs.156110	ENSP00000243173*:DJ1109J22.1 (novel home	1.57	1.46	1.36
	408212	AA297567	Hs.43728	hypothetical protein	1.57	1.55	2.73
5	414699	AI815523	Hs.76930	synuclein, alpha (non A4 component of am	1.57	1.36	1.57 1.13
	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	1.57 1.57	1.70 1.75	1.57
	432946	U60899	Hs.279854	mannosidase, alpha, class 2B, member 1 Human T-cell receptor active alpha-chain	1.57	2.26	2.10
	417929 431629	R27219 AU077025	Hs.74647 Hs.265827	interferon, alpha-inducible protein (clo	1.57	2.09	1.57
10	402876	AUUTTUZS	113.200021	NM_022161*:Homo sapiens livin inhibitor-	1.56	2.28	1.45
••	439627	BE621702	Hs.29076	hypothetical protein FLJ21841	1.56	2.97	1.54 1.88
	414839	X63692	Hs.77462	DNA (cytosine-5-)-methyltransferase 1	1.56 1.56	1.75 2.76	1.67
	450663	H43540	Hs.25292	ribonuclease HI, targe subunit matrix metalloproteinase 17 (membrane-in	1.56	2.36	1.83
15	425818 422765	AB021225 AW409701	Hs.159581 Hs.1578	baculoviral IAP repeat-containing 5 (sur	1.56	1.78	2.06
13	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	1.56	1.32	2.70
	453613	F06838		ESTs	1.56	1.76	1.84 1.56
	428379	X06026	Hs.2259	CD3G antigen, gamma polypeptide (TiT3 co	1.56 1.56	1.43 1.47	3.15
20	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotactin) actin related protein 2/3 complex, subun	1.56	2.01	1.56
20	444652 420842	BE513613 AI083668	Hs.11538 Hs.50601	hypothetical protein MGC10986	1.55	2.24	1.90
	447513	AW955776	Hs.313500	ESTs, Moderately similar to ALU7_HUMAN A	1.55	1.24	3.07
	408901	AK001330	Hs.48855	hypothetical protein FLJ 10458	1.55	1.79	2.17 1.96
0.5	437669	Al358105	Hs.123164	ESTs, Wealty similar to match to ESTs AA	1.55 1.55	1.83 1.63	2.20
25	439437	AI207788	Hs.343628	sialytransferase 48 (beta-galactosidase hypothetical protein dJ511E16.2	1.55	1.73	1.50
	418835 448633	AL023694 AA311426	Hs.88977 Hs.21635	tubulin, gamma 1	1.54	2.02	1.67
	447763	BE619911	Hs.115803	hypothetical protein	1.54	2.52	1.52
	430223	NM_002514	Hs.235935	nephroblastoma overexpressed gene	1.54	1.54 1.97	- 3.03 1.53
30	448258	BE386983	Hs.343214	hypothetical protein FLJ20396	1.54 1.54	1.53	2.55
	440165	AW014718	Hs.7753	calumenin caspase 4, apoptosis-related cysteine pr	1.54	1.34	1.69
	433376 445982	A1249361 BE410233	Hs.74122 Hs.13501	pescadillo (zebrafish) homolog 1, contai	1.54	2.21	1.54
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	1.54	2.50	1.94
35	416926	ноз109	Hs.263395	HT018 protein	1.54	1.41	2.01 1.23
	431630	NM_002204	Hs.265829	integrin, alpha 3 (antigen CD49C, alpha	1.54 1.54	1.89 1.93	1.23
	442159	AW163390	Hs.278554	heterochromatin-like protein 1 exosome component Rrp41	1.53	2.47	1.61
	420421	AF281133 M34996	Hs.343589 Hs.198253	major histocompatibility complex, class	1.53	1.62	1.19
40	406973 422530	AW972300	Hs.118110	bone marrow stromal cell antigen 2	1.53	1.74	1.37
-0	423420	AI571364	Hs.128382	Homo sapiens mRNA; cDNA DKFZp76111224 (f	1.53	2.49	1.59
	429359	W00482	Hs.2399	matrix metalloproteinase 14 (membrane-in	1.53 1.53	2.72 1.64	1.54 2.40
	429837	NM_003896	Hs.225939	sialytransferase 9 (CMP-NeuAc:lactosylc	1.52	1.98	0.98
45	412939	AW411491 BE540516	Hs.75069 Hs.293732	eukaryotic translation elongation factor hypothetical protein MGC3195	1.52	1.39	2.17
45	410678 431186	NM_012249		ras-like protein	1.52	1.91	1.82
	406868	AA505445	Hs.300697	immunoglobutin heavy constant gamma 3 (G	1.52	1.57	1.82 1.19
	422532	AL008726	Hs.118126	protective protein for beta-galactosidas	1.51 1.51	2.08 1.50	0.67
50	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote KIAA0101 gene product	1.51	1.42	7.41
50	417308 424902	H60720 NM_003866	Hs.81892 Hs.153687	inositol polyphosphate-4-phosphatase, ty	1.51	2.75	1.51
	405204	14M_003600	113.133001	NM_002086*:Homo sapiens growth factor re	1.51	1.44	1.53
	424481	R19453	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	1.51	1.92 1.61	2.32 1.47
<i></i>	422516	BE258862	Hs.117950	multifunctional polypeptide similar to S	1.50 1.50	1.35	3.53
55	418827	BE327311	Hs.47166 Hs.311609	HT021 nuclear RNA helicase, DECD variant of DE	1.50	1.55	2.09
	427550 432992	BE242818 BE270472	Hs.279900	HSPC015 protein	1.50	1.82	0.82
	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	1.50	1.34	4.87
	413566	AW604451	Hs.285814	sprouty (Drosophila) homolog 4	1.50 1.50	3.05 1.36	1.51 0.46
60	422616	BE300330	Hs.118725	selenophosphate synthetase 2 zona pellucida glycoprotein 3A (sperm re	1.50	2.05	1.78
	431222 421861		Hs.273790 Hs.108966	phosphatidylinositol-4-phosphate 5-kinas	1,49	1.52	2.62
	421661 422684		Hs.119192	H2A histone family, member Z	1.49	1.53	2.02
	452363		Hs.94953	Homo sapiens, Similar to complement comp	1.49	2.02	1.41
65	411825			hypothetical protein FLJ20327	1,49 1,49	2.55 1.77	1.38 1.49
	409425		Hs.54452	zinc finger protein, subfamily 1A, 1 (lk transcription factor 19 (SC1)	1.49	1.79	1.75
	431070			ras-related C3 botulinum toxin substrate	1.49	1.57	2.14
	427080 440676			LIM and senescent cell antigen-like doma	1.49	1.42	1.46
70	411296			growth suppressor 1	1.49	1.74	1.50
	442894		Hs.8836	parvin, beta	1.49 1.49	2.25 2.06	1.51 1.89
	416361			ESTs, Weakly similar to CA13_HUMAN COLLA ESTs, Weakly similar to ALU2_HUMAN ALU S	1,49	1.59	1.65
	424162			retinoic acid receptor responder (lazaro	1.49	2.00	1.22
75	44713 42775			perforin 1 (pare forming protein)	1.49	2.12	1.41
	42284			neutrophil cytosofic factor 1 (47kD, chr	1.49	1.61	1.67
	41700	7 AF224741	Hs.80768	chloride channel 7	1,48 1,48	1.94 1.68	1.71 1.67
	42192		Hs.109606 Hs.170121	coronin, actin-binding protein, 1A protein tyrosine phosphatase, receptor t	1,48	1.43	2.25
80	42224 41074		Hs.324473	mitogen-activated protein kinase 1	1.48	1.37	3.17
00	44747			sprouty (Drosophila) homolog 2	1.48	1.35	1.46
	42724	7 AW50422	1 Hs.174103	integrin, alpha L (antigen CD11A (p180),	1.47 1.47	1.58 1.73	1.48 1.38
	44294	5 Al024849	Hs.131853	ESTs	1.47	1.73	1.30

	447200	BE543146	U- 201424	Harry annions of the El 114079 for stone UE	9.47	4.00	1.60
			Hs.281434	Homo sapiens cDNA FLJ14028 fis, clone HE	1.47	1.89	
	424085	NOM_002914	Hs.139226	reptication factor C (activator 1) 2 (40	1.47	2.03	1.47
	422857	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	1.47	1.86	1.93
5	416350	AF188625	Hs.189507	phospholipase A2, group IID	1.47	2.92	1.49
)	458207	T28472	Hs.7655	U2 small nuclear ribonucleoprotein auxil	1.47	1.61	1.73
	447940	D86982	Hs.20060	KIAA0229 protein	1,47	1.93	1.72
	445106	AA377165	Hs.44833	ESTs .	1.47	1.56	1.63
	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, impor	1.47	1.78	1.84
	432615	AA557191	Hs.55028	ESTs, Weakly similar to 154374 gene NF2	1.47	2.04	1.47
10	435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	1.47	1.76	1.83
	402294			Target Exon	1.47	1.27	1.46
	430147	R60704	Hs.234434	hairy/enhancer-of-split related with YRP	1.46	2.00	1.59
	414324	Y14768	Hs.890	lymphotoxin beta (TNF superfamily, membe	1.46	1.58	2.15
	400270			NM_000025":Homo sapiens adenylosuccinate	1.46	1.42	2.32
15	414806	D14694	Hs.77329	phosphatidylserine synthase 1	1.46	2.07	1.40
	419625	U91616	Hs.182885	nuclear factor of kappa light polypeptid	1.45	1.78	1.53
	430594	AK000790	Hs.246885	hypothetical protein FLJ20783	1.45	1.31	0.90
	419556	U29615	Hs.91093	chitinase 1 (chitotiosidase)	1.45	2.13	1.46
	453350	AI917771	Hs.61790	hypothetical protein FLJ23338	1.45	2.00	1.39
20	448412		Hs.42532		1.45		
20		AJ219083		ESTs, Moderately similar to ALUS_HUMAN A		1.37	3.17
	411619	AJ418609	Hs.71040	hypothetical protein FLJ20425	1.45	1.39	3.01
	424218	AF031824	Hs.143212	cystatin F (leukocystatin)	1.45	1.82	1.44
	450395	BE048545	Hs.161757	EST _B	1.45	2.40	1.33
25	438555	AI222089	Hs.143878	Homo sapiens mRNA for FLJ00024 protein,	1.45	1.91	1.65
25	422497	D29642	Hs.1528	KIAA0053 gene product	1.45	1.94	1.49
	400991			Target Exon	1.45	2.10	1.42
	431779	AW971178	Hs.268571	apolipoprotein C-I	1.45	1.53	0.42
	424618	L29472	Hs.1802	major histocompatibility complex, class	1.44	1.96	1.86
	423032	A1684746	Hs.119274	RAS p21 protein activator (GTPase activa	1.44	1.34	- 3.36
30	424232	AB015982	Hs.143460	protein kinase C, nu	1.44	1.28	2.94
	438291	BE514605	Hs.289092	Homo sapiens cDNA: FLJ22380 fis, ctone H	1.44	1.63	1.45
	445745	AB007924	Hs.13245	KIAA0455 gene product	1.44	1.17	1.52
	449209	BE616830	Hs.294145	ESTs	1.44	1.35	2.48
	410129	BE244074	Hs.58831	regulator of Fas-induced apoptosis	1.44	2.10	1.79
35	401284	OCETION	113.30001	Target Exon	1.44	1.71	1.44
55	422675	BE018517	Hs.119140		1.44	1.68	1.45
				eukaryotic translation Initiation factor			
	433020	AI375726	Hs.279918	hypothetical protein	1.44	1.37	2.02
	420042	AW015140	Hs.161723	ESTs	1.44	2.02	1.29
40	453878	AW964440	Hs.19025	DC32	1,44	1.69	1.44
40	427268	X78520	Hs.174139	chloride channel 3	1,44	1.45	1.96
	417386	AL037228	Hs.82043	D123 gene product	1.43	1.32	2.81
	409197	N54706	Hs.303025	chromosome 11 open reading frame 24	1.43	1.80	1.17
	411009	W37572	Hs.285864	ESTs	1.43	1.57	1.72
	433160	AW207002	Hs.134342	TASP for testis-specific adriamycin sens	1.43	1.36	1.49
45	416084	L16991	Hs.79006	deoxythymidylate kinase (thymidylate kin	1.43	2.15	1.57
	407826	AA128423	Hs.40300	catpain 3, (p94)	1.43	1.61	1.69
	439070	AI733278	Hs.7621	ESTs	1.43	2.10	1.40
	444090	S69115	Hs.10306	natural killer cell group 7 sequence	1.43	2.09	1.24
	420162	BE378432	Hs.95577	cyclin-dependent kinase 4	1.43	2.13	1.54
50	442591	AW292797	143.90017	hypothetical protein MGC10772	1.43	2.11	1.61
-	451668	Z43948	Hs.326444	cartilage acidic protein 1	1.43	1.49	1.16
	423639	AB037826	Hs.130411	KIAA1405 protein	1.42	2.08	1.51
	426234				1,42	1.57	
		BE314534	Hs.168159	apoptosis regulator			1.31
55	424263	M77640	Hs.1757	L1 cell adhesion molecule (hydrocephalus	1.42	1.88	1.63
55	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	1.42	1.46	3.18
	447126	AW150632	Hs.170307	Ral guanine nucleotide exchange factor R	1.42	1.36	1.38
	432241	AI937060	Hs.6298	KIAA1151 protein	1.42	1.58	1.98
	412471	M63193	Hs.73946	endothelial cell growth factor 1 (platel	1,41	2.09	1.29
60	434262	AF121858	Hs.12169	sorting nexin 8	1.41	3.07	1,41
60	432238	AL133057	Hs.274135	Homo sapiens mRNA; cDNA DKFZp434K1815 (f	1.41	1.82	1.43
	402474			NM_004079:Homo sapiens cathepsin S (CTSS	1.41	1.32	1.24
	419897	X90826	Hs.93649	upstream transcription factor 2, c-fos i	1,41	1.69	1.80
	417621	AV654694	Hs.82316	interferon-induced, hepatitis C-associat	1.41	1.22	1.74
	424441	X14850	Hs.147097	H2A histone family, member X	1,41	1.74	2.15
65	406663	U24683		immunoglobutin heavy constant mu	1.41	1.51	2.03
	409614	BE297412	Hs.55189	hypothetical protein	1.41	1.54	2.20
	443885	H91806	Hs.15284	ESTs	1,41	1.19	1.41
	412276	BE262621	Hs.73798	macrophage migration inhibitory factor (	1.40	1.88	1.24
	425179	AJ224442	Hs.155020	putative methyltransferase	1.40	1.84	1.47
70	418699	BE539639	Hs.173030	ESTs, Wealth similar to ALUS_HUMAN ALU S	1.40	1.27	2.79
. •	432403	AA550815	Hs.124840	ESTs	1.40	1.83	1.44
	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	1.40	1.65	2.51
	422596	AF063611 N20514	Hs.118633	2-5-oligoadenylate synthetase-like	1.40	2.57	1.44
75	435292		Hs.172965	ESTs	1.40	1.91	1.43
75	419424	86041820	Hs.38516	Homo sapiens, clone MGC:15887, mRNA, com	1.39	1.57	1.37
	425068	AL048716	Hs.154387	KIAA0103 gene product	1.39	1.27	3.18
	426020	AL110195	Hs.166017	microphthalmia-associated transcription	1.39	2.26	1.40
	427740	8E242604	Hs.180616	CD36 antigen (collagen type I receptor,	1.39	1.76	0.99
00	403022			C21000178*:gij7341207 gb AAF61215.1 AF22	1.39	1.74	1.36
80	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (	1.39	1.72	1.39
	410103	AW903666		gb:CM4-NN1032-280300-122-b02 NN1032 Homo	1.39	1.46	1.34
	439180	A1393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	1.39	1.35	1.79
	414057	AI815559	Hs.75730	signal recognition particle receptor (d	1.39	1.49	1.17
				- · · · · · · · · · · · · · · · · · · ·			

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	416511	NM_006762	Hs.79356	Lysosomal-associated multispanning membr	1.39	1.52	1.44
	423984	AF163825	Hs.136713	pre-B lymphocyte gene 3	1.39	3.02	1.52 1.39
	448484	BE613340	Hs.334725	Homo sapiens, Similar to RIKEN cONA 9430	1.38 1.38	1.81 1.35	0.99
_	436856	AI469355	Hs.127310	ESTs serologically defined colon cancer antig	1.38	1.26	4.14
5	437179 437912	AA393508 BE278594	Hs.5912	F-box only protein 7	1.38	2.03	1.40
	448664	AIB79317	Hs.334691	splicing factor 3a, subunit 1, 120kD	1.38	1.52	1.38
	439981	AI348408	Hs.124675	ESTs, Weakly similar to T14742 hypotheti	1.38	1.48	1.38
	432812	AI935412	Hs.50162	ESTs	1.38	1.43 1.87	2.18 1.28
10	406826	AW516005	Hs.84298	CD74 antigen (invariant polypeptide of m	1.38 1.38	1.46	2.23
	446962	AI351421	Hs.279709	muscle specific ring finger protein 1  Rho guanine exchange factor (GEF) 11	1.38	1.98	1.50
	408787 428044	NM_014784 AA093322	Hs.47822 Hs.301404	RNA binding motif protein 3	1.38	1.29	2.04
	412926	AI879076	Hs.75061	macrophage myristoylated alanine-rich C	1.38	1.52	2.62
15	418255	AW135405	Hs.37251	ESTs	1.38	1.44	1.75 1.37
	419745	AF042001	Hs.93005	strg (chicken homolog), zinc finger prot	1.37 1.37	1.51 1.98	1.45
	448977	X91809	Hs.22698	regulator of G-protein signalling 19	1.37	1.75	1.31
	422609	Z46023 F11872	Hs.118721 Hs.4892	sialidase 1 (lysosomal sialidase) Homo sapiens clone 24841 mRNA sequence	1.37	1.38	2.80
20	435458 425081	X74794	Hs.154443	minichromosome maintenance deficient (S.	1.37	1.61	1.62
20	429849	U33053	Hs.2499	protein kinase C-like 1	1.37	1.71	1.45
	407103	AA424881	Hs.256301	hypothetical protein MGC13170	1.37	1.62 1.86	1.82 1.37
	452923	BE276018	Hs.288940	five-span transmembrane protein M83	1.37 1.37	1.59	1.37
25	453941	U39817	Hs.36820	Bloom syndrome serine/threonine kinase 10	1.37	1.82	1.48
25	446755 439755	AW451473 AW748482	Hs.16134 Hs.77873	B7 homolog 3	1.36	2.10	1.35
	447630	AI660149	Hs.44865	tymphoid enhancer-binding factor 1	1.36	1.79	1.67
	413821	AA844126	Hs.55964	ESTs, Wealdy similar to C4HU complement	1.36	1.91	1.39 0.33
	445823	A1478563	Hs.145519	FKSG87 protein	1.36 1.36	1.29 1.33	2.01
30	456760	AW961251	Hs.127828	guanine nucleotide binding protein (G pr	1.36	1.66	1.46
	402542	414027420		Target Exon ESTs	1.36	2.00	1.36
	451050 444501	AW937420 AW247624	Hs.11342	ninjurin 1	1.36	1.59	1.14
	413291	NM_006278	Hs.75268	siatytransferase 4C (beta-galactosidase	1.36	2.55	1.42
35	438129	AA778647		gb:af87d03.s1 Soares_testis_NHT Homo sap	1.36	1.46	1,32 4,95
	428398	AI249368	Hs.98558	ESTs	1.36 1.36	1.25 1.84	1.48
	439704	AW020018	Hs.293267	ESTs	1.36	1.27	0.58
	428782	X12830	Hs.193400 Hs.46801	interleukin 6 receptor GCN5 (general control of amino-acid synt	1.35	2.10	1.29
40	437316 439246	A1683454 A1498072	FIS.40001	membrane-associated tyrosine- and threon	1.35	1.81	1.63
40	403409	74450072		NM_005929:Homo sapiens antigen p97 (meta	1.35	1.64	1.35
	446342	BE298665	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (fr	1.35	1.37 1.91	2.33 1.35
	437740	AA810265	Hs.122915	ESTs	1.35 1.35	1.53	1.10
15	423973	AF038461	Hs.136574	arachidonate 12-lipoxygenase, 12R type thymidine kinase 1, soluble	1.35	1.89	1.57
45	421506 457760	BE302796 AA668123	Hs.105097 Hs.134170	ESTs	1.35	2.03	1.43
	439769	AA448828	Hs.30596	Homo sapiens mRNA full length insert cDN	1.35	2.06	1.41
	406824	AW515961	Hs.84298	CD74 antigen (invariant polypeptide of m	1.35	1.77	1.27 0.51
50	429852	AB010445	Hs.225948	small inducible cytokine subfamily A (Cy	1.35 1.34	1.52 1.65	1.61
50	421777	BE562088	Hs.108196	HSPC037 protein transporter 2, ATP-binding cassette, sub	1.34	1.77	1.02
	400328	X87344 AA913059	Hs. 104433	Homo sapiens, clone IMAGE:4054868, mRNA	1.34	1.77	1.15
	421445 428977	AK001404	Hs.194698	cyclin B2	1.34	1.53	1.82
	418283	S79895	Hs.83942	cathepsin K (pycnodysostosis)	1.34	1.33	3.45
55	425848	BE242709	Hs.159637	valyl-tRNA synthetase 2	1.34 1.34	2.11 1.27	1.32 1.97
	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	1.34	1.61	1.75
	422758		Hs.284180 5 Hs.105927	protocadherin gamma subfamily C, 3 stem cell growth factor, lymphocyte secr	1.34	1.75	1.81
	421579 416374			annexin A5	1.34	1.68	1.55
60	451092		Hs.13766	Homo sapiens mRNA for FLJ00074 protein,	1.34	1.87	0.81
-	424778		Hs.153042	lymphocyte antigen 9	1.34	1.94 2.19	1.42 1.48
	421703		Hs.1416	Fc tragment of IgE, low affinity II, rec	1.33 1.33	1.96	1.18
	416700			cathensin D (lysosomal aspartyl protease phosphoinositide-3-kinase, catalytic, de	1.33	1.70	1.60
65	425923 418803		6 Hs.162B08 Hs.88556	histone deacetylase 1	1.33	1.28	2.65
UJ	427730			granulin	1.33	2.09	1.35
	441174			Homo sapiens, clone IMAGE:3050476, mRNA,	1.33	2.05	1.33
	412738		Hs.74562	siah binding protein 1; FBP interacting	1.33 1.33	1.85 1.31	1.35 2.06
70	424528			ESTs, Weakly similar to KIAA1204 protein	1.33	1.77	1.43
70	422599			non-metastatic cells 1, protein (NM23A)  DNA replication factor	1.33	1.91	1.39
	422997 415323			neutrophil cytosolic factor 2 (65kD, chr	1.33	1.16	0.60
	409119			hypothetical protein MGC2574	1.33	1.52	1.34
	41965			hypothetical protein	1.32	2.07	1.29
75	41569	7 Al365603	Hs.198271	DKFZP566I1024 protein	1.32 1.32	2.00 2.07	1.33 1.39
	43435			F-box only protein 6 bromodomain adjacent to zinc finger doma	1.32 1.32	1.25	1,91
	44293			hypothetical gene DKFZp434A1114	1.32	1.63	1.44
	44402 45697		Hs.169401	apolipoprotein E	1.32	1.47	0.85
80	44773			MAD2 (mitotic arrest deficient, yeast, h	1.32	2.51	1.23
	44861	0 NM_0061	57 Hs.21602	nel (chicken)-like 1	1.31	3.12	1.31 1.65
	42649			aryl hydrocarbon receptor v-myb avian myeloblastosis viral oncogen	1.31 1.31	1.21 1.68	1.05
	42758	4 BE41029	3 Hs.179718	A-tilan saran tilanmenere are menden	1.31	1.00	771

	417059	AL037672	Hs.81071	extracellular matrix protein 1	1.31	1.30	2.14
	407777	AA151071	Hs.71465	squalene epoxidase	1.31	1.45	1.43
	408536	AW381532	Hs.135188	ESTs .	1.31	1.38	0.90 1.49
-	410423	AW402432	Hs.63489	protein tyrosine phosphatase, non-recept	1.31	1.81	1,31
5	422486	BE514492	Hs.117487	gene near HD on 4p16.3 with homology to	1.31 1.31	1.63 1.69	1.29
	409154	U72882	Hs.50842	interferon-Induced protein 35 apurinic/apyrimidinic endonuclease(APEX	1.31	1.74	1.39
	425003	AF119046	Hs.154149	phosphoprotein regulated by mitogenic pa	1.31	1.43	0.94
	441406 421975	Z45957 AW961017	Hs.7837 Hs.6459	hypothetical protein FLJ11856	1.30	2.53	1.34
10	417361	NM_000275	Hs.82027	oculocutaneous albinism II (pink-eye dil	1.30	1.38	1.38
10	425676	AW410656	Hs.159161	Rho GDP dissociation inhibitor (GDI) atp	1.30	2.11	1.36
	427289	AI097346		phosphoserine aminotransferase	1.30	2.27	1.48
	427747	AW411425	Hs.180655	serine/threonine kinase 12	1.30	1.68	1.79
	422296	AA360231	Hs.114416	Homo sapiens, Similar to transducin (bet	1.30	1.50	1.30 2.13
15	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	1,30 1,30	1.42 1.58	1.30
	423062	NM_003655	Hs.5637	ESTs	1.30	1.77	1.35
	439740	AL365512	Hs.6657	hypothetical protein bK1048E9.5 hypothetical protein MGC2771	1,30	1.57	1.51
	409340 416920	BE 174629 AA 176455	Hs.321130 Hs.80475	polymerase (RNA) II (DNA directed) polyp	1.30	1.67	1.44
20	430451	AA836472	Hs.297939	cathepsin B	1.30	1.49	1.16
20	457400	AF032906	Hs.252549	cathepsin Z	1.30	1.40	1.21
	403506			C3001912:gij6677647 ref[NP_033602.1  zin	1.29	1.88	1.26
	424867	AI024B60	Hs.153591	Not56 (D. melanogaster)-like protein	1.29	2.64	1.31
0.5	408815	AW957974	Hs.25485	hypothetical protein FLJ22341	1.29	1.79	1.36 1.80
25	416322	BE019494	Hs.79217	pyrroline-5-carboxylate reductase 1	1.29 1.29	1.59 2.01	1.43
	440795	AA262133	Hs.99741	ESTs, Weakly simitar to PNL1_HUMAN PEANU protein Itinase C substrate 80K-H	1.29	1.70	1.34
	421846	AA017707	Hs.1432 Hs.1973	cyclin F	1.29	1.63	1.50
	425966 446766	NM_001761 AF083208	Hs.16178	apoptosis antagonizing transcription fac	1.29	1.71	. 1.40
30	406827	AA971409	113.10110	gb:op92c04.s1 NCI_CGAP_Lu5 Homo sapiens	1.29	2.04	1.35
-	418613	AA744529	Hs.86575	mitogen-activated protein kinase kinase	1.29	1.41	1.94
	443086	AW977125		sine oculis homeobox (Drosophila) homolo	1.29	1,24	1.29
	439146	AW138909	Hs.156110	immunoglobulin kappa constant	1.29	1.99	1.36
~~	434398	AA121098	Hs.3838	serum-inducible kinase (SNK)	1.29	1.18	1.32 2.19
35	418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	1.29 1.29	1.31 1.59	1.36
	400261	105030	U- OFA	Eos Control  #### (Fession managharahata) dahyutmaanas	1.29	1.67	1.53
	413781	J05272	Hs.850	IMP (inosine monophosphate) dehydrogenas gb:PM2-DT0023-080300-004-a04 DT0023 Homo	1.28	1.26	1.07
	412315 420372	AW936678 AW960049	Hs.293660	Homo sapiens, clone IMAGE:3535476, mRNA,	1.28	1.85	1.40
40	425449	X52056	Hs.157441	spleen focus forming virus (SFFV) provir	1.28	1.45	1.14
40	454478	AW805749	14.151111	superoxide dismutase 2, mitochondrial	1.28	2.29	1.07
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	1.28	1.20	0.93
	406016			Target Exon	1.28	1,47	1.31
4.5	449509	BE246434	Hs.289026	guanine nucleotide binding protein (G pr	1.28	1.26	3.02 1.23
45	426059	BE292842	Hs.166120	interferon regulatory factor 7	1.28	1.76 1.60	1.23
	412773	H15785	Hs.74573	similar to vaccinia virus Hindlil K4L OR	1.28 1.28	1.51	1.22
	452700	AI859390	Hs.288940	five-span transmembrane protein M83 ESTs	1.28	2.02	1.08
	408543 408822	N78098 AW500715	Hs.44289 Hs.57079	Homo sapiens cDNA FLJ13267 fis, clone OV	1.27	1.28	3.51
50	425069	AA687465	Hs.298184	potassium voltage-gated channel, shaker-	1.27	1.66	1.39
50	444681	AJ243937	Hs.288316	chromosome 6 open reading frame 9	1,27	1.47	1.55
	430794	NM_000166		gap junction protein, beta 2, 26kD (conn	1.27	1.81	0.89
	430637	BE160081	Hs.256290	S100 calcium-binding protein A11 (calgiz	1.27	1.35	1.68
٠	440502	AI824113	Hs.78281	regulator of G-protein signalling 12	1.27	1.67 1.30	1.31 1.30
55	441598	AI733219	Hs.58262	ESTs	1.27 1.27	2.00	1.16
	431921	N46466	Hs.58879	ESTS	1.26	1.44	1.33
	459345	AW503672	Hs.31447	gb:UI-HF-BN0-ald-h-11-0-UI.r1 NIH_MGC_50 ESTs, Moderately similar to A45010 X-fin	1.26	1.20	1.45
	452436 426334	BE077546 BE305081	Hs.169358	hypothetical protein	1.26	1.22	1.89
60	414044	BE614194	Hs.75721	profilin 1	1.26	1.48	1.51
•	405268	00014104		ENSP000002231741:KIAA0783 PROTEIN.	1.26	1.19	2.25
	416602	NM_006159	Hs.79389	Protein kinase C-binding protein NELL2	1.26	1.19	4.03
	439529	BE293492	Hs.293984	hypothetical protein MGC13102	1.26	1.83	1.19
	421254	AK001724	Hs. 102950	coat protein gamma-cop	1.26 1.26	1.61 1.84	1.23 0.68
65	417785	X59812	Hs.82568	cytochrome P450, subfamily XXVIIA (stero	1.26	1.66	1.34
	419395	BE268326	Hs.90280	5-aminoimidazote-4-carboxamide ribonucle cholesteryl ester transfer protein, plas	1.26	1.42	1.19
	418968	NM_000078	Hs.89538 Hs.121296	ESTs	1.26	1.29	1.28
	441553 446619	AA281219 AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	1.25	1.22	0.65
70	424624	AB032947	Hs.151301	Ca2+dependent activator protein for secr	1.25	1.17	2.95
, ,	450087	BE293180	Hs.24379	MUM2 protein	1.25	1.78	1.28
	429604	AK001851	Hs.210778	hypothetical protein FLJ10989	1.25	1.18	1.25
	429380	AF023268	Hs.200600	secretory carrier membrane protein 3	1.25	2.22	1.25
20	440251	AW796016		Homo sepiens, clone IMAGE:3687782, mRNA,	1.25	1.90 1.32	1.39 1.53
75	416759		Hs.79741	hypothetical protein FLJ10116	1.24 1.24	1.32	1.33
	435466		Hs.29203	G protein beta subunit-like hypothetical protein FLJ11354	1.24	1.61	1.27
	450621 400214		Hs.55918	NM_007002:Homo sapiens cell membrane gly	1.24	1.88	1.32
	435013		Hs.110024	NM_020142:Homo sapiens NADH:ubiquinone o	1.24	1.76	1.25
80	414733		Hs.77171	minichromosome maintenance deficient (S.	1.24	1.82	1.42
	406851		-	major histocompatibility complex, class	1.24	1.68	1.19
	448498	AA418276		ESTs	1.24	1.73	1.29
	440087	W28969	Hs.7718	hypothetical protein FLJ 22678	1.24	1.70	1.38

					1.24	4.61	1.16
	411365	M76477	Hs.289082	GM2 ganglioside activator protein	1.24 1.24	1.61 2.65	1.24
	426502	Y07759	Hs.170157	myosin VA (heavy polypeptide 12, myoxin)	1.24	1.49	1.50
	452056	AW955065	Hs.101150	Homo sapiens, ctone IMAGE:4054156, mRNA, Homo sapiens cDNA: FLJ23111 fis, ctone L	1.24	1.17	2.10
5	427390	AI432163	Hs.268231	ESTs	1.23	1.19	4.77
5	429954	AI918130	Hs.21374	zinc finger protein	1.23	1.62	1.28
	421178 442609	BE267994 AL020996	Hs.102419 Hs.8518	setenoprotein N	1.23	2.30	1.24
	416188	BE157260	Hs.79070	v-myc avian myelocytomatosis viral oncog	1.23	1.18	0.90
	410127	AA354313	Hs.58685	CD5 antigen (p56-62)	1.23	1.68	1.23
10	452244	N33530	Hs.176674	ESTs	1.23	2.93	1.23
10	406718	AA505525	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	1.23	1.56	1.29
	436939	AA853680	Hs.5345	arginyt aminopeptidase (aminopeptidase B	1.23	1.68	1.23
	414457	AW514320	Hs.76159	ATPase, H transporting, lysosomal (vacuo	1.23	1.58	1.20
	416929	N20535		melastatin 1	1.23	1.92	1.20
15	401106			Target Exon	1.23	1.82	1.29
	408981	AW500797	Hs.49427	Gem-interacting protein	1.23	1.40	1.59 1.44
	413317	U53225	Hs.75283	sorting nexin 1	1.23	1.43 1.71	1.24
	422481	AL050163	Hs.117339	DNAX-activation protein 10	1.23 1.23	1.95	1.29
20	425455	AL137522	Hs.157777	casein kinase 1, gamma 1	1.23	2.07	1.27
20	451524	AK001466	Hs.26516	hypothetical protein FLJ10604	1.22	1.87	1.19
	414399	L47345	Hs.155202	transcription elongation factor B (SIII)	1.22	1.55	1.21
	422034	AC006486	Hs.333069	Ets2 repressor factor Interleukin 2 receptor, gamma (severe co	1.22	1.55	1.51
	434224	AA380731	Hs.84	hypothetical protein MGC861	1.22	1.49	1.46
25	429574	BE268321	Hs.208912 Hs.71819	eukaryotic translation initiation factor	1.22	1.64	1.40
23	411742	AW247593	Hs.22880	dipeptidylpeptidase III	1.22	1.63	1.30
	449027 418004	AJ271216 U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	1.22	1.24	0.71
	451481	AA300228	Hs.295866	hypothetical protein DKFZp434N1923	1.22	2.20	1.26
	422739	H20106	Hs.119591	adaptor-related protein complex 2, sigma	1.21	1.55	. 1.21
30	424326	NM_014479	Hs.145296	ADAM-like disintegrin protease, decysin	1.21	1.13	3.29
20	404186		***************************************	NM_019602:Homo sapiens butyrophilin-like	1.21	1.59	1.21
	447604	AW089933	Hs.301342	hypothetical protein MGC4342	1.21	1.25	2.00
	427979	BE379776	Hs.181309	proteasome (prosome, macropain) suburit,	1.21	1.14	1.25
	414509	AW161311	Hs.76294	CD63 antigen (melanoma 1 antigen)	1.21	1.39	1.25
35	428468	AA171388	Hs.184482	DKFZP586D0624 protein	1.21	1.66	1.22
	419700	AF084935	Hs.92357	galactokinase 1	1.21	1.63	0.74
	430948	Al347578	Hs.124015	hypothetical protein MGC2605	1.21	1.48	1.21
	448143	AF039704	Hs.20478	ceroid-lipofuscinosis, neuronal 2, late	1.20	1.75 1.54	1.23 1.29
40	448499	8E613280	Hs.77550	hypothetical protein MGC1780	1.20 1.20	1.54	1.23
40	442173	N76101	Hs.8127	KIAA0144 gene product	1.20	1.18	1.11
	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	1.20	1.83	1.19
	448230	BE395949	Hs.94814	hypothetical protein MGC2865	1.20	1.22	1.61
	403817		11- 74466	NM_015271:Homo sapiens tripartite motif-	1.20	1.15	2,01
45	411678	AI907114	Hs.71465	squatene epoxidase hypothetical protein MGC10966	1.20	1.79	1.20
43	452423	AA991724	Hs.180535 Hs.138202	serine (or cysteine) proteinase inhibito	1.20	2.34	1.20
	424046 447233	AF027866 AW246333	Hs.17901	Homo sapiens, clone IMAGE:3937015, mRNA,	1.20	1.93	1.20
	422565	BE259035	Hs.118400	singed (Drosophila)-like (sea urchin las	1.20	1.32	1.52
	446159	NM_013379		dipeptidyl peptidase 7	1.19	1.64	1.22
50	434563	AW083994	Hs.9469	pleckstrin homology domain-containing, f	1.19	1.53	1.45
	421541	NM_003942		ribosomal protein S6 kinase, 90kD, polyp	1.19	1.75	1.27
	450706	AW167578	Hs.14691	ESTs, Moderately similar to 138022 hypot	1.19	1.71	1.22
	430381	NM_006411	Hs.240534	1-acylglycerol-3-phosphate O-acyltransfe	1.19	1.66	1.21
	426329	AL389951	Hs.271623	nucleoporin 50kD	1.19	1.17 1.73	1.55 1.30
55	421612	AF161254	Hs.106196	8D6 antigen	1.19 1.19	1.75	1.18
	410182	NM_001983		excision repair cross-complementing rode	1.18	1.73	1.09
	434171	BE247688	Hs.347349	KIAA0948 protein N-acetyttransferase, homolog of S. cerev	1.18	2.13	1.22
	424837	BE276113	Hs.333034	solute carrier family 1 (neutral amino a	1.18	1.45	1.30
60	428293	BE250944	Hs.183556 Hs.172753	ESTs	1.18	1,71	1.35
UU	453754 439012	AW972580 BE383814	Hs.6455	RuvB (E coli homolog)-like 2	1.18	1.60	1.23
	422256	M64673	Hs.1499	heat shock transcription factor 1	1.18	1.51	1.28
	439863		Hs.9408	paired immunoglobulin-like receptor beta	1.18	1.89	1.18
	430513		Hs.241586	G6C protein	1.18	2.07	0.81
65	427283		Hs.174185	ectonucleotide pyrophosphatase/phosphodi	1.18	1.13	3.25
•	441648		Hs.30559	ESTs	1.18	1.56	1.23
	418219		Hs.137319	ESTs	1.18	1,77	1.23
	406422			Target Exon	1.18	1.43	1.31
	414823	AA156531	Hs.103902	ESTs, Weakly similar to A44861 keratin,	1.18	1.66	1.23
70	425720		Hs.293984	hypothetical protein MGC13102	1.18	1.58 1.74	1.15 1.21
	419250			U5 snRNP-specific protein, 116 kD	1.17	1.33	1.35
	454390			KIAA0906 protein	1.17 1.17	1.19	1.24
	428471		Hs.184510	stratifin	1.17	1.13	1.96
75	430200			geminin procellagen-lysine, 2-oxoglutarate 5-dio	1,17	1.50	1.22
75	412965		Hs.75093	TCF3 (E2A) fusion partner (in childhood	1.17	1.69	1.32
	430122			U6 snRNA-associated Sm-like protein LSm8	1.17	1.12	2.44
	430512 417080			small nuclear ribonucleoprotein polypept	1,17	1.93	1.18
	423102			chromosome 11 open reading frame 24	1.17	1.89	1.17
80	408393			ESTs	1.16	1.10	1.91
00	424292			gb:EST43554 Fetal brain I Homo sapiens c	1.16	1.61	1.21
	446759		Hs.16165	expressed in activated T/LAK lymphocytes	1.16	1.45	1.23
	42732			hypothetical protein FLJ23322	1.16	1.50	1.23

	446055	AI815981	Hs.12909	mucolipin 1	1.16	1.49	1.10
	414432	BE378174	Hs.26506	Homo sapiens done CDABP0005 mRNA sequen	1.16	1.67	1.20
	417900	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevi	1.16	1.66	1.32
_	411305	BE241596	Hs.69547	myelin basic protein	1.16	1.15	4.29
5	438930	AW843633	Hs.343261	hypothetical protein AL110115	1.16	1.37	1.34
	407239	AA076350	Hs.67846	teukocyte immunoglobufin-lika receptor,	1.15	1.82	1.17
	427458	BE208364	Hs.29283	ESTs, Weakly similar to LKHU proteoglyca	1.15	1.46	1.32
	402160			Target Exxon	1.14	1.23	1.12
10	416881	N32520	Hs.141358	ESTs	1.14	2.42	1.14
10	420223	N27807		ribosomal protein L4	1.14	1.23	1,14
	450778	U81375	Hs.25450	solute carrier family 29 (nucleoside tra	1.14	1.38	1.27
	429538	BE182592	Hs.139322	small proline-rich protein 2A	1.14	1.16	3.52
	428342	AJ739168		Homo sapiens cDNA FLJ13458 fis, clone PL	1.13	1.13	1.13
	436696	AA725678	Hs.120487	ESTs	1.13	1.22	1.13
15	448950	AF288687	Hs.9275	CGI-152 protein	1.12	1.52	1.19
	437696	283844	Hs.5790	hypothetical protein dJ37E16.5	1.12	1.31	1.08
	425009	X58288	Hs.154151	protein tyrosine phosphatase, receptor t	1.12	1.08	1.20
	412099	U64198	Hs.73165	interleukin 12 receptor, beta 2	1.12	2.93	1.12
	407951	W77762	Hs.79015	antigen identified by monoclonal antibod	1.12	1.11	3.43
20	408116	AA251393	Hs.289052	Homo sapiens, Similar to RIKEN cDNA 5430	1.12	1.50	1.12
	450296	AL041949	Hs.24756	hepatocyte growth factor-regulated tyros	1.11	1.48	1.12
	420697	AA827705	Hs.26605	ESTs	1.11	2.19	1.11
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	1.11	2.73	1.11
	418399	AF131781	Hs.84753	hypothetical protein FLJ 12442	1.10	1.43	1.14
25	450358	AB010098	Hs.24907	coronin, actin-binding protein, 2B	1.10	1.35	1.19
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	1.10	1.43	1.10
	408801	AI866590	Hs.63405	Homo sapiens, clone IMAGE:3609337, mRNA,	1.10	1.53	1.14
	402622			C1003392*:gi]12314272 emb[CAC00591.1] (A	1.10	1.59	1.06
	418661	NM_001949	Hs.1189	E2F transcription factor 3	1.09	1.82	1.09
30	442680	BE270707	Hs.8583	similar to APOBEC1	1.09	1.49	1.24
-	439702	AW085525	Hs.55964	ESTs	1.09	1.68	1.09
	423858	AL137326	Hs.133483	Homo sapiens mRNA; cDNA DKFZp434B0650 (f	1.09	1.10	1.73
	443759	BE390832	Hs.134729	FXYD domain-containing ion transport reg	1.09	1.23	1.25
	414396	BE548266	Hs.76057	galactose 4 epimerase, UDP-	1.09	1.07	1.23
35	401558			ENSP00000220478":SECRETOGRANIN III.	1.08	1.54	1.08
	428411	AW291464	Hs.10338	ESTs	1.08	1.07	6.19
	422051	AW327546	Hs.111024	solute carrier family 25 (mitochondrial	1.08	1.25	0.93
	414694	NM_015362	Hs.76907	HSPC002 protein	1.08	1.18	1.12
	453883	AJ638516	Hs.347524	cofactor required for Sp1 transcriptiona	1.07	1.15	1.31
40	420856	BE513294	Hs.205736	HLA class II region expressed gene KE2	1.06	1.47	1.08
	412265	AA101325	Hs.86154	hypothetical protein FLJ12457	1.06	1.17	1.22
	429259	AA420450	Hs.292911	Płakophilin	1.06	1.08	0.73
	417381	AF164142	Hs.82042	solute carrier family 23 (nucleobase tra	1.05	1.04	0.84
	415825	Y18024	Hs.78877	inositol 1,4,5-trisphosphate 3-kinase B	1.05	1.09	1.37
45	444438	N32755	Hs.322489	ESTs	1.04	1.13	1.05
	407394	AF005081	113.022.403	gb:Homo sapiens skin-specific protein (x	1.04	1.22	0.78
	404960	A 003001		eyes absent (Drosophila) homolog 3	1.04	1.06	1.04
	408972	AL050100	Hs.49378	DKFZP586D0919 protein	1.04	1.09	1.13
	414477	U41635	Hs.76228	amplified in osteosarcoma	1.03	1.11	1.03
50	409327	L41162	Hs.53563	collagen, type IX, alpha 3	1.03	1.02	2.33
50	435056	AW023337	Hs.5422	glycoprotein M6B	1.03	1.02	3.56
	415314	N88802	Hs.5422		1.02	1.02	4.02
	408591	AF015224	Hs.46452	glycoprotein M68 mammaglobin 1	1.02	1.02	0.05
	401203	PA 013224	NS.404J2		1.00	1.02	0.03
55	400304	AF005082	Hs.113261	Target Exon Homo sapiens skin-specific protein (xp33	1.00	1.49	0.56
55	407395	AF005082	MS. (13201	gb:Homo sapiens skin-specific protein (x	1.00	1.69	0.56
	411388	X72925	Hs.69752	desmocollin 1	1.00	3.12	1.00
	428618	AA885360	NS.03/32		1.00	1.77	1.00
	402860	A4003300		Target CAT ENSP0000239210:DJ50O24.4 (novel protein	1.00	1.53	1.00
60	437211	AA382207	Hs.5509		1.00	1.33	1.00
O	409269			ecotropic viral integration site 2B	1.00		1.00
		AA576953	Hs.22972	steroid 5 alpha-reductase 2-like; H5AR g		1.46	1.00
	409190	AU076536	Hs.50984	sarcoma amplified sequence	1.00	0.80	
	416143	A1955650		glutaminyl-peptide cyclotransferase (glu	1.00	1.96	1.00
65	401588	44400740	11. 476070	C15000180*:gij544344 sp Q05859 FOR4_MOUS	1.00	2.04	1.00
U)	419519	AI198719	Hs.176376	ESTs	1.00	1.91	1.00
	448816	AB033052	Hs.22151	KIAA1226 protein	1.00	1.82	1.00
	440270	NM_015986	Hs.7120	cytokine receptor-like motecule 9	1.00	1.15	1.00
	418618	U66097	Hs.86724	GTP cyclohydrolase 1 (dopa-responsive dy	1.00	1.66	0.74
70	422836	AL037365	Hs.194093	AKAP-binding sperm protein ropports	1.00	2.21	1.00
70	452461	N78223	Hs. 108106	transcription factor	1.00	1.61	1.00
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	1.00	1.42	1.00
	422420	U03398	Hs.1524	tumor necrosis factor (ligand) superfami	1.00	1.81	1.00
	429477	AI275514	Hs.6658	ESTs	1.00	1.67	1.00
75	454027	R40192	Hs.21527	Human DNA sequence from clone GS1-115M3	1.00	1.05	1.00
75	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	1.00	1.79	1.00
	451993	AA765776	Hs. 122983	ESTs	1.00	2.15	1.00
	416947	N23282	Hs.184341	ESTs, Weakly similar to B34087 hypotheti	1.00	1.67	1.00
	44 1606	R37263	Hs.21065	ESTs, Moderately similar to PC4259 ferri	1.00	1.87	1.00
00	442590	A#002686	Hs.130313	ESTs	1.00	2.59	1.00
80	404831			C1002937*:gil7499208[pir][T20993 hypothe	1.00	1.44	1.00
	428454	U55936	Hs.184376	synaptosomal-associated protein, 23kD	1.00	1.47	1.00
	419717	H07970	Hs.92458	G protein-coupled receptor 19	1.00	1.78	1.00.
	408611	NM_004367	Hs.46468	chemokine (C-C motif) receptor 6	1.00	1.64	1.00

	421666	AL035250	Hs.1408	endothelin 3	1.00 1.00	0.63 1.60	1.00 1.00	
	446155		Hs.159422	Homo sapiens cDNA FLJ13997 fis, clone Y7 engrailed homolog 2	1.00	2.91	1.00	
	423899		Hs.134989 Hs.21213	ESTs	1.00	1.65	1.00	
5	423130 433843		Hs.112819	FSTs	1.00	2.08	1.00 1.00	
,	458574		Hs.135265	Homo sapiens done FLB8436 PRO2277 mRNA,	1.00 1.00	1.00 1.41	1.00	
	430205		Hs.235168	carbonic anhydrase XIV	1.00	1.15	1.00	
	427335		Hs.251677	G antigen 7B ESTs	1.00	1.80	1.00	
10	439951 420248	AI347067 AI377191	Hs.124636 Hs.44714	ESTS ESTS	1.00	2.15	1.00	
10	446259	AA425204	Hs.334721	hypothetical protein FLJ13391	1.00	2.35	1.00 1.00	
	447164	AF026941	Hs.17518	vipirin; similar to inflammatory respon	1.00 1.00	1.53 1.73	1.00	
	447289	AW247017	Hs.36978	melanoma antigen, family A, 3	1.00	1.59	1.00	
1.5	408758	NM_003686	Hs.47504 Hs.63908	exonuclease 1 hypothetical protein MGC14726	1.00	1.73	1.00	
15	453745 436609	AA952989 AJ022514	Hs.131380	FSTs	1.00	1.96	1.00	
	419308	N40321		gb:yx80g07.r1 Soares melanocyte 2NbHM Ho	1.00 1.00	2.28 1.74	1.00 1.00	
	421650	AA781795	Hs.122587	ESTs	1.00	2.16	1.00	
20	459578	AW612538	Hs.304491	EST ESTs	1.00	1.66	1.00	
20	446152 449579	AI292036 AW207260	Hs.134014	ESTs, Weakly similar to T46425 hypotheti	1.00	2.04	1.00	
	418673	NM_005582	Hs.87205	lymphocyte antigen 64 (mouse) homolog (	1.00	1.75 1.85	1.00 1.00	
	415004	AA158925	Hs.240849	ESTs, Weakly similar to GBP1_HUMAN INTER	1.00 1.00	1.92	1.00	
0.5	426274	D38122	Hs.2007	tumor necrosis factor (ligand) superfami budding uninhibited by benzimidazoles 1	1.00	1.72	1.00	
25	453922	AF053306 AW965339	Hs.36708 Hs.44269	ESTs	1.00	1.52	1.00	
	417791 424905	NM_002497	Hs.153704	N1MA (never in mitosis gene a)-related k	1.00	2.02	1.00 1.00	
	416445	AL043004	Hs.79337	KIAA0135 protein	1.00 1.00	1.28 1.92	. 1.00	
	408375	AI224520	Hs.40930	ESTS	1.00	0.46	1.00	
30	406964	M21305	Hs.46320	FGENES predicted novel secreted protein Small proline-rich protein SPRK [human,	1.00	1.00	2.48	
	408522 412828	AI541214 AL133396	Hs.74621	prion protein (p27-30) (Creutzfeld-Jakob	0.98	0.98	3.24	
	422270	AF114494	Hs.114062	protein tyrosine phosphatase-like (profi	0.95 0.94	0.96 0.96	3.06 1.61	
	446488	AB037782	Hs.15119	KIAA1361 protein	0.94	0.94	0.76	
35	433435	BE545277	Hs.340959	Ts translation elongation factor, mitoch cystatin B (stefin B)	0.93	0.91	1.55	
	409402	AF208234 AF209704	Hs.695 Hs.169407	glycolipid transfer protein	0.92	0.93	2.09	
	423942 414219	W20010	Hs.75823	ALL1-fused gene from chromosome 1q	0.91	0.91	4.08 0.73	
	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	0.90 0.90	0.81 0.92	3.89	
40	417632	R20855	Hs.5422	glycoprotein M6B	0.89	0.79	0.84	
	449092	U91641	Un 474021	alpha2,8-sialyttransferase sema domain, immunoglobulin domain (lg),	0.89	0.92	3.70	
	426716 445033	NM_006379 AV652402	Hs.171921 Hs.72901	cyclin-dependent kinase inhibitor 28 (p1	0.88	0.90	2.02	
	408349	BE546947	Hs.44276	homeo box C10	0.88	0.87 0.84	0.73 0.69	
45	429345	R11141	Hs.199695	hypothetical protein	0.85 0.84	0.85	1.32	
	451621	AJ879148	Hs.26770	fatty acid binding protein 7, brain Ras association (RalGDS/AF-6) domain fam	0.84	0.88	3.37	
	417022	NM_014737	Hs.80905	Target Exon	0.81	0.71	1,00	
	405885 407788		Hs.38991	S100 calcium-binding protein A2	0.78	0.78	0.90 0.71	
50	417515		Hs.82237	ataxia-telangiectasia group D-associated	0.77 0.75	0.73 0.78	4.69	
	421100		Hs.124660	Horno sapiens cDNA: FLJ21763 fis, clone C	0.74	0.78	5.42	
	440274		Hs.7122 Hs.154424	scrapie responsive protein 1 deiodinase, iodothyronine, type II	0.70	0.75	4.29	
	425071 412719			FSTe	0.70	0.77	3.99 3.79	
55	432467		Hs.239388	Human DNA sequence from clone RP1-304B14	0.69 0.65	0.73 0.64	1.11	
	437191			serine protease inhibitor, Kazal type, 5 Homo sapiens cONA FLJ13329 fis, clone OV	0.61	0.65	3.20	
	452487		Hs.6630 Hs.73769	foliate recentor 1 (adult)	0.61	0.22	0.49	
	448133 439659			Homo sapiens cDNA FLJ14471 fis, clone MA	0.49	0.30	0.67 0.34	
60	419092		Hs.89603	mucin 1, transmembrane	0.41 0.23	0.11 0.30	0.35	
	41707	9 U65590	Hs.81134	interleukin 1 receptor antagonist	0.20	<b>5</b> .55		
	TABLE	400-						
	Pkey:	; 430. Uk	nique Eos probes	et identifier number				
65		umber: G	ene cluster numb	a.				
	Acces	sion: G	enbank accession	numbers				
	Cha.	CAT Numt	er Accession					
	Pkey 43054		BC017171 E	3C012195 NM_007126 AF100752 AL137377 Z70768 BM474	865 BG754806 AU	124376 BG7	57203 BG7644	20 BG/75028 BG824418
70	1,000	-	BM045810	AU120387 BG770238 BG686740 BG913323 B1759980 BG3	C10040MB 0666	COROR AIASRI	RR A1240408 A	1191843 AI131029 AW768399
75								
				AW245422 A1423847 A1914518 H80534 BE301004 AC35113 M018598 A1689260 AW072450 F20201 AW151405 AW5175 W52648 AA113434 BE785431 B1041981 BG832385 BG253				
80								
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	4040	17 007174		AW613399 AA503435 AA502682 N91138				
	4313	17 997174_1	. MA131001	529				
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	453912	32562_3	BMA72224 BISS6849 BISS6735 AW973032 BISS284 BISS3048 AA548765 AI926504 AA041551 AW043754 AI086702 AW008105 AA974849 AW614893 AA553737 AA916996 AW262982 AI580991 BF726843 AV693312 W35325 AA039927 BG460936 AW388482 AW388420 BF374777 W01360 N94710 H87967
5	420218	191547_1	AW958037 R42557 AU37047 AA948360 AI638005 AA459950 AI624915 AI638047 AI467856 AI521826 AA860305 AI932315 AW003092 AW271756
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	430015	713_2	00017171 D0017105 NN 007176 AF100757 A1137377 770768 RM474R65 RG754R05 AU124376 BG757203 BG754420 BG775028 BG024418
10		_	BIAD45810 AU120337 BG770238 BG886740 BG913323 B1759930 BG395998 BIAD48875 BE881070 BE313689 BE879144 BIA309834 AW245847 AI770171 BF196861 BE856897 AA463876 AI375927 AA648810 AA948193 AA490916 AI459893 AI458188 AI240408 AI191843 AI131029 AW768399
10			A12CE 10E AW22708A AW226150 RE466501 RE674599 AIR18438 AA772197 AI6S1927 AW151143 BI198825 BG819083 BM458764 BE903567
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15			AL35943 BM018598 AL689260 AW072450 F20201 AW151405 AW517572 AA773468 BG259694 BE391163 BG621529 AM21728 BG767231 BM462953 BG340524 W52648 AA113434 BE785431 BI041981 BG832385 BG253168 BG759470 BF369329 BF981332 BE259418 BE785738 BI091658 N72512
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			ADADDAA AADDDADD AAADDDD AADDSTIR AIRATREE AIRTIETO AARIAARE AIDSTIND ROTTOA AATESEOS AATZ4593 AID18399 AID37550 AAA911UJ
20			AW008188 R07703 AA989120 AA746235 AW029893 AA789102 AU185751 AW971465 AA489681 AW971893 AW612086 BE077936 BI860809 BE002760 BG746251 BE962912 BM454584 AL134894 BF104082 H80591
	425231	235504_1	A 4 FORMACA INCOMESTICA A A ESTRICE A A EREADO A MAISTREAD
	417282	2142_2	AKU25474 U11233 AF141304 BM24202 AL539879 AL554793 AL543707 AL549509 BI753328 BG756797 BI856494 BE901116 AL556989 AU133347 BI838505 AW949559 BM012604 BG773980 BG661309 BI260149 BF436764 BG983060 BF822225 BI059728 BF917666 BF917609 BF91474 D31003
25			A 4 3 2 4 3 10 A 14 3 A 4 CE DIANGROSS DESCRIPE DESCRIPES REARRIES DESCRIPES DE 10 1 A 14 3 A
			A193230 A123522 AI656594 A128758 AA975916 AI885224 A1264922 AA256604 AA659637 BE218707 AA195203 AW999239 AW139706 N31717 AW205941 R95955 N39147 BM015411 AL576975 BF689524 AL563130 BI858155 AA417889 AL513995 AL568815 AU160693 AA836028 H84388
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30	406687	0.0	BM011139 AW675130 BEZ76045 BF933396 AL517803 AA886367 BI030596 BG477193 BF973867 M31126
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35			DEDACO 2 A1276555 DE 106021 AA700055 AA609305 AA772596 A1635758 A1635749 H95459 AW610290 BE464994 AA527135 BF3/48U2 A18UU1/5
			AW195227 A189676 BF802049 AL513632 AL554911 AL538845 BE297273 AA315321 BM451920 BE269268 BE292835 BE018128 BG755713 BM041095 BG677009 AL039691 BF995709 BE735586 BE296453 BG393609 BG824453 AL567522 AI745257 AW388641 AW301265 AI141144
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	430441	1438_6	BG108218 BE560548 AW380115 BE269629 AI911518 AW380113 AA302964 AA455001 AI276529 AI685597 AA970496 D61084 AW380068 AW380080 R00283 C15236 AW327776 D80759
45	432810	101919_1	BG292389 C06094 AI668930 AW104534 AA310513 AA830127 AW134897 AA046953 AW965490 AI810530 BF092924 AA334151 AA334725 D31302 R20723 AA263003 BI824635 AI276287 AI684428 AI524234 AI335035 AW014704 AI911443 AA972102 AI367512 AI126670 AW016017 AI286003
	•		R20723 AA263003 BIB24535 AI276287 AI684426 AI524234 AI533033 AW014104 AST1445 ACS72124 ACS73124 ACS731
	446040	050303.4	R46187 BE929954 AA333976 D63102 BF744491 AJ362520 D25917 AJ670784 AJ742347 AW269789 AJ270700 AW610541 AW793036 AW793035 AW610540 AW362220 AW362166 AW362214
50	446019	658727_1	AM/20222 AM/202229 AL 110927
	453331	16559_1	BGS71303 AA410586 AA035018 BG572117 BG620022 AA147247 BG005785 BG014448 R31981 H02668 H12498 R36203 BF992089 R73999 T49904 R75732 BI057974 T53681 AA147933 N50695 R68588 R25671 R31935 R25110 R36105 AK055628 BE157467 AW663674 AA190993 H01642 BF510304
			A ACCOME A AZACOCO ALLEGORA A ADODESA RICEZZERA AIRORRAZO AIRORRAZO AIRORRAS AAA11449 ALBZEZO AAA76929 ALBZEZO AABUSDOO RIZORZ
55			AJ360919 AJ350463 AW069127 AA411621 AA742532 H12451 BE208298 H03612 H12839 N58781 R75957 BF996484 AJ240665 BF989591 BI056086 BC001590 BF107035
55	429978	35194_2	BE738825 BE738323 BM126944 AW629678 AW265195 AI916735 AI394255 AI573090 AI354442 AW612857 AI339558 AI919424 AI377532 AI354441 AI308821 AA772275 AW065215 AI589705 AI336532 AA806547 AV682125 H93575 AW071172 AW769904 AI863985 AW265018 AW196655 D79662
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60		****	AW963196 C06195 AI678018 BC014081 NM_000593 X57522 L21208 L21207 L21206 L21205 L21204 AL561404 AL546423 AL560492 AL556882 AL541576 AL550654 BI823519
60	452203	2630_1	DITTODES AL SEADED DIARDONE ALSOAGES AWYSES AWYSES AND REASON RESPONSE BERNASON FOR THE FIRST BANGES AWYSES AWYSES AWYSES AND RESPONSE AND FOR THE FIRST BANGES AWYSES AWY
			BC742981 AA279685 AA847441 AA313737 BF172639 BF897216 BF914190 BF903647 S70277 AI569694 AW073296 AI361433 AA564544 AA487429 BE858232 AA838610 AI539114 AI719375 AI829129 BG057675 AI423422 AU158860 BE300655 AW170777 AA566956 AL571889 AL556850 AL576404
			AL 502000 DIZECEAA DEZAZZOL DERFEGGA AANSAASR AARSAASR AARSAASA AARSAASA RERIGSZZ AL 577635 AI479850 AW150377 AU154395 AW9512/1 AIU32220
65			AIB19778 AJ346733 AW771150 AW512525 AI249904 AA279809 AJ352549 AW512517 BG056280 AA521222 BE271141 AL581932 AL541575 BI819184 AV660190 AL556475 AI620020 AW089888 AW079179 Z21518 AA687601 F04651 AI783961 T57198 AI433367 T78652 AL554968 AA365648 AL582619
			DEBTAGNI RERNAGGO AL 574458 RM145502 AL266514 AL538823 AL475626 AA948210 AA884054 AA487637 AA031844 AA535221 AW794256
			AW361447 BE788505 AI682892 AA830989 AA852356 AA653084 BMD09154 AA135727 H05927 H23433 R42244 N79997 AW366665 AW366601 AA678742 AL556474 AA135770 BE774050 BF914200 H88457 AA627746 BI560216 BI753586
70	458098	23945_1	AI082245 BE467534 AI797130 BE467063 BE467767 BE218421 AI694996 BE327781 BE327407 BE833829 AA989054 AA459718 BE833855 BE550224 AA832519 AF086393 AV733386 BE465409 N29245 W07677 AA482971 BE503548 H18151 AA461301 W79223 W74510 AI090689 AL600773 AL600781
			MACANA DARANG DAALRA RENTLESA AWRRERST A1276145 A1276696 H97808 N20540 A1468553
	424399	2196_1	NM, 058173 AF414087 W7Z837 BF742809 AW070916 BE092421 AI905687 AA340069 BE074512 AI905623 AI905633 BG202312 W7Z838 AI139456 BG218084 BE926938 BE186013 AW176044 AW291950 BG185269 BG197186 BG192597 BG183176 BG207535 AI127172 BE815819 AI905624
75			P75793 RC202313 AI905R37 RE815R53
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	400222 410600		NM_002082 L16862 BG828886 BE793217 BE994084 BE284326 BE297203 BE394617 BE535127 BE535100 F12351 BG825102 F10710 BF347859 AW499616 AA191322 AW499617 AL601010 AW575742 AA729043 BE463447 AA086179 BE549623 Al335824 AW408712 BM149172
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			BG775668 BG680336 AW991605 AA455904 AW265494 AW265432 BF911380 AA456370 BF911379 AA195677 BF914311 BF913866 BG775059
	417324	292720_1	DCG51874 A1577169 AA072070 AM085313 RIDG7611 HG119864 WU2337 D0U304
	453613	10943_2	TO 100 100 100 100 100 100 100 100 100 10
5	411825	7891_1	ALCONCOL ALCONARD RETUINIBER BL2233300 ATTOURS AND TOUR AND THE PROPERTY A
			AV000224 DEGRADAR AWN15634 AL3/3336 AV00012 AV00030
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			BEZ64146 AWZ65931 AA16541 AI652537 AI803674 AA631209 AI923786 AWZ05704 AI354260 AI198865 BF-593366 AWZ6173 AR655931 AA16541 AI652537 AI803674 AA631209 AI923786 AWZ05704 AI354260 AI198865 BF-593366 AWZ61734 AR655981 AI375483 BGZ21393 AI867580 BE893700 BFZ42879 BE251315 AA534659 AA94551 BI047923 BGG949898 BFZ46869 BI085069 BM007035 AA665981 AI375483 BGZ21393 AI867580 BE893700 BFZ42879 BE251315 AA534659 AA94551 BI047923 BGG949898 BFZ46869 BI085069 BM007035 AA665981 AI375483 BGZ21393 AI867580 BE893700 BFZ42879 BE251315 AA534659 AA94551 BI047923 BGG949898 BFZ46869 BI085069 BM007035 AA665981 AI375483 BGZ21393 AI867580 BE893700 BFZ42879 BE878335 AA121664 AI146666 BI026299 AI872956 AA788642 AA128025 AW612345 R12769 W92325 R40084 AA191625 D51044 AA599257 BE878335 AA121664 AI146666 BI026299 AI872956 AA788642 AA128025 AW612345 R12769 W92325 R40084 AA191625 D51044 AA599257 BE878335 AA121664 AI146666 BI026299 AI872956 AA788642 AA128025 AW612345 R12769 W92325 R40084 AA191625 D51044 AA599257 BE878335 AA121664 AI146666 BI026299 AI872956 AA788642 AA128025 AW612345 R12769 W92325 R40084 AA191625 D51044 AA599257 BE878335 AA121664 AI146666 BI026299 AI872956 AA788642 AA128025 AW612345 R12769 W92325 R40084 AA191625 D51044 AA599257 BE878335 AA121664 AI146666 BI026299 AI872956 AA788642 AA128025 AW612345 R12769 W92325 R40084 AA191625 D51044 AA599257 BE878335 AA121664 AI146666 BI026299 AI872956 AA788642 AA128025 AW612345 R12769 W92325 R40084 AA191625 D51044 AA599257 BE87835 AA121664 AI146666 BI026299 AI872956 AA78864 AA128025 AW61234 AW61234 AA128025 AW61234 AW
			AA128025 AW612/345 R12/05 V132225 R12/05 V13225 R12/05 R1324905 AV747031 AA128068 BF19623 A127591 A435105 A354905 AV747031 BC021240 BF430978 BC056212 AW874052 BI856040 A1572156 A1914600 A1002736 BM023413 H91902 AL563177 AL529967 BM023140 BE391587 BC021240 BF430978 BC056212 AW874052 BI856040 A1572156 A1914600 A1002736 BM023413 H91902 AL563177 AL529967 BM023140 BE391587
15	442591	58995_1	PC761313 RE377571 RH95388 BE309300 H31031 DE301300 DE30130 DE3
	410103	366775_1	BG003993 AW589921 AW892489 AW9U3000
	437179	12239_1	AA134107 BM023515 AA917504 AH593222 AH593419 AA917040 W90430 A1342984 A1378957 AL036486 AW020068 B1491093 BF476021 R41226
20			AID28415 AID/4114 BG690305 BEAVION AID40988 R54266 R31422 R56631 F04125 C02343 AA115589 R56480 AI400988 R54266 R31422 BM453041 AA760783 BE218582 AI340046 AW166131 BF515854 AI530296 AA461307 AI090881 AW023059 AA155797 AA115486 AL597396 BM453041 AA760783 BE218582 AI340046 AW166131 BF515854 AI530296 AA461307 AI090881 AW023059 AA155797 AA115486 AL597396
	451050	11847_4	AMBROANA AMRO77/70 AA137(DZ AAU133/4 DG0154/0 DG154/0
25	438129	497522_1	BES04404 AA778647 BF431889 AW070999 BG17012 BG18712 BG18712 BG1871 BG1875 A3861301 A1674602 BF001506 AW004996 A1446292 A189883 A1608601
25	439246	388_5	AW131794 AI356096 AI433040 BG05/016 AI639100 AI 578056 AA316669 RER04796 AA768324 AI285396 BG745142 BG325246 BG475289 AL580901
			4 A 022/45 A 4 222/68 RFING(/42 AW/2) 1003 DF 343017 DE 01 1003 D 343012 A 022/22 AW/2) 2072 AW/2) AW/2) AW/2
30	427289	1820_2	**************************************
			AW612240 AA505495 AA515380 BG76075 AV3645 B1361407 B1018403 RE376945 T75578 BF933325 BF932853 BG502266 AW868934 AV663504
			BIO18121 N41953 BF933343 BF93267 1 H06554 KH40 12 Dr 05754
35	406827 443086		BE896316 BC619393 AA187888 AW753172 BE896316 BC619393 AA187888 AW753172 BE896316 BC619393 AA187888 AW753172 BE896316 BC619393 AA187888 AW753172
	400261	23110_1	BC006097 XUSUBO NM_UCTU WILSON XXIVSTRO41 AA909398 AW768606 AI357070 AI865365 AW014799 AI767973 AW518041 AA909398 AW768606 AW936678 AW936821 AW936883 AW936822 AW936781 AW936817 AW936811 AW936653 AW936823 AW936685 AW936815 AW936817 AW936817 AW936811 AW936653 AW936823 AW936828 AW936818 AW936819 AW9368
	412315	1163860_1	AW936678 AW936682 AW936682 AW9366732 AW936730 AW936762 AW936682 AW936732
40	454478		AW796921 AW798102 AW805749 AW805072 BF965000 AW79650 B B B B B B B B B B B B B B B B B B B
	459345 40021		AW853325 AW503672 AK59839 BE897640 BE907077 BC003059 BC017245 BC010733 BM423383 AL537826 AL580324 BG749884 BE910412 BI085225 BG830374 AK59839 BE897640 BE907077 BC003059 BC017245 BC010733 BM423383 AL537826 AL580324 BG749884 BE910412 BI085225 BG830374 BG765711 BE513420 BE513706 AW249005 BE378229 BE250756 BG389441 BF998736 H61321 BF869238 BG979991 H49658 AA353290 D64154 BG765711 BE513420 BE513706 AW249005 BE378229 BE250756 BG389441 BF998736 H61321 BF869238 BG979991 H49658 AA353290 D64154 BG765711 BE513420 BE513706 AW249005 BE378229 BH208270 BI546248 BG750170 BG480128 AL561553 BI559389 BG762029 BG741197 BI551200
			014470420 AT EXDORR RITHARY AT 2003244 DIRECTOR OF THE PROPERTY OF THE PROPERTY RITHARD AND ACCORD DISCRETE RITHAR
45			DI750061 RG751116 RE905428 BG704402 AC322114 BG701429 BG70402 AC322114 BG704039
			BG573991 BG389305 BF971754 BG903059 BE754960 BF811388 D31335 AW951318 BF992435 BF811453 NM_0070UZ A318634
			AL574934 AL523534 AL523534 AL52454 AL521769 AL524508 R13328 BC489456 BF102495 BF693420 AL526597 BG104181 BG740214 BE393189 Al966312
50			HE LEGE AWNELLED RINNER AVYSOOLS DOODS AVYSOOLS AND AVYSOOLS AND AVYSOOLS A
	40685 44845		AA60978A R97304 BG167206 AA677217 A1703389 A1051577 A1912137 H39571 AA650047 A1399798 H24807 AA341614 BG945259 A1074162 AW960920 BG167206 AA677283 AA677217 A1703389 A1051577 A1912137 H39571 AA650047 A1399798 H24807 AA341614 BG945259 A1074162 AW960920 AA628934 AA659498 AA699917 H14450 H21758 H39576 AA095608 A1049973 BG054505 BG319545 A1742408 AA421324 A1580138 A1375883 AA628934 AA659498 AA699917 H14450 H21758 H397376 AA095608 A1049973 BG054505 BG319545 A1742408 AA421324 A1580138 A1375883 AA628934 AA659498 AA699917 H14450 H21758 H397376 BA77368 A1373751 A779885 A1801494 BE349021 A1220937 AW338397 AA253409 AA418327
55		-	BG167205 AA6599498 AA6599617 H14450 H21758 H39576 AA095608 AIQA9973 BG064505 BG318345 AI742408 AA461323 AA55949 AA628934 AA6599498 AA699617 H14450 H21758 H39576 AA095608 AIQA9973 BG064505 BBC349021 AIZ20937 AW338397 AA253409 AAA18327 AI374848 AI367657 AI374767 AI304678 AA007357 BF477168 AI373751 AA779885 AI801494 BE349021 AIZ20937 AW338397 AA253409 AAA18327 AI374848 AI367657 AI374767 AI3747674 AI475074 AI475079 AI77478 AIR747847 AIR
55		29 14596_3	A872682 A1572030 A1521517 A157294 A11600 A1260 A0292 N33332 N33330 N20535
	4169 4192		1 BG755078 BI226909 N41827 AW404060 Bi050921 TH 1233 AM767046 AA815039 AW403510 AI868663 AA815462 AA235654 AW292253
60	) .		AW959582 AV725205 AW959578 AA300091 W24553 100710 AW1
	4242 4202		4 NOTEO AA256634 HEZ/DJZ4
	428		DEALGOOG AW118719 AUSS2765 AW500000 AW570550 AUGS57 TT AMAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA
6.	5		AW070509 AIS21500 ALDX295 AA019337 AA01315 A301151 A3011618 AW291137 BI061872 BI069498 AA134476 AW084888 AA036967 AW370823 155263
			01002756 AAARG664 RF827261 W74741 BF903100
	428	394 27110_ 618 2668_1	PC017009 RIS26643 BG715794 BG722097 BIADUTOT DG773-03 TISECOT TOTAL PROPERTY PROPERT
7	0	5143 40539_	
	410	,,,,,	AW342041 BG217293 BE619664 BE403807 AV143003 AR703247025 B AA262267 AI969523 N25559 AI760218 BG217318 BF893160
_	_ 419	3308 24992	1 NAN321 AA236322 AA236215
7		6152 28579 9092 4406_	
			RF111429 GRIDGE I KW_G12500 DE 200005 GRESSES CO.
Q		ABLE 49C: sey:	Unique number corresponding to an Eos probesel  Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA  Sequence source. The 7 digit numbers at al. (1900) Network 417 489-495.
C	Re		Sequence source. The 7 digit numbers in ruis country are destroated with the sequence of the s
	St	rand:	Indicates DNA strand from which exons were predicted.
			531

	Mt_position	: Indic	ates nucleotide	positions of predicted exons.				
	Pkey	Ref	Strand	Nt_position				
	402075	8117407	Plus	121907-122035,122804-122921,124019-124	6			
5	405451	7622517	Minus	145949-146227				
	401747	9789672	Minus	118596-118816,119119-119244,119609-119	76			
	401454	9186923	Minus	114659-114832				
	405545	1054740	Plus	118677-118807,119091-119296,121626-121				
	401780	7249190	Minus	28397-28617,28920-29045,29135-29296,294	1			
10	403328	8469086	Minus	120428-120703				
	405547	1054740	Plus	124361-124520,124914-125050				
	403532	8076842	Minus	81750-81901				
	400750	8119067	Plus	198991-199168,199316-199548				
15	405506	6466489	Ptus	80014-80401,80593-81125 277132-277595				
13	400533 405779	6981826 7280331	Minus Minus	33048-33856				
	402779	2996643	Minus	4727-4969				
	401781	7249190	Minus	83215-83435,83531-83656,83740-83901,847	3			
	401994	4153858	Minus	42904-43124,43211-43336,44607-44763,45				
20	403969	8569909	Plus	31237-31375,32405-32506	•			
	401760	9929699	Plus	83126-83250,85320-85540,94719-95287				
	401797	6730720	Plus	6973-7118				
	401151	9438288	Plus	30848-31228				
	404872	9650523	Minus	18540-18718				
25	402876	9864669	Plus	5679-6027,7485-7584				
	405204	7230116	Ptus	126569-126754				
	402294	2282012	Minus	2575-3000				
	400991	8096825	Plus	159197-159320			_	
30	401284	9800819	Minus Minus	101307-101421 53526-53628,55755-55920,57530-57757				
30	402474 403022	7547175 3132351	Plus	92097-92864				
	402542	9801558	Minus	67076-67594				
	403409	9438598	Plus	6860-7054,12573-12771				
	403506	7596863	Plus	105008-105650				
35	406016	8272661	Plus	41341-41940				
•	405268	4156151	Minus	24404-24521				
	401106	8568931	Plus	122694-122893				
	404186	4481839	Plus	829-1110				
40	403817 406422	8962065 9256411	Plus Plus	110297-111052 163003-163311				
70	402160	8516165	Plus	166063-166354				
	402622	9930984	Minus	129861-130099				
	401558	7139678	Plus	103510-104090				
	404960	7408010	Minus	146186-146377.147747-147943				
45	401203	9743387	Minus	172961-173056,173868-173928				
	402860	9588237	Minus	76423-76560				
	401588	7230871	Plus	46412-46561	-00			
	404831	6624702	Minus	16833-17020,20007-20120,21605-21799,23	33			
50	405885	7677703	Minus	42574-42998				
30								
	TABLE 5	DA: ABOUT 39	8 GENES UPF	EGULATED IN PRIMARY MELANOMAS OR I	KELANOMA METASTAS	ES RELATIV	E TO BENIGN NE	:VI m 50690 emberate on the
	Table 50/	A lists about 39	8 genes upreg	ulated in primary melanoma or melanoma meta Gene expression data for each probeset obtains	or ngilisu a sveisisi zaesis Mamathir analysis was	everecced o	wele selection il or s average intensif	v (Af), a normalized value reflecting the
55		ivel of mRNA e		Selle extression data ion easi brosser opravi	, non and brojos was	<b></b>		, 4 4,, 2
33	Pkey:			set identifier number				
	ExAccn:			on number, Genbank accession number				
	Unigenel		igene number	•				
	Unigene	Tide: Un	igene gene titt	•				
60	R1:	70	th percentile of	primary melanoma and melanoma metastasis	Als divided by the maximi	m Al of ben	ign nevi. ion nevi udam lib	a 46th passaction of passact ficture Ata
	R2:			primary melanoma and melanoma metastasis	us divided by the maxim	um AI OI DEN	Mu usar' musi a na	a four percenture of florities ossoe Ala
		wa	s subtracted in	om both the numerator and denominator				
	Pkey	ExAcon	UnigenelD	Unigene Title		R1	R2	•
65	422424	Al186431	Hs.296638			13.73	16.82	
•	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopo	ntin,	11.67	11.84	
	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator,		9.35	7.59	
	444381	BE387335	Hs.28371			8.63	7.90	
	417880	BE241595	Hs.82848	setectin L (lymphocyte adhesion mo		8.21	4.09	
70	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine		7.13 6.70	6.10 6.26	
	447210	AF035269	Hs.17752	phosphatidylserine-specific phospho		6.79	6.26 6.36	
	417693	AW959741	Hs.40368 Hs.28911	adaptor-related protein complex 1, s hexabrachion (tenascin C, cytotactir		6.55 6.43	7.11	
	429500	X78565 X72755	Hs.77367	monokine induced by gamma interfe		6.43	7.51	
75	414812 451736	AV080356		ESTs, Weakly similar to ALU7_HUA		6.31	4.28	
, ,	451730	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4		6.20	4.32	
	428291	AA534009			•	6.03	4.52	
	417308	H60720	Hs.81892	KIAA0101 gene product		6.01	6.78	
	448569	BE382657			ans	5.99	7.51	
80	439310	AF086120			1-	5.95	4.79 6.65	
	452838	U65011	Hs.30743			5.95 5.76	5.55 4.82	
	422241 442379	Y00062 NM_00461	Hs.17012 3 Hs.8265	<ol> <li>protein tyrosine phosphatase, receptransglutaminase 2 (C polypeptide,</li> </ol>		5.76	2.19	
	447313	<u></u> 0	- 13.0203	and an another to be be being				

					5.65	4.63
	409274		Hs.52644	SKAP55 homologue cytosolic acyl coenzyme A thioester hydr	5.58	3,41
	442739	NM_007274	Hs.8679 Hs.8645	hypothetical protein	5.45	5.79
	442711 425118	AF151073 AU076611	Hs.154672	methylene tetrahydrofolate dehydrogenase	5.42	5.56
5	412918	BE563957		activated RNA polymerase II transcriptio	5.35 5.33	4.31 4.83
	428125	AA393071	Hs.182579	leucine aminopeptidase small inducible cytokine subfamily A (Cy	5.33	5.13
	446921	AB012113	Hs.16530 Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	5.30	6.27
	431183 414219	NM_006855 W20010	Hs.75823	ALL1-fused gene from chromosome 1q	5.16	5.13
10	426600	NM_003378	Hs.171014	VGF nerve growth factor inducible	5.05 5.03	13.72 4.93
	415444	BE247295	Hs.78452	solute carrier family 20 (phosphate tran ESTs, Moderately similar to 178885 serin	5.03	3.42
	436701	AW959032	Hs.277477	major histocompatibility complex, class	4.99	3.36
	406648 410850	AA563730 AW362867	Hs.302738	Homo sapiens cDNA: FLJ21425 fis, clone C	4.98	5.30
15	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	4.98 4.97	4.85 4.46
	432469	AL080084		CGI-100 protein	4.85	3.49
	404854	000000	Hs.78619	Target Exon gamma-glutarnyl hydrolase (conjugase, fol	4.82	4.90
	415701 425397	NM_003878 J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	4.81	5.26
20	408958	T99607	Hs.49346	signal recognition particle 54kD	4.78	2.34 5.18
	453949	AU077146	Hs.36927	heat shock 105kD	4.78 4.77	4.13
	458079	AJ796870	Hs.54277	DNA segment on chromosome X (unique) 992 hypothetical protein	4.74	3.32
	440245	AK001913	Hs.7100 Hs.73792	complement component (3d/Epstein Barr vi	4.74	1.55
25	412228 417834	AW503785 BE172058	Hs.82689	tumor rejection antigen (gp96) 1	4.73	4.25
20	451003	AF058696	Hs.25812	Nijmegen breakage syndrome 1 (nibrin)	4.67 4.62	4.69 3.02
	424571	BE379766		polymerase (RNA) II (DNA directed) polyp	4.61	5.45
	434203	BE262677	Hs.283558 Hs.28777	hypothetical protein PRO1855 H2A histone family, member L	4.60	2.88
30	452268 421311	NM_003512 N71848	Hs.283609	hypothetical protein PRO2032	4.60	3.24
20	410491	AA465131	Hs.64001	Homo sapiens clone 25218 mRNA sequence	4.60	4.34 3.58
	425706	AW406678	Hs.122559	hypothetical protein FLJ22570	4.59 4.57	3.82
	450293	N36754	Hs.171118	hypothetical protein FLJ00026 immunoglobulin kappa constant	4.57	9.27
35	406836	AW514501	Hs.156110 Hs.75367	Src-like-adapter	4.53	3.60
. 33	413441 431129	AJ929374 AL137751	Hs.263671	Homo sapiens mRNA; cDNA DKFZp434l0812 (f	4.48	4.89
·	418506	AA084248	Hs.85339	G protein-coupled receptor 39	4.47 4.47	3.72 3.96
	411060	NM_006074		Homo sapiens mRNA full length insert cDN	4.45	2.40
40	417501	AL041219	Hs.82222	sema domain, immunoglobulin domain (lg). tissue inhibitor of metalloproteinase 1	4.43	4.27
40	437763	AA469369 BE614989	Hs.5831 Hs.7503	hypothetical protein FLJ14153	4.42	3.91
	448883 417274	N92036	Hs.81848	RAD21 (S. pombe) homolog	4.41	3.80
	419285	D31887	Hs.89868	KIAA0062 protein	4.40 4.38	3.20 2.79
4.5	418321	D63477	Hs.84087	KIAA0143 protein serine (or cysteine) proteinase inhibito	4.37	3.86
45	430154	AW583058		KIAAD175 gene product	4.36	4.65
	428450 428297	NM_014791 AA236291	Hs.183583	serine (or cysteine) proteinase inhibito	4.36	3.42
	447232			interleukin 10 receptor, alpha	4.36 4.35	3.31 3.10
	409598	NM_014011	8 Hs.55097	mitochondrial ribosomal protein S28 hypothetical protein FLJ23468	4.34	5.61
50	442432		Hs.38178	gb:H.sapiens SOD-2 gene for manganese su	4.33	3.31
	407047 443991	X65965 NM_00225	0 Hs.10082	potassium intermediate/small conductance	4.33	3.57
	452322			glutaredoxin (thioltransferase)	4.32 4.32	2.20 3.60
	420991			Homo sapiens mRNA for FLJ00111 protein,	4.31	5.79
55	449722			cyclin B1 diubiquitin	4.30	3.62
	408380 427127			pyruvate dehydrogenase phosphatase	4.28	4.18
	417933		Hs.82962	thymidylate synthetase	4.28 4.25	5.06 4.15
	432828			chondroitin 4-sulfotransferase thioredoxin domain-containing	4.24	3.15
60	450306 440266			hypothetical protein FLJ22794	4.23	3.65
	407951		Hs.79015	antigen identified by monoclonal antibod	4.22	4.21
	427337		Hs.176663	Fc fragment of IgG, low affinity IIIb, r	4.20 4.20	4.11 4.26
	408989			KIAA0746 protein zinc finger protein 258	4.19	2.65
65	44962			neutrophil cytosolic factor 1 (47kD, chr	4.18	6.80
	422841 41572		Hs.78712	aminolevulinate, delta-, synthase 1	4.16	4.28
	44420			cathensin () (lysosomal aspartyl protease	4.16 4.14	1.89 3.32
	41698	0 AA38113		high-mobility group (nonhistone chromoso uncharacterized hypothalamus protein HTO	4.14	3.02
70	43871			ESTs	4.12	4.18
	43780 44639			homolog of mouse quaking QKI (KH domain	4.12	3.87
	40946		9 Hs.54483	N-myc (and STAT) interactor	4.11	3.80 5.71
	42724	7 AW5042	21 Hs.174103	integrin, alpha L (antigen CD11A (p180).	4.11 4.10	4.25
75			Hs.75929	cadherin 11, type 2, OB-cadherin (osteob Homo sapiens cDNA FLJ11174 fis, clone PL	4.10	291
	45007 45288			folate transporter/carrier	4.10	4.25
	41452			Immunoglobutin J chain	4.09	3.99
	40775	6 AA11602		ubiquitin specific protease 18	4.09 4.08	4.60 3.64
80			12 Hs.301005	Target Exon purine-rich element binding protein B	4.07	2.43
	44467 41749			CD53 antigen	4.07	6.55
	4137			Homo sapiens cDNA: FLJ22139 fis, clone H	4.06	3.27
				522		

	484888					
	421508	NM_004833	Hs.105115	absent in melanoma 2	4.05	4.39
	408688	A1634522	Hs.152925	KIAA1268 protein	. 4.05	3.32
	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	4.04	3.53
5	445701	AF055581	Hs.13131	lymphocyte adaptor protein	4.02	4.20
J	451131	AI267586	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	4.01	3.96
	449291	BE176893	Hs.23440	KIAA1105 protein	4.01	2.34
	443071	AL080021	Hs.8986	complement component 1, q subcomponent,	4.00	6.97
	417615	BE548641	Hs.82314	hypoxanthine phosphoribosyltransferase 1	3.99	4.27
10	408246	N55669	Hs.333823	mitochondrial ribosomal protein L13	3.98	3.66
10	408819	AW163483	Hs.48320	double ring-finger protein, Dorfin	3.98	3.76
	424058	AL121516	Hs.138617	thyroid hormone receptor interactor 12	3.97	2.38
	418942	AJ566004	Hs.141269	Homo sepiens cDNA: FLJ21550 fis, clone C	3.97	3.40
	424756	AW504657	Hs.152931	tamin B receptor	3.93	2.67
15	421958	AA357185	Hs.109918	ras homotog gene family, member H	3.89	2.39
13	440692	AL031591	Hs.7370	phosphotidylinositol transfer protein, b	3.88	3.23
	433001	AF217513	Hs.279905	clone HQ0310 PR00310p1	3.68	4.24
	418255	AW135405	Hs.37251	ESTs .	3.87	2.53
	444371	BE540274	Hs.239	forkhead box M1	3.86	4.29
20	450515	AW304226	400000	biphenyl hydrolase-like (serine hydrolas	3.85	3.73
20	416114	AI695549	Hs.183868	glucuronidase, beta	3.85	3.74
	440596	H13032	Hs.103378	hypothetical protein MGC11034	3.84	1.90
	417020	178413		heterogeneous nuclear ribonucleoprotein	3.82	2.04
	448503	BE243146	Hs.21332	BTB (POZ) domain containing 1	3.81	3.07
25	446506	AI123118	Hs.15159	chemokine-like factor, alternatively spl	3.81	3.69
25	417059	AL037672	Hs.81071	extracellular matrix protein 1	3.80	6.01
	410668	BE379794	Hs.159651	hypothetical protein	3.80	5.22
	420107	AL043980	Hs.7886	pellino (Drosophila) homolog 1	3.79	3.93
	446071	N51527	Hs.13659	hypothetical protein DKFZp585F2423	3.79	2.74
20	419731	S47242	Hs.92909	SON DNA binding protein	3.77	1.85
30	443710	AI928136	Hs.9691	Homo sapiens cDNA: FLJ23249 fis, clone C	3.77	4.98
	406837	R70292	Hs.156110	immunoglobulin kappa constant	3.77	7.42
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	3.76	3.55
	419381	AB023420	Hs.90093	heat shock 70kD protein 4	3.76	3.81
25	423979	AF229181	Hs.136644	CS box-containing WD protein	3.76	3.97
35	402474			NM_004079:Homo sapiens cathepsin S (CTSS	3.76	4.01
	412828	AL133396	Hs.74621	prion protein (p27-30) (Creutzfeld-Jakob	3.75	3.77
	454080	A1199711	Hs.576	fucosidase, atpha-L-1, tissue	3.74	6.15
	408085	N25929	Hs.342849	ADP-ribosylation factor-like 5	3.74	2.92
40	426096	D87436	Hs.166318	lipin 2	3.72	2.98
40	417105	X60992	Hs.81226	CD6 antigen	3.72	2.78
	418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	3.72	3.37
	447735	AA775268	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L	3.70	4.09
	409264	NM_014937	Hs.52463	KIAA0966 protein	3.69	4.79
4.5	429170	NM_001394	Hs.2359	dual specificity phosphalase 4	3.69	2.94
45	428398	AI249368	Hs.98558	ESTs	3.68	3.82
	423494	AW504365	Hs.24143	Wiskott-Aldrich syndrome protein interac	3.67	3.52
	413235	BE243445	Hs.75248	topoisomerase (DNA) II beta (180kD)	3.67	2.79
	423712	W46802	Hs.81988	disabled (Drosophila) homolog 2 (mitogen	3.66	3.42
	409703	NM_006187	Hs.56009	2-5-oligoadenylate synthetase 3 (100 k	3.66	6.44
50	447225	R62676	Hs.17820	Rho-associated, coiled-coil containing p	3.65	2.93
	414829	AA321568	Hs.77436	pleckstrin	3.65	2.30
	400219			Eas Control	3.64	2.76
	437239	AW503395	Hs.5541	ATPase, Ca transporting, ubiquitous	3.63	2.73
	422445	M23114	Hs.1526	ATPase, Ca transporting, cardiac muscle,	3.62	3.60
55	449971	AA807346	Hs. 288581	Homo sapiens cDNA FLJ14296 fis, clone PL	3.62	3.62
	424460	BE275979	Hs.296014	polymerase (RNA) II (DNA directed) polyp	3.62	3.06
	427609	AK000436	Hs.179791	hypothetical protein FLJ20429	3.62	2.31
	400750			Target Exon	3.61	2.74
	424541	AW392551	Hs.180559	ESTs, Wealdy similar to A56194 thromboxa	3.61	2.25
60	427051	BE178110	Hs.173374	Homo sapiens cDNA FLJ 10500 fis, clone NT	3.60	4.20
	433867	AK000596	Hs.3618	hippocatcin-like 1	3.59	4.19
	421986	AL137438	Hs.110454	SEC15 (S. cerevisiae)-like	3.59	1.58
	414841	H55601	Hs.77490	glutathione S-transferase theta 1	3.58	1.00
	429693	BE254962	Hs.211612	SEC24 (S. cerevisiae) related gene famil	3.57	3.00
65	425204	NM_002436	Hs.1861	membrane protein, palmitoylated 1 (55kD)	3.56	3.09
	441669	R78195	Hs.29692	Homo sapiens cDNA FLJ11436 fis, clone HE	3.56	3.26
	442043	BE567620	Hs.99210	ESTs	3.55	3.56
	406636	L12064		gb:Homo sapiens (clone WR4.12VL) anti-th	3.55	3.83
	446341	AL040763	Hs.310735	ESTs, Moderately similar to ALU7_HUMAN A	3.54	3.52
70	432485	N90866	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)	3.54	4.66
-	422765	AW409701	Hs.1578	bacutoviral IAP repeat-containing 5 (sur	3.54	3.25
	412630	AA738437	Hs.26226	Homo sapiens cDNA: FLJ21286 fis, clone C	3.54	1.87
	432841	M93425	Hs.62	protein tyrosine phosphatase, non-recept	3.53	3.96
	425177	AF127577	Hs.155017	nuclear receptor interacting protein 1	3.53	3.40
75	426643	AA857131	Hs.171595	HIV TAT specific factor 1	3.51	2.21
	420137	AA306478	Hs.95327	CD3D antigen, della polypeptide (TiT3 co	3.51	2.51
	429248	U96759	Hs.198307	von Hippel-Lindau binding protein 1	3.51	2.85
	452852	AK001972	Hs.30822	hypothetical protein FLJ11110	3.51	2,71
	451791	Z78407	Hs.27023	vesicle transport-related protein	3.49	2.91
80	418310	AA814100	Hs.86693	ESTs	3.49	1.45
	406868	AA505445	Hs.300697	immunoglobulin heavy constant gamma 3 (G	3.48	6.81
	400200	-		NM_002788*:Homo sapiens proteasome (pros	3.48	2.51
	438746	AI885815	Hs.184727	Human melanoma-associated antigen p97 (m	3.47	6.94
				• • •		

					3.47	3.38
	441646	AB023169	Hs.7935	KIAA0952 protein cathepsin S	3.45	2.71
	427968	AI857607 AL359588	Hs.181301 Hs.7041	hypothetical protein DKFZp762B226	3.45	3.45
	440201 434608	AA805443	Hs.179909	hypothetical protein FLJ22995	3.44 3.44	3.68 6.70
5	427527	AI809057	Hs.153261	immunoglobulin heavy constant mu	3.44	2.72
	413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase H.sapiens polyA site DNA	3.43	2.76
	435550 453857	A1224456 AL080235	Hs.324507 Hs.35861	DKFZP586E1621 protein	3.43	3.64 2.29
	423392	AA195037	Hs.169341	HTPAP protein	3.43 3.43	2.78
10	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	3.41	3.06
	453915	AA588721	Hs.286218	ribosomal protein L44 hypothetical protein FLJ13187	3.41	4.23
	442485	BE092285 NM 002104	Hs.29724 Hs.3066	oranzyme K (serine protease, granzyme 3;	3.40	3.93 2.12
	432606 417410	AF063020	Hs.82110	PCA and SERS1 interacting protein 1	3.40 3.40	4.70
15	436810	AA353044	Hs.5321	ARP3 (actin-related protein 3, yeast) ho	3.39	7.58
	422545	X02761	Hs.287820	fibronectin 1 SMC4 (structural maintenance of chromoso	3.36	4.12
	409142	AL136877 AF155661	Hs.5075B Hs.22265	ovruvate dehydrogenase phosphatase	3.34	5.05 4.31
	434826 448410	AK000227	Hs.21126	hypothetical protein FLJ20220	3.33 3.33	4.60
20	416065	BE267931	Hs.78996	proliferating cell nuclear antigen	3.32	4.49
	432642	BE297635	Hs.3069	heat shock 70kD protein 9B (mortalin-2) ESTs, Weakly similar to 138022 hypotheti	3.24	4.22
	425234	AW152225 AA345519	Hs.165909 Hs.9641	complement component 1, q subcomponent,	3.23	12.31 5.07
	443623 426490	NM_001621		aryl hydrocarbon receptor	3.23 3.16	4.97
25	443958	BE241880	Hs.10029	cathepsin C	3.14	4.75
	412577	Z22968	Hs.74076	CD163 antigen coatomer protein complex, subunit beta 2	3.13	4.00
	414050	NM_004766	Hs.75724 Hs.106260	corting payin 10	3.12	4.45
	421633 413936	AF121860 AF113676	Hs.297681	corino (or cysteine) amteinase inhibito	3.11 3.10	4.00 . 4.03
30	428797	AA496205	Hs.193700	Homo saciens mRNA; cDNA UKFZp30010324 (1	3.06	4.49
-	430314	AA369601	Hs.239138	pre-B-cell colony-enhancing factor small inducible cytokine A5 (RANTES)	3.04	4.98
	430413	AW842182	Hs.241392 Hs.85838	course carrier family 16 (monocarboxylic	3.03	4.49
	418526 452139	BE019020 AA099969	Hs.16331	Homo sapiens cDNA: FLJ21482 lis, clone C	3.01 2.95	4.75 5.55
35	439237	AW408158	Hs.318893	ESTs, Weakly similar to A47582 B-CEII gr	2.94	4.64
	422684	BE561617	Hs.119192	H2A histone family, member Z gb:zw20f11.s1 Soares ovary tumor NbHOT H	2.93	10.28
	406782	AA430373	Hs.21858	trinucleotide repeat containing 3	2.91	5.40
	438549 450455		Hs.25035	entorida intracellular channel 4	2.90 2.89	4.86 4.04
40	427528			minichromosome maintenance deficient (5.	2.87	9.61
-10	422530		) Hs.118110	bone marrow stromal cell antigen 2	2.83	4.86
	423605			cadherin 19, type 2 proteasome (prosome, macropain) 26S subu	2.82	5.02
	410231 419956			catherin 19 Ivne 2	2.80 2.79	4.30 5.80
45	416511			Lysosomal-associated multispanning membr	2.78	4.21
45	42973		Hs.2488	hymphocyte cytosolic protein 2 (SH2 doma hypothetical protein FLJ22649 similar to	2.78	4.23
	44851			hypothetical protein PCS22043 Similar to lumican	2.78	4.40
	41678		2 Hs.79914 Hs.180841	hymor necrosis factor receptor superfami	2.77	4.23 4.17
50	42779 41214			RAR6 interacting, kinesin-like (rabkines	2.77 2.76	4.43
50	42708		37 Hs.301175	ras-related C3 botulinum toxin substrate hematopoietic cell-specific Lyn substrat	2.75	4,20
	44627			commically defined colon cancer antig	2.74	4.07
	43717			CRY (sex determining region Y)-box 13	2.72	4.63 4.93
55	42940 42136			eouthrocyte membrane protein band 4.1-8	2.71 2.68	4.15
	40920	2 AA23688	1 Hs.51043	hexosaminidase B (beta polypeptide) phosphatidylinositol glycan, class F	2.68	4.00
	42612		9 Hs.250697 Hs.119129	millionen, tyne IV, alpha 1	2.67	4.72
	4226 4173			midding (neurite growth-promoting factor	2.65 2.65	7.77 4.47
60	4173			Homo saniens cDNA: FLJ21026 hs, clone C	2.64	5.61
•	4103	41 AW4999		ARP2 (actin-related protein 2, yeast) ho putative nucleotide binding protein, est	2.63	4.34
	4330		18 Hs.279923 Hs.151738	matrix metalloproteinase 9 (gelatinase B	2.62	4.95
	4246 4094			splicing factor, arginine/serine-rich 5	2.60 2.60	6.00 4.27
65	4247		51 Hs.153053	CD37 antinen	2.60	4.64
	4093	54 N68188	Hs.159472	Homo sapiens cDNA: FLJ22224 fis, clone H nuclear RNA helicase, DECD variant of DE	2.57	4.27
	4275			proteasome (prosome, macropain) subunit,	2.56	4.20
	4261 4215			orandysio	2.56	4.13 5.46
70	) 425			proteoglycan 1, secretory granule	2.55 2.54	5.78
, ,	428		84 Hs.182793	golgi phosphoprotein 2	2.50	5.15
	429			antizyme inhibitor gb:Human omega light chain protein 14.1	2.50	4.98
	407			UDP-Gal:betaGicNAc beta 1,4- garactosyu	2.45	5.58 7.20
7:	421 5 412			CKSOS binding protein OfficulSOF	2.45 2.44	4.11
, ,	412	025 AI8274	151 Hs.24143	Wiskott-Aldrich syndrome protein interac membrane-spanning 4-domains, subfamily A	2.44	4.67
		523 T6284		headachtafiassa l	2.44	5.44
		350 AF052 1296 AL137		Homo saniens cDNA; FLJ23015 fis, clone L	241	4.31
Q		296 AL137   <b>106</b> 5 <b>W03</b> 4		hypothetical protein MGC4595	2.41 2.39	4.25 5.68
ō		223		Eos Control	2.39	2.22
	42	658 AF231			2.38	
	43	1629 AU07	7025 Hs.265827	Elicitatori, aprioristatorio prosini (***		

	414522	AJ752666	Hs.76669	nicotinamide N-methyltransferase	2.38	5.21
	415149	X12451	Hs.78056	cathepsin L	2.37	7.71
	435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	2.37	5.68
5	427407 426432	BE268649	Hs.177766	ADP-ribosytransferase (NAD; poly (ADP-r	2.31 2.29	4.89 4.83
,	430555	AF001601 AI815486	Hs.169857 Hs.243901	paraoxonase 2 Homo sapiens cDNA FLJ20738 fis, clone HE	2.27	5.03
	413869	NM_000878	Hs.75596	Interleukin 2 receptor, beta	2.25	4.14
	412617	AK001364	Hs.808	heterogeneous nuclear ribonucleoprotein	2.21	4.31
10	447547	NM_007229	Hs.18842	protein kinase C and casein kinase subst	2.19	4.62
10	416232 420842	AW502678 AI083668	Hs.79090 Hs.50601	exportin 1 (CRM1, yeast, homotog) hypothetical protein MGC10986	2.18 2.14	4.84 4.22
	411358	R47479	Hs.94761	KIAA1691 protein	213	4.65
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	2.13	4.03
15	406687	M31126		matrix metalloproteinase 11 (stromelysin	2.11	4.16
13	417331 450344	AW411297 AW994032	Hs.81972 Hs.8768	SHC (Src homology 2 domain-containing) t	2.11 2.11	4.25 4.09
	429642	X68264	Hs.211579	hypothetical protein FLJ 10849 metanoma cell adhesion molecule (MCAM) (	2.11	5.42
	416448	L13210	Hs.79339	lectin, galactoside-binding, soluble, 3	2.10	6.42
20	418613	AA744529	Hs.86575	mitogen-activated protein kinase kinase	2.10	4.00
20	453352 409220	T10446 BE243323	Hs.51233	ESTs	2.09 2.09	4.48 4.98
	414045	NM_002951	Hs.75722	tumor necrosis factor receptor superfami ribophorin II	2.07	4.59
•	422451	AA310753	Hs.42491	ESTs, Weakly similar to S65657 alpha-1C-	2.07	4.09
25	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	2.06	5.06
25	452363 438393	AJ582743	Hs.94953	Homo sapiens, Similar to complement comp	2.04 2.03	11.17
	438393	AA351815 NM_002047	Hs.50740 Hs.283108	Homo sapiens cDNA: FLJ22272 fis, clone H gtycyl-IRNA synthetase	2.02	4.36 4.79
	412994	032257	Hs.75113	general transcription factor IIIA	2.00	4.67
20.	424415	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	1.98	4.79
30	421897	AW583693	Hs.109253	N-terminal acetyltransferase complex and	1.98	4.17
	442159 429451	AW163390 BE409861	Hs.278554 Hs.202833	heterochromatin-like protein 1 heme oxygenase (decycling) 1	1.95 1.95	7.53 4.63
	416967	BE616731	Hs.80645	interferon regulatory factor 1	1.95	4.31
2.5	400203			Eos Control	1.94	5.03
35	437317	AA748613	Hs.311977	ESTs, Highly similar to SWI/SNF related,	1.94	4.03
	414945 416224	BE076358 NM_002902	Hs.77667 Hs.79088	hymphocyte antigen 6 complex, locus E reticulocalbin 2, EF-hand calcium bindin	1.93 1.92	4.68 4.12
	445411	AL137255	Hs.12646	hypothetical protein FLJ22693	1.91	4.23
4.0	413945	NM_000591	Hs.75627	CD14 antigen	1.90	5.00
40	413317	U53225	Hs.75283	sorting nexts 1	1.89	4.20
	448719	AA033627	Hs.21858	trinucleotide repeat containing 3	1.89 1.88	4.26 4.15
	430838 427239	N46664 BE270447	Hs.169395	hypothetical protein FLJ12015 ubiquitin carrier protein	1.87	5.72
	450440	AB024334	Hs.25001	tyrosine 3-monooxygenase/tryptophan 5-mo	1.87	5.81
45	433671	AW138797	Hs.132906	19A24 protein	1.85	4.27
	413190	AA151802	Hs.40368	adaptor-related protein complex 1, sigma	1.85	5.19
	414915 430040	NM_002462 AW503115	Hs.76391 Hs.227823	myxovirus (influenza) resistance 1, homo pM5 protein	1.85 1.83	4,31 5.57
	417929	R27219	Hs.74647	Human T-cell receptor active alpha-chain	1.82	4.29
50	414570	Y00285	Hs.76473	insulin-like growth factor 2 receptor	1.81	4.39
	414416	AW409985	Hs.76084	hypothetical protein MGC2721	1.80	4.20
	428977 418707	AK001404 U97502	Hs.194698 Hs.87497	cyclin B2 butyrophilin, subfamily 3, member A2	1.79 1.78	4.17 4.30
	425367	BE271188	Hs.155975	protein tyrosine phosphatase, receptor t	1,78	5.44
55	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, impor	1.77	5.11
	422009	AI742845	Hs.110713	DEK oncogene (DNA binding)	1.77	4.37
	424909 409154	S78187 U72882	Hs.153752 Hs.50842	cell division cycle 25B	1.74 1,74	5.00 4.86
	413892	AI878921	Hs.75607	interferon-induced protein 35 myristoylated alanine-rich protein kinas	1.73	4.37
60	444954	AW247076	Hs.12163	eukaryotic translation initiation factor	1.71	5.02
	424263	M77640	Hs.1757	L1 cell adhesion molecule (hydrocephalus	1.70	4.68
	424825 427378	AF207069	Hs.153357 Hs.177556	procollagen-lysine, 2-oxoglutarate 5-dio melanoma antigen, family D, 1	1.70 1.67	4.59 5.59
	413322	BE515037 AA380158	Hs.75290	ADP-ribosylation factor 4	1.67	4.39
65	442414	8E408758	Hs.8297	ribonuclease 6 precursor	1.65	4.03
	410129	BE244074	Hs.58831	regulator of Fas-induced apoptosis	1.64	4.24
	422976	AU076657	Hs.1600	chaperonin containing TCP1, subunit 5 (e	1.64	4.91
	443051 452472	AA333660 AW957300	Hs.71331 Hs.294142	hypothetical protein MGC5350 ESTs, Weakly similar to C55663 oligodend	1.64 1.63	4.08 4.41
70	446143	BE245342	Hs.306079	sec61 homotog	1.62	4.70
	431142	AA852596	Hs.250641	tropornyosin 4	1.62	4.86
	407752	AA573581	Hs.13328	ESTs	1.62	4.19
	416322 414572	BE019494 AU077174	Hs.79217 Hs.288181	pyrrotine-5-carboxytate reductase 1 cathepsin H	1.61 1.60	4.51 5.25
75	415017	F06434	Hs.77805	ATPase, H transporting, lysosomal (vacuo	1.60	4.56
. •	452056	AW955065	Hs.101150	Homo sapiens, clone IMAGE:4054156, mRNA,	1.58	5.46
	413976	BE295452	Hs.75655	procotlagen-profine, 2-oxoglutarate 4-di	1.58	4.05
	414420 410638	AA043424 N46504	Hs.76095	immediate early response 3 profilin 2	1.58 1.57	4.00 5.57
80	419638 422624	BE616678	Hs.91747 Hs.76152	KOEL (Lys-Asp-Glu-Leu) endoplasmic retic	1.57	4.44
-0	415819	AU077330		transcription elongation factor A (SII),	1.55	4.89
	439627	BE621702	Hs.29076	hypothetical protein FLJ21841	1.55	6.66
	425243	N89487	Hs.155291	KIAA0005 gene product	1.54	4.38

						4.22	
	424799	BE550723	Hs.153179	fatty acid binding protein 5 (psoriasis-	1.53 1.53	4.22 7.41	
	416971	R34657	Hs.80658	uncoupling protein 2 (mitochondrial, pro	1.51	4.12	
	426059	BE292842	Hs.166120	interferon regulatory factor 7 Tax1 (human T-cell leukemia virus type I	1.50	4.02	
5	418879	AW162087	Hs.5437 Hs.279903	Ras homolog enriched in brain 2	1.50	4.18	
5	432999 415661	BE294029 AF057307	Hs.78575	prosaposin (variant Gaucher disease and	1.49	4.19	
	428098	AU077258	Hs.182429	protein disuffide isomerase-related prot	1.49	5.74 4.53	
	452264	AU077013	Hs.28757	transmembrane 9 superfamily member 2	1.48 1.47	4.95	
••	415198	AW009480	Hs.943	natural killer cell transcript 4	1.45	4.61	
10	411794	AL118577	Hs.75658	phosphorylase, glycogen; brain nucleolar protein family A, member 3 (H/	1.45	4.15	
	433271	BE621697	Hs.14317 Hs.104125	adenylyl cyclase-associated protein	1.42	4.67	
	421416 415089	BE302950 N25117	Hs.299465	ribosomal protein S26	1.41	5.19	
	421975	AW961017	Hs.6459	hypothetical protein FLJ11856	1.41	4.03 4.44	
15	400202			NM_002795*:Homo sapiens proteasome (pros	1.41 1.41	4.57	
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	1.40	4.25	
	412968	AW500508	Hs.75102	alanyl-tRNA synthetase insufin-like growth factor binding prote	1.39	4.11	
	440704	M69241	Hs.162	coronin, actin-binding protein, 1C	1.39	4.51	
20	447099	AB030656 AA019912	Hs.17377 Hs.184693	transcription elongation factor B (SIII)	1.38	4.90	
20	428511 413825	BE299181	Hs.75564	CD151 antigen	1.37	4.44	
	441737	X79449	Hs.7957	adenosine dearninase, RNA-specific	1.36	4.29 4.10	
	440087	W28969	Hs.7718	hypothetical protein FLJ22678	1.36 1.35	4.50	
0.5	413566	AW604451	Hs.285814	sprouty (Drosophila) homolog 4 low density lipoprotein-related protein-	1.35	5.14	
25	413019	BE281604	Hs.75140	HSPC035 protein	1.35	4.14	
	433026	AW160616	Hs.279921 Hs.177559	interferon gamma receptor 2 (interferon	1.34	4.35	
	427380 428289	NM_005534 M26301	Hs.2253	complement component 2	1.33	4.23	
	419715	AF070523	Hs.92384	vitamin A responsive; cytoskeleton relat	1.32	4.61 · 4.76	
30	425299	AW505214	Hs.155560	calnexin	1.31 1.30	5.30	
	422242	AJ251760	Hs.273385	guanine nucleotide binding protein (G pr Homo sapiens clone FLB9213 PRO2474 mRNA,	1.29	6.09	
	448483	AA356392	Hs.21321	EST	1.29	4.56	
	407143	C14076	Hs.332329 Hs.75207	glyoxalase i	1.26	5.56	
35	413125 439053	BE244589 BE244588	Hs.6456	chaperonin containing TCP1, subunit 2 (b	1.26	4.98	
22	413929	BE501689	Hs.75617	collagen, type IV, alpha 2	1.25	4.76 4.56	
•	419663	AA394208	Hs.92198	calcium-regulated heat-stable protein (2	1.24 1.21	4.50 8.96	
	422166	W72424	Hs.112405	S100 calcium-binding protein A9 (calgran	1.21	4.02	
40	416636	N32536	Hs.42645	solute carrier family 16 (monocarboxylic	1.18	4.29	
40	425335	BE394327	Hs.296267	follistatin-fike 1 S100 calcium-binding protein A13	1.17	4.32	
	446211	AI021993	Hs.14331 Hs.10432	KIAA0878 protein	1.13	4.17	
	428542 454117	NM_014899 BE410100	Hs.40368	adaptor-related protein complex 1, sigma	1.10	4.00	
	428216	M18468	Hs.183037	protein kinase, cAMP-dependent, regulato	1.09	4.40 4.70	
45	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	1.00 0.98	4.40	
-	422158		Hs.112341	protease inhibitor 3, skin-derived (SKAL	0.90	4.78	
	408522	AI541214	Hs.46320	Small proline-rich protein SPRK (human,	0.00		
	T. O. F	500.					
50	TABLE	50B:	nimus Ens nombes/	et identifier number			
50	Pkey: CAT nu	_	ene cluster numbe				
	Access	-	enbank accession				
	Pkey	CAT Numb	per Accession	L519009 AV755430 AV756363 AV711927 BI523434 AI521	453 AAB46815 AW0	24829 AW949	702 BG218926 AA626658 AI445621 AI452815
55	412918	3 2764_3					
			AA940333 A	A723580 AA612925 BG105326 BG532616 AW513934 AW BG190378 AA483698 BE066066 BE066067 BE066062 AW	304207 BE939361 A	W795569 BG2	10592 AW795644 BE939358 AW102886
			DE065977 F	3C182971 H97042 D58090 BIQ46351 H81248 AI75UTT AV	V372079 C05492 D5	8287 D57835	AA935095 BF /00910 BG213002 BG135439
			AW368467	BG495535 BG533177 BI087962 BE541579 BF130753	0 4 4 4 4 0 0 0 C 4 1 4 7 0 E	E2 AMONOST A	1360304 AA418828 AW301673 BE218952
60	43670	1 28142_1	Z69892 AA	210833 BM353155 AI473754 AI147901 AI8U3109 AA84329	6 AA418923 AI4783 60640 61222671 613	47724 AW0017	711 Al028652 AA398130 Al470582 Al915936
			AI632804 B	F433234 AA394157 BF378047 BE467036 AA319724 AW2 C75102 N36920 H50440 AI919034 AI004399 AI383862 AI1	23606 AA648518 A	516258 AI865	321 N22865 AA848101 AL589792 AA758196
			AA908929	C75102 N36920 H50440 A1919034 A1004,399 A1383862 A1 A1373911 AW194733 AA213447 A1290291 BF437165 AA7!	7592 BF086904 AW	959032 AW99	2466 BF446888 AI936337 BE938849
65	43246	9 58644_1			N967497 BE219482	BE018650 AV	7770511 AW459095 AW470133 BM130101
05	43240	3 30011_1					
				N990100 AW087624 AA668793 AL080084 BI333666 BI620 NW954201 BM145846 BG111760 AI750065 BG655794 A N184602 AI343932 AW136586 AW029464 AI708651 AA8			
70			AA976614	A1344537 AA609603 A1873901 A1859995 AA833389 AA76 E243185 AA282179 AA831098 AA112676 A1702407 BG621	752 BE006492 AA3	53202 BG6742	256 N46921 BI048774 AW300233 BF739890
75			00044444	AAN 12000 HON207 AW575477 AW150918 AW5913/1 AU	82111 N1 1320 M144	197 A1285602 A	A/43033 AI281047 BF3/10/0 10320
				BG721680 AA285143 H27167 AW500235 BG494497 BF6 AW152643 AI803450 AI564343 AI092711 AI140525 AW1		54689 AI16120	9 AI290242 AI339745 AI374611 AI347388
	4245	71 9758_1					
80	,						
9(	,						
			BG94235	1370715 BE244980 AA548596 AW449673 A1191006 BF22. 6 A1474968 BE858217 BF793358 AV756758 BG483603 A1	)93724 BF693395 B	6545345 AI/4	TETERPOO ETTI FONN EPERCI PESA
				•			

	444207	9172_3	BE739425 AA514221 AA865491 AIB28293 AA <i>A</i> 70456 AI276739 AA169357 BE932464 AA514889 AW819039 AW819083 BE843048 AI432496 AI470335 AI247243 BCS33994 AA513783 AI887309 AA528036 AW972006 AW873028 AI924914 AIB18810 AW152378 AW084946 AI521413 AI669583 BE932521 AI581370 BE180238 AW089750 AW771461 AW089714 AI590349 AI819148 AA731056 BF815234 BF911506 AA235803 AA485373 AI735658
5			AW393133 AW073080 AJ707637 BF353320 BE843111 AW819036 AW393135 BG697291 AV648670 AV654332 AV687530 BG566964 AI807430 AI676072 AA837010 AI452482 AI625817 AW241750 BE048616 AI290928 AI680714 AA485530 BE175687 AV648513 AW130312 AI000556 AA632893 BE674169 BF001208 AA948166 BE175650 AA524664 AA490345 AI244948 AA602956 AA483492 AA58818178 AW802049 BG675859 AV658871 BG678060 AI565004 AW819026 BE843092 AV866437 AV723049 BG616948 AI911647 AI743490 A091096 BE857251 AI956074 AA040027 AW769317 AA343477 AA640112 BF876213 R82948 H26425 H82876 BE843095 BE843140 BG536641 BG617830 AA235802 BE774985 BE005682 BF342375
10	450515	13638_2	AA903144 BF338083 BF984258 AV657996 A1749542 BF768614 BE857252 BE932516 BE768573 AV657993 AV657777 AV752631 BE774974 T55847 BF095761 BF911611 BE710793 BE180119 BG617338 H45942 T55897 AV657718 BG563497 BE299805 A1589870 AA847598 A470122 BF93896 A1304356 BE223045 BF435800 A1394207 A1708171 AW025415 A079409 AW008420 AW304226 N34543 AW603578 AA526961 AA983631 N99134 AA626645 R45023 AA902417 AW672925 AA449985 AA953982 AW675471 AA010062 N80194
15	417020	74857_1	H14620 H28475 H26247 BF333581 AW842369 H06848 H05608 H81745 H15016 R51905 AA860423 AI860904 AA876023 AK024824 BI089104 AL596792 AI880004 BF969921 BE349489 AA843097 AI475644 AW676123 AW731676 AI339951 AI128503 AW243903 BG231992 BG057353 AA987811 AA575927 AI889162 N68847 AA464693 AA962541 AA844323 AI969978 AW731676 AI333994 R19260 AI338984 R24078 AI128953 T886956 AA808038 AA694545 H02091 BF439007 AI189805 AI279912 AA730423 R26552 AA455017 AI264219 AI446015 R19187 D51331 T24484 AI522034 AV721528 BI056340 BG009879 AW371368 Z36733 BE707682 BG501334 BG180238 BE177547 H48381 BF055495 AI948528 AW994256 BF109394 AI817046 W58758 H48807 H01994 T78413 BG750345 R24132 N92060 R25367
20	400219	8366_1	BC003552 L10284 NM_001746 AJ271880 BI834281 BI597016 AU133331 BI668332 BI463073 BG720694 AL046729 BI460138 BI461052 AV647588 BG823268 AW889757 BE001258 AA31256 AA476446 AU098976 AA312196 BF749977 M94859 AF070646 BC5654196 BG623397 AU1173322 BG680963 BI667083 AU134542 AU138830 A4761459 BG679882 AA209406 AW512644 AW514818 AU706585 BE547592 BG655418 AI459204 BF725673 BE870032 BF001968 AL047245 BF724470 BF058818 H18415 BE076849 BE076887 BE076848 BE076827 BE076886 BE076827 BE076886 AV708687 AA380923 BE076851 F08118 L18887 BF785701 AU128383 BE908383 AW6733350 AW500108 BE079837 BE929419 BF868758 AW503373 AW580528 BE005524
25			BI917505 BI457781 BE883812 BI668159 AA213643 AA374821 BF969974 BM480200 AU136152 BE395635 AV685066 AV693755 AL040984 AA676820 BG896408 BE082272 BE082312 C05287 BE082264 AA378850 AW672902 AI625955 BF033526 AW296557 AA728815 BE077058 AW081700 AA911707 AA362640 BE707179 BG913228 BG116191 BG752367 AA074678 AL036937 BG113760 H03524 BG681802 AI664688 AU149556 BE178600 AI813488 AU452433 AI208989 AA593932 AA580385 AA486274 AA629899 AA565929 AA114046 AA094252 BM450328 BG529568 R68320 BE076792 BE030073 BE076855 BE076859 BE076829 AA361719 AA379164 AI202712 BG223315 BE122741 BGC534531 AA903494 H24978 BF035674 B
30	406636 400200	0_0 3806_1	BM456787 N40286 T80096 N39642 H42119 BG483861 AW381621 R69347 AW128895 AJ367416 AJ095285 AA099344 BE568161 AA180109 BF246488 BI561938 AW379170 BG567212 L12064 L12083 L12065 L12075 L12066 L12085 L12072 L12082 L12081 L12062 L12080 BC005265 BG176720 AW006027 BM352064 AW026316 AJ635822 AJ880584 AJ693769 AJ092211 BJ492387 AJ400449 AW166297 BF939910 AA232282
35.			AW021432 AI333893 AA494308 AA854899 A436795 AW069256 AA682373 AI092748 AA993184 AI126077 AI081758 AI240586 AI261863 AI378423 AA465237 AI376096 AA035579 AI087306 AA48162 AA129977 AI090903 AI080686 AI288939 N33004 AI801240 AW021546 AI370773 AI086064 AA669528 AI250053 AI870113 AA853181 AA858014 BC055562 BC939559 AW080765 AA032283 AW467587 H40506 D00762 NM_002788 AA641134 AI582295 AI417525 AI563975 AI093566 AI707743 AI290741 AW073417 BE875418 BM264076 BG876884 AI680535 AW854219 BE774635 AW854212 BG952443 AW854221 AW854208 BE156348 BE843056 AW858991 BE937569 BG878291 BG876450 AW819099 AI908570 AA449871 AU135228 BM478404 BF126296 AA375499 AA248473
40	406782 437179	0_0 12239_1	AA430373 AA968771 AK055109 BC019085 AA187684 BG656226 BM023227 A1932311 AW264381 AA398371 BM021483 A1432433 A1375777 A1129580 AW262782 AA134107 BM023515 AA977504 A1859222 A1348454 R69725 AA975268 BM021207 AL080074 AA129218 AW207842 N90581 AA771919 A1092259 A1028416 A1074114 BG656536 BE501677 AW193419 AA917040 W90430 A1342984 A1378957 AL036486 AW020068 B1491093 BF476021 R41226
45	426143	3806_1	R69631 F04125 C02343 AA115589 R56480 AI400988 R54266 R31422 BC005265 BG176720 ANY006077 BM352064 AW026316 AI635822 AI880584 AI693769 AI092211 BI492387 AI400449 AW166297 BF939910 AA232282 AW021432 AI3333893 AA494308 AA854899 AI436795 AW069256 AA682373 AI092748 AA993184 AI126077 AI081758 AI240686 AI261863 AI378423 AA465237 AI376096 AA035579 AI087306 AA448162 AA12977 AI090903 AI080686 AI288939 N33004 AI801240 AW021546 AI370773 AI086064 AA669528 AI250053 AI870113 AA853181 AA858014 BG055562 BG939559 AW080765 AA032283 AW467587 H40506 D00762 NM_002788 AA641134 AI582295 AI417525 AI563975 AI093566 A707743 AI290741 AW073417 BE875418 BM264076 BG876884 AI680535 AW854219 BE774635 AW854212
50	400223	2368_1	BG952443 AW854221 AW854208 BE156348 BEB43056 AW858991 BE937569 BG878291 BG876450 AW819099 AI908570 AA449871 AU135228 BM478404 BF126296 AA375499 AA248473 NM_005648 BC013809 L34587 BF103775 BG702618 BG716553 BI667090 BG505863 BF983483 BG718195 BI857891 BG501016 BM043599 AL521812 BG705730 BI495545 BI495546 BF112248 BM023182 BM023123 AI075173 AW051799 BF058224 BI324885 BF436008 AA398446 BG822375
55			BM019558 BM023382 BG164174 N56909 BI467064 BM023464 AI207475 BM311415 BG758430 BG758807 AI934826 N90351 BG422026 BE910312 AI027778 AI081950 AI360890 BM009115 AI191829 BG759697 AI138728 AA393403 AI355589 AI336427 AA688702 AA393660 AA025127 BG027630 AA952774 AA631224 BG940967 BE791087 AA57315 W81685 AA393525 BG944103 AI339125 AI149864 AA977655 N90314 BE612839 BG491847 AI129091 AA461234 AA781198 AA759256 AA888954 AA975844 AI184099 AI018025 AA398363 AI003331 AI193380 AA626020 AI244476 AI601114 AW135664 AI206607 AW263599 AA813219 AI684453 AA878626 AA772222 AI085496 AI630226 BG940966 AI022010 AA770649 AA887624 AA491739 AA974295 BG530040 AA037091 AA019912 BI160457 H64512 BG503896
60	406687 453352	0_0 12299_2	M31126 BC619646 AA367158 BI850421 AW998556 BF107010 BF969630 BF185964 AA361080 AW960026 AA147486 AI807023 AW770262 BI492178 BM145577 AA829932 AW021238 AW629477 AI337862 AI457141 BI712705 BM194542 BI712465 AI380070 N27407 AI609764 AI274152 AI206228 AI076874 AI261827 AI610982 AI469158 AI420690 AI168768 AA491675 C16249 C16232 C16209 C16275 C16274 C16243 R23287 BF246254 R66738
65	400203	11774_1	R23212 C14593 NM_002794 D26559 BM469989 BF305151 BG821966 BI089030 AW007738 BI222910 BM049422 BG028749 A1189162 AI831230 AW131497 BM272215 BE791105 AW778828 AA479594 AA480133 AA131997 AA284572 AA453009 BF928258 AA152127 AA393918 BF765307 BE247542 BF334697 BF341798 BE253409 AA470620 AI828932 AW379902 AV762678 AV741784 AV760892 AI025755 AA878562 AA630630 AA761708 AA862518 AA855831 AA862947 N53065 AA131821 AA293499 N23342 N26856 A1147345 AW951549 AA772963 BE245986 BG208493 AI831666 BG474873 BI023168 AU149547 BG197069 BG191102 BF304178 BE536135 AA706900 AA443583 AI002710 AW275192 AU149842 BG214797
70	427239	20459_2	BG198193 AW197923 AW627799 198683 BG194788 BG214656 BF345259 BG716363 Al066528 BI546220 AA393815 AA132004 AA353826 H97858 BG187823 BF841463 AJ351714 AV735966 BG196439 BG216840 BG198439 BG400762 AL523260 BE794750 AA582906 AI015067 AW271034 BG271636 AW075177 AW071374 AJ345565 AJ307208 BE138953 BE049086 AI334881 AW075005 AW075181 AA464019 AW302733 AW075100 AW073433 AI802854 AJ334909 AI802853 AJ345036 AJ348921 AJ340734 AJ37478 AJ251289
75			AW302327 AW072520 AJ312145 AW073656 AW072513 AW071289 AJ307559 AA876186 T29587 AJ307493 AJ255068 AJ252686 AJ252839 AW074809 AJ252926 AJ252160 AJ251662 AJ251362 AJ610913 AJ270787 AJ270156 AJ252075 AW073469 AW072901 AW072495 AW071420 AJ305762 AJ254764 AJ802837 AJ251284 AW073049 AW071311 AJ340643 BE138965 BE138502 AW073456 AJ334733 AJ054333 BE139260 AJ054050 AJ054
80	415819	40015_1	BE739429 BM60292 AL549095 BF752457 BE783002 BC035869 AW601528 AL880413 BF593762 AA974415 AW305318 AA716501 AJ936239 AB99486 AI744171 AW804992 BF108747 AW804693 BE219333 AIB07707 AA306963 BC012140 BF741621 BF741618 BF741619 AW062543 AA155832 AU151381 AU158043 AU150410 AU145605 AU150252 AA188205 AU153035 A1147293 AA084507 AA868165 AI887120 AI468336 AW023112 H44035 F01513 AA747672 AW779630 AA757298 R77738 AU150931 R38473 AA189022 H96984 AL550490 AW949737 AU150194 AU149258 AI749453 AW172950 AW276160 AI753604 AI421762 AW575512 AI275633 AW516120 AI340167 AJ567728 AI797326 AI471532 AU074080 AI633122 AW674646 AW316571 AA258187 AA102780 AA258186 AI363307 AA862862 AI206836 AA629555 AA486287 AI185097 AI872389 BE465687

5	400202 1	Al246746 Al351453 Al189679 AA594582 Al038639 AA862764 AA644332 AA912423 AA601552 AW014502 AA694605 AW068949 BF941650 AW297886 BF941649 Al077854 Al027442 AA705602 AW020757 BI491734 AA977135 AA653973 BI522334 AA398723 Al280083 Al419671 AW009199 AA496011 AU144081 Al538440 BF741690 BF741680 H41990 AV724108 AW955578 BE698790 T29312 BG954488 R33179 BI832621 BF742040 BE091493 H92122 BG614879 AW993709 Al216562 H44107 AA393530 BE173154 BG285054 BF751883 AA489308 BF741676 R64496 BE183198 H97097 AW062534 BF036430 AW192614 BF431707 N30258 AA629072 BG954496 Al401616 BG590357 BE873890 BF745945 AA156007 AA573157 AW874610 AA916387 N75963 BM083306 AW044671 BC013008 NM_002795 D26598 BG118716 BI910891 BF972860 BG119842 BI094093 AL538757 BE271653 BI856538 BE909573 BG109826 BE784430 BE899255 BI833973 BM010809 BE621321 BG684956 BF904726 BI871370 AV708990 BF971483 BE298241 BI197007 BE272092 BG120374 AW963509 BE540572 AV744947 BG943041 AW327463 BG472870 BE393697 N28533 AA316042 N42043 AW404246 AW892094 AA379896 AW801110 AW406977 AA379791 BG941889 BE076254 AA360459 AA379385 AA320056 BG942618 D31230 AA308300 AA360371 AA371733 AA732937 AA494241 W32225 BF745937 A1383690 BG202360								
	TABLE 50C:									
	Pkey: Unique number corresponding to an Eos problems on Cookenk Identifier (Cl) numbers. "Dunham, et al." refers to the publication entitled "The DNA									
15	Ref:	CONTRACT	ce of human ct	romosome 22" Dunham, el al. (1999) <u>Nature</u> 402.º	189-495.					
1.5	Strand:	Indicate	s DNA strand i	rom which exons were predicted.						
	Nt_position:	Indicate	s nucleodoe p	ositions of predicted exons.						
				N_position						
20				.4260-14537 10014-80401,80593-81125						
			Minus !	3526-53628,55755-55920,57530-57757						
		8119067	Plus	198991-199168,199316-199548						
25										
23	TABLE 51A Table 51A I Gene expre Pkey:	ists about 453 ge ssion data for ea	enes upregulati ach probeset ol a Fos probeset	ULATED IN PRIMARY MELANOMAS RELATIVE ad in primary melanomas relative to normal skin. ( ctained from this analysis was expressed as avera- identifier number	Genes were selected from 59 ge intensity (AI), a normalize	580 probesets on I value reflecting	the Eos/Affymetrix Hu03 Genechip array. the relative level of mRNA expression.			
30	ExAccn:	Exemp	olar Accession	number, Genbank accession number						
-	UnigenelD:	d Haina	ne number							
	Unigene Tr R1:	ne: Uniger 90th o	ne gene title ercentile of prid	mary melanoma Als divided by 90th percentile of n	ormal skin Als	h accounting of the	omal lissue Als was subtracted from both			
	R2:	90th p	ercentile of pri	nary melanoma Als divided by 90th percentile of n	ormal skin Als, where the 10	n percentile of the	Milital USSOCO PUS Was South Court I Think The			
35		the nu	rmerator and de	enominator ·						
•	Pkey	ExAcon	UnigenelD	Unigene Title	R1 14.06	R2 15.56				
	452838	U65011	Hs.30743	preferentially expressed antigen in mela dopachrome tautomerase (dopachrome delta	13.64	11.62				
40	430377	NM_001922	Hs.301865 Hs.2053	tyrosinase (oculocutaneous albinism IA)	13.50	7.98				
40	426555 438549	NM_000372 BE386801	Hs.21858	trinucleotide repeat containing 3	12.78	13.80 15.56				
	422424	AI186431	Hs.296638	prostate differentiation factor	11.88 10.14	22.46				
	426600	NM_003378 AJ005371	Hs.171014 Hs.248017	VGF nerve growth factor inducible glyceraldehyde-3-phosphate dehydrogenase	9.33	7.25				
45	430822 457211	AW972565	Hs.32399	ESTs. Weakly similar to S51797 vasodilat	8.66	9.62 9.58				
	438380	T06430	Hs.6194	chondroitin sulfate proteoglycan BEHAB/b	7.87 7.66	4.63				
	417355	D13168 AF035269	Hs.82002 Hs.17752	endothelin receptor type B phosphatidylserine-specific phospholipas	7.38	9.04				
	447210 413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	6.64	7.32 4.65				
50	415752	BE314524	Hs.78776	putative transmembrane protein	6.46 6.44	7.00				
	421508	NM_004833	Hs.105115 Hs.148324	absent in melanoma 2 ESTs	6.43	5.92				
	449644 426312	AW960707 AF026939	Hs.181874	interferon-induced protein with tetratri	6.27	6.47 3.70				
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	6.17 6.09	3.92				
55	429500 414812	X78565 X72755	Hs.289114 Hs.77367	hexabrachion (tenascin C, cytotactin) monokine induced by gamma interferon	6.04	7.73				
	452973	H88409	Hs.40527	ESTs	6.04	5.89 2.50				
	402075			ENSP00000251056":Plasma membrane calcium	n 5.96 5.72	5.29				
60	436856 425088	AI469355 AA663372	Hs.127310 Hs.169395	ESTs hypothetical protein FLJ12015	5.68	5.88				
UV	439310	AF086120	Hs.102793	ESTs	5.62 5.62	6.30 3.30				
	429170	NM_001394		dual specificity phosphatase 4 hypothetical protein, expressed in osteo	5.50	4.28				
	413670 409512	AB000115 AW979187	Hs.75470 Hs.293591	melanoma differentiation associated prot	5.36	4.14				
65	430540	AW245422		Homo sapiens cDNA: FLJ22105 fis, clone H	5.36 5.35	4.64 4.31				
	436315	BE390513	Hs.27935	hypothetical protein MGC4837 hypothetical protein MGC5370	5.28	4.03				
	442426 435056	AI373062 AW023337	Hs.332938 Hs.5422	glycoprotein M6B	5.23	3.25				
	432828	AB042326	Hs.287402	chandroitin 4-sulfotransferase	5.20 5.14	5.52 4.82				
70	430294	AI538226	Hs.32976 Hs.266175	guanine nucleotide binding protein 4 phosphoprotein associated with GEMs	5.09	4.35				
	431639 430838	AK000680 N46664	Hs.169395	hypothetical protein FLJ12015	5.06	3.68				
	414004	AA737033	Hs.7155	FSTs. Moderately similar to 2115357A TYK	5.04 4.94	4.23 6.29				
75	407366		Hs.17518 Hs.113019	gb:Homo sapiens cig33 mRNA, partial sequ fs485	4.88	5.62	·			
75	422192 420208		Hs.95972	silver (mouse homolog) like	4.88					
	445006	NM_00440	3 Hs.13530	deafness, autosomal dominant 5	4.77 4.74					
	440065		Hs.26633 Hs.10592		4.74	5.75				
80	421574 440274		Hs.7122	scrapie responsive protein 1	4.77					
55	417166	AA431323	Hs.42146	ESTs	4.66 4.63					
	415314		Hs.5422 Hs.16372	glycoprotein M68 4 ESTs	4.6					
	443983	H04482	113.10072		530					

	432642	BE297635	Hs.3069	heat shock 70kD protein 9B (mortalin-2)	4.62	2.87
	437179	AA393508		serologically defined colon cancer antig	4.62	5.08
	417933 431620	X02308 AA126109	Hs.82962 Hs.264981	thymidylate synthetase 2-5'-oligoadenylate synthetase 2 (69-71	4.58 4.50	3.02 4.37
5	431629	AU077025	Hs.265827	interferon, alpha-inducible protein (clo	4.49	16.82
•	447937	AL109716	Hs.20034	Homo sapiens mRNA full length insert cDN	4.44	5.95
	409264	NM_014937	Hs.52463	KIAA0966 protein	4.42	2.94
	434203 422309	BE262677	Hs.283558 Hs.114924	hypothetical protein PRO1855 solute carrier family 16 (monocarboxylic	4.42 4.38	3.54 3.30
10	449722	U79745 BE280074	Hs.23960	cyclin B1	4.32	4.07
••	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	4.30	3.82
	450065	AL050107	Hs.24341	transcriptional co-activator with PDZ-bi	4.28	4.36
	424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	4.27 4.25	3.05 4.68
15	413916 420267	N49813 N37030	Hs.75615 Hs.173337	apolipoprotein C-II ESTs	4.24	4.24
13	442739	NM_007274	Hs.8679	cytosolic acyl coenzyme A thioester hydr	4.21	3.00
	433576	BE080715	Hs.161091	ESTs	4.20	6.31
	412652	AJ801777		ESTs	4.20 4.20	2.73 5.18
20	438209 441553	AL120659 AA281219	Hs.6111 Hs.121296	aryi-hydrocarbon receptor nuclear transi ESTs	4.20	4.94
20	407856	AA045281	Hs.266175	phosphoprotein associated with GEMs	4.14	3.14
	439926	AW014875	Hs.137007	ESTs	4.12	4.76
	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	4.12 4.10	4.85 5.20
25	400860 409415	AA579258	Hs.6083	Target Exon Homo sapiens cDNA: FLJ21028 fis, clone C	4.08	6.02
23	416636	N32536	Hs.42645	solute carrier family 16 (monocarboxylic	4.08	2.42
	452826	BE245286	Hs.301636	peroxisomal biogenesis factor 6	4.06	2.96
	407748	AL079409	Hs.38176	KIAA0606 protein; SCN Circadian Oscillat	4.06	2.28
30	417632 418064	R20855	Hs.5422 Hs.83384	glycoprotein M68 S100 catcium-binding protein, beta (neur	4.01 4.00	2.96 4.62
50	448111	BE387287 AA053486	Hs.20315	interferon-induced protein with tetratri	4.00	2.82
	420674	NM_000055	Hs.1327	butyrylcholinesterase	4.00	2.90
	451668	Z43948	Hs.326444	cartilage acidic protein 1	3.99	5.17
35	430015	AW768399	N= 20200	ESTs	3.96 3.94	3.89 2.91
. 33	407756 430223	AA116021 NM_002514	Hs.38260 Hs.235935	ubiquitin specific protease 18 nephroblastoma overexpressed gene	3.93	3.89
•	433364	AI075407	Hs.296083	ESTs, Moderately similar to 154374 gene	3.93	4.70
	448719	AA033627	Hs.21858	trinucleofide repeat containing 3	3.92	7.78
40	419381	AB023420	Hs.90093	heat shock 70kD protein 4	3.87 3.87	3.34 3.69
40	402609 408083	BE383668	Hs.42484	KIAA1209 protein hypothetical protein FLJ10618	3.86	4.04
	409703	NM_006187	Hs.56009	2-5-oligoadenylate synthetase 3 (100 k	3.85	3.64
	420218	AW958037		ribosomal protein L4	3.84	3.20
45	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	3.84	5.19
45	410600	AW575742	U= 120000	ESTs, Moderately similar to S65657 alpha ESTs; hypothetical protein for IMAGE:447	3.82 3.82	5.74 2.96
	442117 428513	AW664964 BE220806	Hs.128899 Hs.184697	Homo sapiens clone 23785 mRNA sequence	3.82	4.03
	417381	AF164142	Hs.82042	solute carrier family 23 (nucleobase tra	3.80	3.56
50	432094	A1658580	Hs.61426	Homo sapiens mesenchymal stem cell prote	3.79	3.23
50	443105	X96753	Hs.9004	chondroitin sulfate proteoglycan 4 (mela	3.77 3.72	3.66 2.28
	423605 407846	AF047826 AA426202	Hs.129887 Hs.40403	cadherin 19, type 2 Cbp/p300-interacting transactivator, wit	3.72	5.34
	442578	AK001643	Hs.8395	hypothetical protein FLJ 10781	3.71	3.42
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	3.68	3.31
55	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	3.68 3.68	4.24 2.74
	400750 447217	BE465754	Hs.17778	Target Exon neurocilin 2	3.66	3.60
	459373	BE408266	Hs.301406	hypothetical protein PP3501	3.66	3.48
<b>60</b>	419628	H67546	Hs.49768	ESTs	3.62	4.13
60	406868	AA505445	Hs.300697	immunoglobulin heavy constant gamma 3 (G	3.61 3.59	4.40 3.53
	421866 421709	M24470 AA159394	Hs.1435 Hs.107056	guanosine monophosphate reductase CED-6 protein	3.57	2.63
	438501	Z44110	Hs.86149	phosphoinositol 3-phosphate-binding prot	3.56	3.54
	408962	BE386436	Hs.44317	SRY (sex determining region Y)-box 10	3.55	2.70
65	425139	AW630488	Hs.25338	protease, serine, 23	3.50 3.49	2.80 2.58
	428411 452744	AW291464 AI267652	Hs.10338 Hs.246107	ESTs Homo sapiens mRNA; cDNA DKFZp434E082 (fr	3.48	4.61
	411305	BE241596	Hs.69547	myelin basic protein	3.48	3.37
	447343	AA256641	Hs.236894		3.47	2.68
70	429954	AI918130	Hs.21374	ESTs	3.47	2.63 2.34
	417621 435256	AV654694 AF193766	Hs.82316 Hs.13872	interferon-induced, hepatitis C-associat cytokine-like protein C17	3.46 3.46	2.47
	450534	AI570189	Hs.25132	KIAA0470 gene product	3.42	3.65
	421100	AW351839	Hs.124660		3.41	2.63
75	418506	AA084248	Hs.85339	G protein-coupled receptor 39	3.40	4.02 2.95
	442711 453344	AF151073 BE349075	Hs.8645 Hs.44571	hypothetical protein ESTs	3.39 3.38	2.38
	436700	AI693690	Hs.301406		3.36	4.60
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	3.36	2.61
80	433867	AK000596	Hs.3618	hippocalcin-like 1	3.36	4.26 2.10
	408393 447484	AW015318 AA454839	Hs.23165 Hs.292566	ESTs hypothetical protein FLJ14697	3.36 3.36	2.49
	412828	AL133396	Hs.74621	prion protein (p27-30) (Creutzfeld-Jakob	3.35	2.27

					3.35	2.58
	426158			v-erb-b2 avian erythroblastic leukemia v	3.35 3.34	2.55
	440325	NM_003812	Hs.7164	a disintegrin and metalloproteinase doma regulator of G-protein signalling 20	3.34	5.96
	420602 439963	AF060877 AW247529	Hs.99236 Hs.6793	olatelet-activating factor acetylhydrola	3.34	2.73
5	406663	U24683	1,0.0.00	immunoglobulin heavy constant mu	3.31	5.21 3.40
•	427540	R12014	Hs.20976	ESTs	3.30 3.29	2.80
	412141	AI183838	Hs.48938	hypothetical protein FLJ21802 NM_005313:Homo sapiens glucose regulated	3.29	3.46
	400282	AW403911	Hs.266175	phosphoprotein associated with GEMs	3.28	5.20
10	419870 416539	Y07909	Hs.79368	epithetial membrane protein 1	3.28	2.79
10	431518	AA743462	Hs.165337	FSTs	3.27 3.26	2.51 6.38
	402994			NM_002463":Homo sapiens myxovirus (influ	3.26	4.48
	419956	AL137939	Hs.40096 Hs.103982	cadherin 19, type 2 small inducible cytokine subfamily B (Cy	3.26	3.71
15	421379 444371	Y15221 BE540274	Hs. 103902 Hs. 239	forkhead box M1	3.25	3.72
13	432874	W94322	Hs.279651	melanoma inhibitory activity	3.25 3.24	5.33 3.20
	417282	AA195203		RABSC, member RAS oncogene family	3.24 3.24	2.32
	439569	AW602166	Hs.222399	CEGP1 protein bone marrow stromat cell antigen 2	3.24	6.20
20	422530	AW972300	Hs.118110	NM_015271:Homo sapiens tripartite motif-	3.23	3.70
20	403817 407857	AI928445	Hs.92254	synaptotagmin-like 2	3.22	2.49 2.46
	426334	BE305081	Hs.169358	hypothetical protein	3.21 3.19	5.50
	453837	AL138387	Hs.256126	baculoviral IAP repeat-containing 7 (liv ectonucleotide pyrophosphatase/phosphodi	3.18	2.04
25	427283	AL119796	Hs.174185 Hs.23765	Homo sapiens mRNA; cDNA DKFZp547M123 (fr	3.18	3.73
25	437379 424090	AL359575 X99699	Hs.139262	XIAP associated factor-1	3.18	4.44
	410491	AA465131	Hs.64001	Homo sapiens clone 25218 mRNA sequence	3.18 3.16	3.26 2.21
	408418	AW963897	Hs.44743	KIAA1435 protein	3.16	4.04
20	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous C1002500:gij6754254 ref NP_034610.1  hea	3.15	4.57
30	402829	AW978107	Hs.5884	Homo sapiens mRNA; cDNA DKFZp586C0224 (f	3.15	3.07
	437862 425935	Z98200	Hs.163724	HSPC019 protein	3.14	3.08 2.73
	417124	BE122762	Hs.25338	ESTs	3.14 3.11	2.16
	425071	NM_013989		deiodinase, iodothyronine, type II Homo sapiens cDNA: FLJ22528 fis, clone H	3.10	2.43
35	412490	AW803564	Hs.288850 Hs.8180	syndecan binding protein (syntenin)	3.10	2.83
•	442271 415817	AF000652 U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	3.10	1.78
	429083	Y09397	Hs.227817	BCL2-related protein A1	3.10 3.10	3.17 3.32
	437673	AW565665	Hs.153034	ESTs	3.10	3.90
40	407813	AL120247	Hs.40109	KIAA0872 protein KIAA0455 gene product	3.10	3.35
	445745	AB007924 R56631	Hs.13245 Hs.26550	retinoid X receptor, gamma	3.09	4.45
	451537 408654	BE018882	Hs.46721	UCC1 protein	3.08	3.65 2.12
_	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	3.08 3.08	2.12
45	446019	AI362520		histone deacetylase 3	3.08	5.29
	434276		Hs.93605 Hs.59622	leucine zipper, putative tumor suppresso Homo sapiens, clone IMAGE:3507281, mRNA,	3.06	3.36
	427871 403532		NS.33022	NM_024638:Homo sapiens hypothetical prot	3.06	3.37
	433160			TASP for testis-specific adriamycin sens	3.04 3.03	3.17 2.98
50	446341	AL040763	Hs.31073		3.03	2.01
	426501		Hs.29361 Hs.91973	6 ESTs ESTs	3.02	2.19
	450325 418941		Hs.23952		3.02	3.29
	431797		Hs.27013		3.02 3.00	2.54 1.96
55	442064		Hs.88594	ESTs	3.00	2.98
	40545		52 Hs.76391	dihydropyrimidinase-like 3 myxovirus (influenza) resistance 1, homo	2.99	6.41
•	414915 454117				2.98	3.25
	45295			FSTs	2.98 2.96	4.14 3.30
60	42764	7 W19744	Hs.1800	9 Homo sapiens cDNA FLJ20653 fis, clone KA	2.96	2.47
	40919				2.96	4.16
	42881 42845				2.96	2.41
	41421		Hs.7582	ALL1-fused gene from chromosome 1q	2.95	2.79 4.70
65	41135		Hs.9476		2.95 2.94	2.65
	43248		Hs.2393	Human DNA sequence from clone RP1-304B14 NM_002082*:Homo sapiens G protein-couple	2.94	2.69
	40022			NM 025184":Homo sapiens hypothetical pro	2.94	2.55
	40578 40978		0	nh FST10534 Adinose tissue, white I Homo	2.94	2.57
70	41811		Hs.8348	4 SRY (sex determining region Y)-box 4	2.93 2.93	2.52 2.43
	40903		Hs.5000		2.92	3.20
	45670				2.91	4.45
	4597 4113			KIAA1802 protein	2.90	2.72
75	4275			65 minichromosome maintenance deficient (S.	2.90 2.90	2.27 2.03
	4069	64 M21305		FGENES predicted novel secreted protein	2.50 2.89	3.55
	4288				2.89	3.87
	4131 4386		-	TU12B1-TY protein	2.88	2.37
80	4424		89 Hs.381	78 hypothetical protein FLJ23458	2.87	2.00 2.51
	4287	82 X12830	Hs.193		2.86 2.86	3.07
	4540		Hs.215 Hs.279 Hs		2.86	5.58
	4531	07 NM_016	1113 113.273	To the second to the second se		

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	414737	AI160386	Hs.125087	ESTs	2.84	2.79
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	2.84	3.80
	447735	AA775268	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L	2.83 2.83	2.11 3.32
5	416091 442445	AF295370 AA082665	Hs.283082 Hs.209561	defensin, beta 3 KIAA1715 protein	2.81	2.17
,	408208	BE018717	113.203001	ESTs	2.81	2.43
	430066	AI929659	Hs.237825	signal recognition particle 72kD	2.80	2.25
	424755	AB033094	Hs.152925	KIAA1268 protein	2.80	2.74
10	422616	BE300330	Hs.118725	selenophosphate synthetase 2	2.79 2.78	201 265
10	405506 411619	AI418609	Hs.71040	Target Exon hypothetical protein FLJ20425	2.78	3.10
	400236	AM 10003	113.7 1040	Eos Control	2.78	2.21
	452698	NM_001295	Hs.301921	chemokine (C-C motif) receptor 1	2.78	3.15
	446488	AB037782	Hs.15119	KIAA1361 protein	2.78	2.80
15	439778	AL109729	Hs.99364	putative transmembrane protein	2.78 2.78	3.78 2.86
	420005 428642	AW271106 NM_014899	Hs.133294 Hs.10432	ESTs KIAA0878 protein	2.77	3.07
	453779	N35187	Hs.43388	28kD interferon responsive protein	2.76	4.56
	425289	AW139342	Hs.155530	interferon, gamma-inducible protein 16	2.76	1.83
20	437723	AI672731	Hs.13256	ESTs	2.76	4.23
	416730	T99937		gb:ye72d04.r1 Soares fetal liver spleen	2.76 2.76	2.98 3.21
	426153	AF057169 H58373	Hs.182771 Hs.332938	vitelliform macular dystrophy (Best dise hypothetical protein MGC5370	2.76	3.97
	444670 421351	AU076667	Hs.103755	receptor-interacting serine-threonine ki	2.74	3.50
25	406673	M34996	Hs.198253	major histocompatibility complex, class	2.74	3.24
	427268	X78520	Hs.174139	chloride channel 3	2.74	2.82
	428403	AI393048	Hs.326159	leucine rich repeat (in FUI) interaction	2.74 2.74	1.95 2.99
	409417	AA156247	Hs.104879	serine (or cysteine) proteinase inhibito ESTs	274	2.33
30	419705 440457	AW368634 BE387593	Hs.154331 Hs.21321	Homo sapiens clone FLB9213 PRO2474 mRNA,	2.72	3.60
50	413599	AJ006239	Hs.75438	quinoid dihydropteridine reductase	2.72	2.43
	447164	AF026941	Hs.17518	vipirin; similar to inflammatory respon	2.72	4.77
	430594	AK000790	Hs.246885	hypothetical protein FLJ20783	2.72	3.67
35	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa 2,3'-cyclic nucleofide 3' phosphodieste	2.71 2.70	12.06 2.40
33	424572 409142	M19650 AL136877	Hs.179600 Hs.50758	SMC4 (structural maintenance of chromoso	2.70	3.81
	425996	W67330	16.50700	hypothetical protein AL110115	2.69	3.85
	430441	BE398091		desmoplakin (DPI, DPII)	2.68	2.55
40	442355	AA456539	Hs.8262	lysosomal-associated membrane protein 2	2.68	1.67
40	421362	AK000050	Hs.103853	hypothetical protein FLJ20043	2.68 2.68	2.94 1.89
	437158 412315	AW090198 AW936678		KIAA1150 protein gb:PM2-DT0023-080300-004-a04 DT0023 Homo	2.68	2.80
	432878	BE386490	Hs.279663	Pirin	2.68	2.58
	408822	AW500715	Hs.57079	Homo sapiens cDNA FLJ13267 fis, clone OV	2.68	2.74
45	426759	AI590401	Hs.21213	ESTs	2.68	2.35
	405486		14. 47000	Target Exon	2.67 2.67	2.70 3.33
	410326	Al368909 AW444613	Hs.47650 Hs.288809	ESTs hypothetical protein FtJ20159	2.66	2.54
	434040 437396	BE140396	Hs.21621	hypothetical protein DKFZp7620076	2.66	1.91
50	412719	AW016610	Hs.816	ESTs	2.66	4.21
	451708	Al306536	Hs.60975	ESTs	2.66	5.69
	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	2.66 2.66	2.31 2.73
	425017 400235	AL119305	Hs.26409	ESTs NM_005336:Homo sapiens high density lipo	2.66	2.29
55	444809	BE207568	Hs.208219	oculospanin	2.64	2.86
-	436291	BE568452	Hs.344037	protein regulator of cytokinesis 1	2.64	2.33
	406382			C16001275*:gi 12698037 dbj BA821837.1  (	2.64	2.48
	432241	AI937060	Hs.6298	KIAA1151 protein	2.63 2.63	3.16 2.10
60	417308 429294	H60720 AA095971	Hs.81892 Hs.198793	KIAA0101 gene product Homo sapiens cDNA: FLJ22463 fis, clone H	2.62	2.43
UU	453935	AI633770	Hs.42572	ESTs	2.62	1.99
	401454	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,		NM_014226*:Homo sapiens renal tumor anti	2.62	3.01
	436456	AW292677	Hs.248122		2.62	5.94
65	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	2.61 2.60	3.02 2.68
65	453256 451622	AI565587 AW139587	Hs.32556 Hs.30579	KIAA0379 protein Homo sapiens cDNA: FLJ23070 fis, clone L	2.60	2.51
	424006	AF054815	Hs.137548		2.60	2.56
	409354	N68188	Hs.159472		2.59	3.00
	425392	N39725	Hs.15220	zinc finger protein 106	2.58	3.52
70	427286	AW732802	Hs.2132	epidermal growth factor receptor pathway	2.58 2.58	1.86 2.15
	418166 413794	AI754416 AF234532	Hs.61638	Cdc42 effector protein 3 myosin X	2.58	2.54
	445707	AI248720	Hs.114390		2.58	1.95
	416640	BE262478	Hs.79404	neuron-specific protein	2.57	2.46
75	427982	NM_016156			2.56	1.74
	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	2.56 2.55	2.22 2.34
	455839 447737	BE145814 AK000643	Hs.19404	gb:MR0-HT0208-101299-202-a04 HT0208 Homo DKFZP564L0862 protein	2.55 2.55	2.31
	423799		Hs.132906		2.54	211
80	442762		Hs.8700	deleted in liver cancer 1	2.54	2.47
	432886		Hs.279704		2.54	3.99
	440676			3 LIM and senescent cell antigen-like doma proteolipid protein 1 (Pelizaeus-Merzbac	2.54 2.53	2.96 6.98
	424481	R19453	Hs.1787	hometho home it is entanged and to a	2.33	5.50

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	422340	AW296219	Hs.115325 F	AB7, member RAS oncogene family-like 1	2.53	3.06
	428844	AW972635		ypothetical protein FLJ12671	2.53 2.53	3.13 1.63
	458997	AW937420		STs	2.53 2.52	2.30
-	419591	AF090900		tomo sapiens cDNA: FLJ21887 fis, ctone H nydroxyprostagtandin dehydrogenase 15-{N	2.52	1.80
5	414807 429238	A1738616 NM_002849		protein tyrosine phosphatase, receptor t	2.52	3.02
	432882	NM_002045 NM_013257		serum/glucocorticoid regulated kinase-li	2.52	3.05
	407260	L09095		gb:Horno sapiens mRNA fragment	2.50	5.00
	431186	NM_012249	Hs.250697	ras-like protein	2.49 2.49	6.16 4.71
10	417542	J04129	Hs.82269	progestagen-associated endometrial prote	2.48	5.77
	419556	U29615		chilinase 1 (chitotriosidase) ets variant gene 5 (ets-related molecule	2.48	3.77
	408209 405885	NM_004454		Target Exon	2.46	3.11
	406837	R70292		immunoglobulin kappa constant	2.44	3.10
15	412609	Z48804	Hs.74124	ocular albinism 1 (Nettleship-Falls)	2.44	4.90 4.31
	421633	AF121860	Hs.106260	sorting nexin 10	2.44 2.42	4,31 3,19
	415929	AA724373	Hs.49344	hypothetical protein FLJ11006	2.37	3.57
	413171	AA318325	Hs.75219	tyrosinase-related protein 1 immunoglobulin lambda locus	2.36	5.87
20	406621	X57809	Hs.8997 Hs.334485	hemicentin (fibulin 6)	2.36	3.04
20	414142 410700	AW368397 AA352335	Hs.65641	hypothetical protein FLJ20073	2.36	3.66
	414283	AW960011	Hs.154993	ESTs	2.34	4.95
	453931	AL121278	Hs.25144	ESTs	2.34 2.32	4.18 3.45
	422515	AW500470	Hs.117950	multifunctional polypeptide similar to S	2.32	4.94
25	435292	N20514	Hs.172965	ESTs macrophage myristoylated alanine-rich C	2.31	3.78
	412926	A1879076	Hs.75061 Hs.317714	pallid (mouse) homolog, pallidin	2.30	3.95
	440197	AW340708 D87119	Hs.155418	GS3955 protein	2.29	5.08
	425262 439979	AW600291	Hs.6823	hypothetical protein FLJ10430	2.28	4.05
30	403969	7111000201		ENSP0000034663:Zinc finger protein 131	2.28	3.64
-	421686	AB011156	Hs.106794	KIAA0584 protein	2.26 2.24	3.31 4.08
	432800	BE391046	Hs.278962	AIM-1 protein	2.24	3.47
	406782	AA430373	11. 70472	gb:zw20f11.s1 Soares ovary turnor NbHOT H	2.22	3.66
35	415539	AI733881	Hs.72472 Hs.21938	BMP-R1B hypothetical protein FLJ12492	2.20	3.43
33	447523 433180	BE613328 AB038651	Hs.31854	K562 cell-derived leucine-zipper-like pr	2.20	3.52
•	415825	Y18024	Hs.78877	inositol 1,4,5-trisphosphate 3-kinase B	2.19	3.76
	407241	M34516		gb:Human omega light chain protein 14.1	2.18	3.17
	422243	AW803733	Hs.23585	hypothetical protein MGC12250	2.18 2.16	3.28 5.85
40	417324	AW265494		ESTS	2.14	3.49
	412819	T25829	Hs.24048	FK506 binding protein precursor	2.13	4.39
	432342	AL036128	Hs.274404 Hs.301406	plasminogen activator, tissue hypothetical protein PP3501	2.13	5.48
	427923 417437	AW274357 U52682	Hs.82132	interferon regulatory factor 4	2.13	3.08
45	425535	AB007937	Hs.158287	KIAA0468 gene product	2.13	8.66
-13	429638	AI916662	Hs.211577	kinectin 1 (kinesin receptor)	2.12	3.01 4.66
	409154	U72882	Hs.50842	interferon-induced protein 35	2.12 2.12	3.71
	429951	AL040521	Hs.15220	zinc finger protein 106	211	4.27
50	418918	X07871	Hs.89476	CD2 antigen (p50), sheep red blood cell EST	2.11	3.58
50	419200	AW966405 L13210	Hs.79339	tectin, galactoside-binding, soluble, 3	2.10	5.34
	416448 425069	AA687465	Hs.298184	potassium voltage-gated channel, shaker-	2.07	7.86
	445133			ESTs	2.06	3.68 3.36
	411492		Hs.70337	immunoglobulin superfamily, member 4	2.04 2.03	3.41
55	408015		Hs.244349	epidermal differentiation complex protei	2.03	3.82
	424412		Hs.10043	hypothetical protein FLJ13074 ESTs, Weakly similar to 834087 hypotheti	2.02	3.03
	431657 427536		Hs.105448 Hs.115803		2.02	3.09
	400533		110.110000	ENSP00000209376*:PRED65 protein (Fragmen	2.00	3.29
60	432680		Hs.278613	interferon, alpha-inducible protein 27	1.99 1.97	3.07 4.52
	410129		Hs.58831	regulator of Fas-induced apoptosis	1.97 1.97	3.26
	417312				1.94	3.79
	423952			MIAA0853 protein ESTs, Wealdy similar to zinc finger prot	1.93	3.16
65	455705 419723				1.93	3.11
05	438866		Hs.32549	5 fissue inhibitor of metalloproteinase 2	1.93	3.47
	448410				1.92	3.00 4.07
	400293	2 AA250737			1.92 1.90	3.04
70	43679			7 hypothetical protein MGC14879	1.90	6.53
70	40685			major histocompatibility complex, class 5 CGI-76 protein	1.89	3.39
	42843 43183				1.89	4.04
	42468		Hs.15173		1.87	3.64
	42632		Hs.2012	transcobalamin I (vitamin B12 binding pr	1.85	4.21
75	42522	1 AV649864			1.85 1.85	3.13 3.04
	42016				1.85	3.20
	44353			binder of Arl Two 5 19A24 protein	1.84	3.39
	43367				1.82	3.22
80	42441 40099			Target Exon	1.82	4.11
00	41867		Hs.8722	SRY (sex determining region Y)-box 5	1.82	3.43
	42444	11 X14850	Hs.1470	7 H2A histone family, member X	1.81 1.79	3.12 5.31
	42482	25 AF20706	9 Hs.1533	57 procottagen-lysine, 2-oxoglutarate 5-dio	1./3	

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	425818	AB021225	Hs.159581	matrix metalloproteinase 17 (membrane-in	1.79	3.40
	416426	AA180256	Hs.210473	Homo sapiens cDNA FLJ14872 fis, clone PL	1.78	3.38
	414945	BE076358	Hs.77667	lymphocyte antigen 6 comptex, locus E	1.77	3.69
5	440942	AW246547	Hs.17901	Horno sapiens, clone IMAGE:3937015, mRNA,	1.77	3.12
5	401591	NIN 000000	Un 100000	Target Exon	1.75 1.75	4.30 3.68
	425923 412844	NM_005026 AI828045	Hs.162808 Hs.18016	phosphoinositide-3-kinase, catalytic, de Homo sapiens mRNA; cDNA DKFZp586H0324 (f	1,74	3.53
	417237	H86385	Hs.81737	palmitoyi-protein thioesterase 2	1.73	3.06
	419849	BE041436	Hs.93379	eukaryotic translation initiation factor	1.72	4.38
10	454429	BE273437	Hs.301406	hypothetical protein PP3501	1.72	4.38
	440672	AF083811	Hs.7345	MAD1 (mitotic arrest deficient, yeast, h	1.72	3.61
	408204	AA454501	Hs.43666	protein tyrosine phosphalase type IVA, m	1.72	3.06
	430148	BE387620	Hs.234489	lactate dehydrogenase B	1.71	4.38
15	426502	Y07759	Hs.170157	myosin VA (heavy polypeptide 12, myoxin)	1.70 1.70	3.13 3.08
13	413317 417333	U53225 AL157545	Hs.75283 Hs.173179	sorting nexin 1 bromodomain and PHD finger containing, 3	1.68	3.15
	407223	H96850	113.113113	gb:yw03b12.s1 Soares melanocyte 2NbHM Ho	1.68	4.19
	413566	AW604451	Hs.285814	sprouty (Drosophila) homolog 4	1.67	5.74
	404067			Target Exon	1.67	4.73
20	447630	A1660149	Hs.44865	lymphoid enhancer-binding factor 1	1.66	3.22
	443337	Y07604	Hs.9235	non-metastatic cells 4, protein expresse	1.65	3.17
	427747	AW411425	Hs.180655	serine/threonine kinase 12	1.64	3.35
	437912	BE278594	Hs.5912	F-box only protein 7	1.64	3.24
25	404140 414214	D49958	Hs.75819	NM_006510:Homo sapiens ret finger protei	1.64 1.64	3.10 3.45
23	427239	BE270447	NS./3013	glycoprotein M6A ubiquitin carrier protein	1.62	3.58
	427289	AI097346		phosphoserine aminotransferase	1.62	5.89
	452923	BE276018	Hs.288940	five-span transmembrane protein M83	1.62	3.23
	426020	AL110195	Hs.166017	microphthalmia-associated transcription	1.62	4.00
30	439627	BE621702	Hs.29076	hypothetical protein FLJ21841	1.61	5.00
	451489	NM_005503	Hs.26468	amyloid beta (A4) precursor protein-bind	1.60	3.06
	414699	AJ815523	Hs.76930	synuclein, alpha (non A4 component of am	1.58	3.34
	411825	AK000334		hypothetical protein FLJ20327	1.56	3.18
35	438552	AJ245820	Hs.6314	type I transmembrane receptor (seizure-r	1.56	3.23
33	428081	AA421048	Hs.95011	syntrophin, beta 1 (dystrophin-associate	1.55 1.54	3.10 3.33
	401914 424902	NM_003866	Hs. 153687	Target Exon inositol polyphosphate-4-phosphatase, ty	1.54	3.15
	441648	H05734	Hs.30559	ESTs	1.52	3.36
	439769	AA448828	Hs.30596	Homo sapiens mRNA full length insert cDN	1.52	3.17
40	437696	Z83844	Hs.5790	hypothetical protein dJ37E16.5	1.52	4.93
	413019	BE281604	Hs.75140	low density apoprotein-related protein-	1.52	3.01
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	1.52	3.83
	422596	AF063611	Hs.118633	2-5-oligoadenylate synthetase-like	1.50	3.04
45	421851	R18686	Hs.108896	tambda-crystallin	1.47	3.10
43	448499	8E613280	Hs.77550	hypothetical protein MGC1780	1.44	3.07
	427378	BE515037	Hs.177556	melanoma antigen, family D, 1 heat shock 90kD protein 1, beta	1.44 1.42	3.00 3.66
	412641 448143	M16660 AF039704	Hs.74335 Hs.20478	ceroid-lipofuscinosis, neuronal 2, late	1.42	4.16
	413291	NM_006278	Hs.75268	sialytransferase 4C (beta-galactosidase	1,41	3.30
50	435968	AW161481	Hs.111577	integral membrane protein 3	1,41	3.30
	422486	BE514492	Hs.117487	gene near HD on 4p16.3 with homology to	1.40	3.01
	443759	BE390832	Hs.134729	FXYO domain-containing ion transport reg	1.39	3.82
	444441	AW613841	Hs.301394	hypothetical protein MGC3101	1.39	3.43
55	430205	AB025904	Hs.235168	carbonic anhydrase XIV	1.36 1.35	3.32 3.03
22	406827	AA971409 Z25424		gb:op92c04.s1 NCI_CGAP_Lu5 Homo sapiens gb:H.sapiens protein-serine/threonine to	1.34	6.25
	406906 426890	AA393167	Hs.41294	ESTs	1.34	3.66
	433320	D60647	Hs.250879	ESTs, Highly similar to CTXN RAT CORTEXI	1.34	3.18
	450358	AB010098	Hs.24907	coronin, actin-binding protein, 28	1.33	3.19
60	421612	AF161254	Hs.106196	806 antigen	1.33	3.03
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	1.32	3.68
	428342	AJ739168		Homo sapiens cDNA FLJ13458 fis, clone PL	1.32	3.10
	449444	AW818436		solute carrier family 16 (monocarboxylic	1.30	3.30
65	404700			Target Exon	1.30	3.14 4.22
UJ	403043	NIV OCCUC	Un 60000	Target Exon	1.30 1.29	3.09
	409858 424679	NM_006586 AL117477	Hs.56828 Hs.119960	trinucleotide repeat containing 5 DKFZP727G051 protein	1.27	3.13
	406908	Z25437	119.113300	gb:H.sapiens protein-tyrosine kinase gen	1,27	3.66
	432665	AW603880		ATPase, H transporting, lysosomal (vacuo	1.26	3.09
70	423130	AW897586	Hs.21213	ESTs	1.24	3.34
-	453220	AB033089	Hs.32452	Horno sapiens mRNA for KIAA1263 protein,	1.24	3.15
	442680	BE270707	Hs.8583	similar to APOSEC1	1.22	3.94
	422319	AW403342	Hs.115232		1.21	3.36
75	402408	NIL 000407	U- 150701	NM_030920*:Homo sapiens hypothetical pro	1.04	3.37
75	424905	· NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	1.00	3.02

TABLE 51B:
Pkey: Unique
CAT number: Gene of
Accession: Genbar Unique Eos probeset identifier number Gene cluster number Genbank accession numbers

80

Pkey CAT Number Accession

	430540		BC017171 BC012195 NM_007126 AF100752 AL137377 Z70768 BM474865 BG754806 AU124376 BG757203 BG764420 BG775028 BG824418 BM045810 AU120387 BG770238 BG686740 BG913323 B1759980 BG395998 BM048875 BE881070 BE313689 BE879144 BM309834 AW245847 AJ770171 BF196861 BE856897 AA463876 AJ375927 AA648810 AA948193 AA490916 AJ459893 AJ458188 AJ240408 AJ191843 AJ131029 AW768399 AJ365196 AW337984 AW026150 BE466591 BE674599 AI818438 AA772197 AJ651927 AW151143 B1198825 BG819083 BM458764 BE903567 AJ365196 AW337984 AW026150 BE466591 BE674599 AI818438 AA772197 AJ651927 AW151143 B1198825 BG819083 BM458764 BE903567
5			BE732715 BMM33200 BE900263 BE900706 BE731097 BE390023 BG875394 BF995406 BF985930 BM73322 ANT-2675 BE3075 BE50537 BE903782 BE732947 BI227204 BG761305 BE526342 BE52642 BE31848 BE382475 BG008258 BI547991 BI459099 BE391391 BE259420 BE596150 AW7245422 AM423847 AI914618 H80534 BE301004 AL531791 AI435581 BF793112 AL577303 AA373265 BE746965 BF743630 BE679296 BE298109 AW7245422 AM423847 AI914618 H80534 BE209109 AW745422 AM423847 AI914618 H80534 BE301004 AL531791 AI435581 BF793112 AL577303 AA373265 BE746965 BF743630 BE6787231 BM462953 AI359493 BM018598 AI689260 AW072450 F30201 AW151405 AW517572 AA773468 BG259694 BE39163 BG675231 BM62953 AI359493 BM018598 AI689260 AW072450 F30201 AW151405 AW517572 AA773468 BG259694 BE391319163 BG651259 AI4217369 AI6767231 BM462953 AI359493 BW018598 AI689260 AW072450 F30201 AW151405 AW517572 AA773468 BG259694 BE391319 BE259418 BE785738 BW91659 N72512
10			WS8732 W85690 BG958989 AI205206 H19721 W17051 W17958 BILSZD10 AA64319 W7415 W722 H1851W E17 H8515W
15	437179	12239_1	AK055109 BC019085 AA187684 BG656226 BM023227 AI932311 AW7626381 AA398371 BM021493 A432433 AIG7517 A129930 AV76227 AI932311 AW76259 BM021307 AL080074 AA129218 AW207842 N90581 AA771919 AI092259 AI34107 BM023515 AA977504 AI859222 AI348454 R69725 AA975688 BM021207 AL080074 AA129218 AW207842 N90581 AA771919 AI092259 AI028416 AI074114 BG656536 BE501677 AW193419 AA977040 W90430 AI342984 AI378957 AL036486 AW020068 BI491093 BF476021 R41226
20	412652	18858_2	AB01777 BE677762 AW008210 AW009441 BE350994 BE207949 AU91475 AI802774 AI82733 AU75363 AU05397 AA687632 AV007437 AA670058 AA602411 AA683472 A436058 AA612826 AU038932 BC057726 A1167355 BF449023 A1289476 AW074381 BF972912 A1991780 AA889119 A4537472 Z39730 A1868953 A1192337 BE812978 BE812939 AA115248 H99006 A1915784 F08973 T16748 D20468 AA609899 BF081234 AA115336
25	430015	713_2	BE812876 BE812972 BE812982 BE813005 BE813015 ME813015 ME8
30			A159493 BM018598 A1689260 AW072450 F20201 AW151405 AW51/572 AA7/3406 BG23999 BT981332 BE259418 BE785738 BI091658 N72512 BG340524 W52648 AA113434 BE785431 BI041981 BG832385 BG253168 BG759470 BT 389329 BF981332 BE259418 BE785738 BI091658 N72512 BG340524 W85690 BG958989 A1205206 H19721 W17051 W77958 B1262010 AA844319 W74143 W72214 N85194 BE734033 BG164099 AA931069 W58732 W85690 BG9589899 A1205206 H19721 W17051 W77958 B1262010 AA844319 W74143 W72214 N85194 BE734033 BG164099 AA931069 H13645 R41394 AK025758 BG180977 BE349455 AA812018 AA774574 A027722 A150356 AA886393 AW977527 BE220225 AA884082 AW518114 B73645 R41394 AK025758 BG180977 BE349455 AA812018 AA774573 AP156766 AA774593 AP159399 AI537550 AA491103
35	420218	191547_1	AV23844 AA80993 AA451029 AA8576 A1347604 A315760 A28150 A2
40	410600 400282	497855_1 7778_2	BF347859 AW499616 AA191322 AW499617 AL501010 AW575742 AA729043 BE403447 A0080179 BE593623 AV35362 AV4767 AL50103 AL548510 AL542531 BC014433 Z49835 D16234 U42068 D83485 NM_005313 AL53156 AL53202 AL533596 AL531770 AL542767 AL551050 AL548510 AL542531 AL540818 BE799237 AL547374 AL560312 AL543505 AL540727 AL541255 BG765697 AU126498 BI829574 BG576125 AL519304 AL54821 AL542983 AL546818 BE799237 AL547374 AL560312 AL543505 AL540727 AL541255 BG765697 AU126498 BI829574 BG576125 AL519304 AL548281 AL542983 BI596431 BI829284 AL045490 BE407984 BI668702 BI713725 BE547233 BM312673 BG822625 AW29391 Z BM3126285 BE296719 BM312059 BI712618 BI596431 BI829284 AL045490 BE407984 BI668702 BI713725 BE547233 BM312673 BG822625 AW29391 Z BM312635 BG472541
45	417282	2142_2	BF724689 AA353713 BF477104 Bi838605 BG170854 BE612762 BF917301 BF-332271 BI049160 BE7-15315 AUT-25716 DE1-16315 AUT-25716 DE1-
50			AA234218 A.M. 2046 B.M. 2016 120 BE 206937 ALSO 120 AVG 120 AV
	446019	658727_1	AU362520 D25917 ABC0184 A174234 AW259165 A22107 W ARTON ARTO
55	400222 409760 438619	865166_1	AA302840 T93016 T92950 AU184997 AA077551 NM_016575 AB032773 AI765521 BF593742 AI497757 AI761233 AW467938 BF000670 AI818496 N24761 AL043306 BF476138 BF593836 AA132787 NM_016575 AB032773 AI765521 BF593742 AI497757 AI761233 AW467938 BF000670 AI818496 N24761 AL043306 BF476138 BF593836 AA132787 AI147248 AI086795 AA151317 T95288 AW083548 AA058371 N27951 AI769860 AI784548 AW205506 AI800679 AI041733 AI459902 BE327641 AI147248 AI086795 AA151317 T95288 AW083548 AA058371 N27951 AI769860 AI784948 AW205506 AI800679 AI041733 AI459902 BE327641
60	408208	642734_1	A1127616 N35901 AA682443 AA678249 AA719371 AA132582 T15981 N99958 N40717 AW959402 AX67251 BF909329 A142005 193579 N29720 R59632 H17318 H17331 H29327 R40829 R3395 R59573 A1749561 R56599 H16755 A1694500 AA027907 R59632 H17318 H17331 H29327 R40829 R53279 R59573 A1749561 R56599 H16755 A1694500 AA027907
65	400238	3 231_3	BITS/7837 XW419843 XW11/2763 BEU107176 GEU30726 BES00208 BF968374 XI806648 BG774205 XW250728 BE265845 AA290719 M80359 NM_002376 AU132239 AU120606 AU124963 AU665116 BE900808 BF968374 XI806648 BG774205 XW250728 BE265845 AA290719 AU125196 BG428863 AA333580 AA604551 W73300 XI932646 AA082201 AA627618 BF038887 BF337051 BI021159 XW057581 XI983156 AI268004 T71931 T90093 XW194009 H93969 XI742843 XI935080 BE041751 H93970 XW797399 W05032 T87824 T82912 XW129639 XI221821 XI911810 AA703093 AA160135 XW779124 AA102559 AA969546 D29560 BI915937 AA707716 BI085679 AA700887 AA081085
	416730 425990		
70	43044	1 1438_6	AI796380 AW117545 AI749657 AI537634 N50122 BG108218 BE560548 AW380115 BE269629 AI911518 AW380113 AA902964 AA455001 AI276529 AI685597 AA970496 D61084 AW380068 AW380080
	43715	8 59575_1	R00283 C15236 AW327776 D80759 AL050068 AA160485 AW173544 AW296506 AW439860 AI521563 AI702529 AI393606 AW138323 AA570109 H19504 BM021968 BF063327 BF593552 AA530766 AI597717 AI807128 AA523012 AI356250 AW451857 AA974203 AI762577 BF512552 AW007307 BE675286 AW450602 AA962057
75			AW516069 AI582546 BF221924 BF222543 AI801808 AW468599 AW000736 AI866625 AW235356 BM021837 AA911956 AI66000 W66316 103370 AW611634 H41653 AI468349 H19588 AW090188 AW063993 R39847 AW036625 AW236363 AW036685 AW236635 AW236637 AW23667 AW23667 AW23667 AW23667 AW23667 AW23667 AW23667 AW2367 AW236
	41231		ALLMOST ON ALLMOST ON ALLMOST ON ALMOST OF THE STATE OF T
80	40023	5 3084_1	AW936/30 AW336/32 AW336/32 AW336/32 AW336/32 BI27845 BI318183 AU124191 AU125604 AU140930 AL043307 BG7636/70 BG824279 AU125959 BI518466 BC001173 NM_005336 M64098 BC014305 BI827845 BI31838 AU124191 AU134388 BE163488 BE163483 BC421980 BC768130 AW300482 AU310178 AW868323 BI318438 BI3184388 BE163483 BC421980 BC768130 AW300482 AU3101078 AW368323 BI70 AW450290 BM466817 BG255224 BE394282 AU140278 BB7464 AL042675 BI195986 BE883385 BE544751 BE270148 BM011334 AU933482 AAD28903 AM510705 BE38609 F06628 AW408605 BF814085 BC007961 BM451548 BG768053 BM452948 AU140330 BG489566 BI870474 BM014013 AU131264 BG679824 BI225752 BI457400 BE410173 BM044254 BG763690 BE251495 BG179862 BE513489
			545

			8E712976 BE	064815 BF569858 BI712614 BG655891 BG424940 BE175180 BM313160 BC471936 BM091124 BF885884 BF870522 BE004490 712862 AA401033 BF569477 BE712936 BF353839 BE713042 AA316561 BE712974 BE712977 BE712938 BE712937 BE712867 713023 N42463 BE712901 BE713041 BE712904 BE712895 BE713012 BE713049 BE713025 BE712998 BE712988 BE712987 BE712986
5			BE712984 BE BE712902 BE BF060840 BC AI720319 AI8	712982 BE712975 BE712970 BE712953 BE712929 BE712922 BE712875 BE712865 BE712861 BE712860 BE712864 BE712853 712897 BE712912 BE984910 BE712903 BE764759 BE715723 BE715745 BE712915 AA441839 BE713040 BE713555 BF872528 3395104 BG744878 AU124081 A1893823 A1801072 A1633102 A1678670 A493608 AW194294 A1354559 A1686736 AW152477 A1419496 66190 AA047013 AA039625 BE049622 AA369065 AA025686 A1570198 AA706304 AW439251 H64553 AW168006 A1983753 AW081999 1851400 BE886341 AW931246 A1190143 A1151074 A1499541 A1050934 AA402167 AA382049 T16207 T03299 A1932691 AW571663
10			BG479797 8I W25087 BM4 BF948864 BE R72666 H395 AW374086 B	E408436 B1450153 BG385046 BE616501 AW151629 BG236164 BF852743 BF852046 T57801 W37881 AA482668 H43740 W58142 559852 AU125403 BG767992 BE258516 A1114509 BE394494 BE386905 AA450315 BG750593 AA557855 BG766487 BG766998 5279327 BE870900 AA577098 BF365851 AA745058 N29867 A1625038 AA641801 AA846174 H26395 AA025568 BF680282 R67845 554 T78959 W01317 H45860 W80837 N53985 BG757202 BE838055 BE072895 BE072668 BE867012 BM042833 AA083591 BG745462 GB31325 BE715757 BG767243 BG763272 AA113402 A1024044 BF818501 BE081938 BF3533818 AA7463336 BM019086 BE712894 H16977 743 BE778619 BE577467 AA593938 AA064857 T78097 AA578485 T78907 AA346590 F00017 BE966368 N58726 AA732431 T54379
15			W80749 BF2 AA064680 N BF923672 BI	38314 BE279768 AA325106 T19241 BE409339 BF852119 W23803 T54011 AW392638 BI465185 AW516784 AA211335 BI159846 80615 W49676 BF851406 R88120 AA434028 H44546 T61029 N44804 AA114948 H26960 BI261965 AA82599 BG469385 BF818172 024270 AW362633 BE883122 BM470779 BE935760 AW856056 AW856103 BE828607 AW381799 AL121058 BE828618 BE769545 0749778 BI770417 BI662544 A1110687 AF063562 BE740347 BE874864 AJ305113 BE513675 BE091369 BI046660 BE091453 BI046648 868704 AJ025179 BF336840 BF886357 BF886313 BG951884 AJ347880 AW627563 BF932536 AW820377 BF739372 BF831620 BE068264
20	418166	18858_1	AK055915 BI BE835295 A Al096810 AV R93989 AA3	asa1745 wo1130 H2052 E867252 a1523348 aa765350 BF446858 z43675 R19529 al.133837 BG389444 aw382942 BE702956 aa081961 BE835247 BE835308 E8376302 BE645790 aa376590 aa376592 aw954423 NB5732 aa249770 a1754416 aa213816 BF592044 aa811729 aw514842 a1633486 V183016 a1635738 N27524 BE645916 a1247842 aw991230 a1754277 H16814 a1766892 BF108422 a1800361 T95129 F11313 R97946 75242 BF109388 a1860939 a1680060 aw953899 BF971486 a1972337 aw953841 aa372437 a1216746 H11384 R38484 aa249043
25	455839 458997	1518842_ 11847_4	BM453041 A AW889004 A	E145830 BE145884 BE145814 BE145905 BE145833 BE145834 BE145883 BE145889 A760783 BE218582 A1340046 AW166131 BF515854 A1630296 AA461307 A1090881 AW023059 AA155797 AA115486 AL597396 IW937420 AA137082 AA013374 BG619478 BG401839
30	406782 417324	0_0 292720_1		G680336 AW991605 AA455904 AW265494 AW265432 BF911380 AA456370 BF911379 AA195677 BF914311 BF913866 BG775059
	419200	9531_1	A 4937302 A	MY190446 BG194731 AW662036 AI445021 BE937550 AW818972 AW393132 AA834685 BF112058 AV721682 H16423 AI270167 AI857345 W818444 BE929780 BG498678 BF155010 BI598271 BI599811 BE161728 AW578737 AW753711 AW379707 AW381918 BG506608
35			AI167170 A/ BE827256 R BE093545 A BE702099 R	N336627 AA43828 AW592922 AA233129 AA730278 AW439062 AW474332 BI043239 AW474342 BG708553 AW362423 BF090028 116550 R39478 R39479 R94368 BG540916 BM314745 AA251087 D54231 D55274 BF085805 D31589 AW966405 AW994425 D81879 W901107 AA383529 BI021552 R56420 N39976 AA573281 H82595 AA234955 BE0933539 AW367006 BF358697 BF366318 AA663856 F035969 AI267384 AI267232 BE348320 AA621574 AA861212 BF083343 BF083341 AY745131 D53074 AW954476 AW954472 AA376836 55065 C14928 AA093287 AA062638 BG483558 BE940050 AA765954 T70171 BE938775 BE940057 D53502 AW373300 AL118798
40			BM128728 / AA625761 / AIR63860 H	XA193411 AW444709 AW952455 A1887612 BF431948 B1498876 A1264159 BM128481 A1624657 A1689301 A1969467 AA861685 AA251595 XAB72090 A1826730 AA328366 BE827416 R75951 D65918 R68122 BE827384 AL118797 A1184164 AA164411 B1495332 BE858113 M06A0 T69849 AW780389 C14667 BF934995 B1018662 R92801 AA164410 H00752 AW373305 AW373299 AW373302
45	455705	77478_2	AA864334 A BF355591 E	IE513812 AA133359 AW581719 BF434402 AL600619 BG699731 BI551395 AW027136 AW055130 BF939512 AI076048 H18584 AW161061 NB16101 BE049456 AW044012 AA954079 AI274682 AI370526 AW131990 AA853195 AA853191 BG118295 AA761620 BG705371 NF336596 AA360497 H28072 BG198352 AW364709 H40926 H44214 AA836538 BI059563
	406851 427239	0_0 20459_2	AW075006	19/304 EP744750 AA582906 A1015067 AW271034 BG271636 AW075177 AW071374 A1345565 A1307208 BE138953 BE049086 A1334881 AW075181 AA464019 AW302733 AW075100 AW073433 A1802854 A1334909 A1802853 A1345036 A1348921 A1340734 A1307478 A1251289 AW072520 A1312145 AW073656 AW072513 AW071289 A1307559 AA876186 T29587 A1307493 A1255068 A1252868 A1252839 AW074809
50	427289	1820_2	AI252926 A AI802837 A AI053722 A	1252160 AI251662 AI251262 AI610913 AI270787 AI270156 AI252075 AW073469 AW072901 AW072496 AW071420 AI305762 AI254764 1251264 AW073049 AW071311 AI340643 BE138965 BE138502 AW073456 AI334733 AI054335 BE139260 AI054302 AI054060 AI054057 1289711 BE139228 AW470478 AW271039 AW302085 BE041872 AI254494 AI271496 AI252427 BF718773 BF718645 AW074866 BE857822 BG766159 BG769338 BG761999 BG744385 BG770572 AW370510 AW370581 AA978353 AW327973 AW402425 AI889380 AA868504
55	427203	1020_2	AW612968 AW612240 AV7034201	AA630644 A1751211 N26980 A1394506 AA747849 BF154926 BF477185 AA649647 R39135 A1750216 T35363 W36278 AW079375 AA505495 AA515380 BG760793 AW370651 BG766029 AW370595 BF229885 BG762422 BG764907 T50662 AA025671 AW815715 H65047 AA485582 R56186 H90385 R55913 B1261497 B1018403 BF376945 T75578 BF933325 BF932853 BG502266 AW868934 AV683504 I41953 BF933343 BF932871 H08334 R14012 BF897622 T50816 BG698803 BF340083 Z20199
<b>CO</b>	411825	7891_1	AK000695	AK000489 BC001688 BG235988 AW006329 A1887644 A1207230 A1148213 A1304333 A1634653 AW662636 A1281247 AA946921 AA424487 A1830689 AA150183 AA977141 RC231801 AA631793 AA975194 RFR17537 AA477798 B1906631 AW083424 AA625199 NM. 017767
60	406827	0_0	AA971409	BF984048 AW815634 AL573992 AA430612 AA928390 AA46447 AW340827 AA424290 AI927759 BG951502 AW881353 BI765535 AID15524 AA724079 BI713619 AI377728 AW293682 AI928140 AI092404 AI085630 AA731340 BM469629 AW968804 AA425658 AA769094
	428342	6712_1	BF446026	AW118719 A1332765 AW500888 AW576556 A1859571 AW499664 AW614573 AW629495 AW505314 W74704 A1356361 A1923640 A1521500 A1 042095 AA609309 AA761319 A1381489 H45700 AA761333 AW265424 AA909524 AA635311 AA649040 A1392620 Z40708
65			A1985564 A	W263513 AA913892 AI693486 AW263502 AI806164 AW291137 BI061872 BI059498 AA134476 AW084888 AA036967 AW370823 T55263 AA89664 RF877761 W74741 BF963166
	449444	2735_1	AU155762 RE382644	4 004696 AV734324 AI245349 AA369517 H88760 D79128 AA970406 H01059 H88761 H03446 BG620383 AU135008 AU136895 AU158158 R73608 R65751 R23756 N74630 AW078687 BE439761 BE786351 R68994 BE785867 AW297502 AW297553 BG431545 AW814843 BG429539 BE929862 BF811258
70	432665	27095_3	BG165971	BE143233 Al.577712 A1400326 AA769318 AA427856 AW088714 A1150755 A1924874 A1186243 AA804195 AA768972 AW574769 AW204520 AA235326 A1005076 BE826687 AW004816 AW007235 BE826639 BE826634 BF222941 BE826631 BE826643 AA292639 A1690331 A1673409 AA627727 A1923685 AA931499 A1249783 A1810663 AA548622 AA702095 AA832395 B1259508 AA262993 AW075840
75	TABLE S	i1C:	Mana a t -	
	Pkey: Ref:		Sequence source sequence of huma	mesponding to an Eos probeset  The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA and chromosome 27 Dunham, et al. (1999) Nature 402:489-495.
80	Strand: Nt_posit	ion:	Indicates DNA 8th Indicates nucleotic	and from which exons were predicted. de positions of predicted exons.
	Pkey 402075	Ref 8117407	Strand Plus	Nt_position 121907-122035,122804-122921,124019-12416

PCT/US02/29560 WO 03/025138

	400860	9757499	Minus	151830-152104,152649-152744
	402609	9926446	Minus	113464-113633,114264-114654
	400750	8119067	Plus	198991-199168,199316-199548
	402994	2996643	Minus	4727-4969
5	403817	8962065	Plus	110297-111052
•	402829	8918414	Plus	101532-101852,102006-102263
	403532	8076842	Minus	81750-81901
	405451	7622517	Minus	145949-146227
	405785	9581533	Minus	98702-98925
10	405506	6466489	Plus	80014-80401,80593-81125
	405486	6651379	Pkis	179441-179598
	406382	9256148	Plus	122336-122851
	401454	9186923	Minus	114659-114832
	405885	7677703	Minus	42574-42998
15	403969	8569909	Plus	31237-31375,32405-32506
	400533	6981826	Minus	277132-277595
	400991	8096825	Plus	159197-159320
	401591	9966977	Minus	55410-55835
	404067	3282162	Plus	1415-2071
20	404140	9843520	Plus	37761-38147
	401914	9369520	Plus	62537-62945,63155-63308
	404700	9800123	Minus	159621-160203
	403043	7768753	Minus	314423-316252
	402408	9796239	Minus	110326-110491
25				

TABLE 52A: ABOUT 204 GENES UPREGULATED IN PRIMARY MELANOMAS RELATIVE TO MELANOMA METASTASES
Table 52A lists about 204 genes upregulated in primary metanomas relative to metanoma metastases. Genes were selected from 59680 probesets on the Eos/Affymetrix Hu03
Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Peer:

30

Unique Eos probeset identifier number Exemplar Accession number, Genbank accession number Unigene number

35

MKNA expressi Pkey: ExAccn: UnigeneID: Unigene Title: R1: R2: Unique gene title

90th percentile of primary metanoma Als divided by the 90th percentile of metanoma metastasis Als

90th percentile of primary metanoma Als divided by the 90th percentile of metanoma metastasis Als, where the 15th percentile of normal tissue Als was subtracted from both the numerator and denominator

	Pkey	ExAcon	UnigenelD	Unigene Title	R1	R2
40	421948	L42583	Hs.334309	keratin 6A	21.90	16.66
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	21.36	43.65
	401781			Target Exon	18.70	18.58
	401780			NM_005557*:Homo sapiens keratin 16 (foca	15.34	16.00
	431360	NM_000427	Hs.251680	loricrin	12.34	9.86
45	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	11.24	8.73
73	412636	NM 004415		desmoplakin (DPI, DPII)	11.20	6.62
	417366	BE185289	Hs.1076	small protine-rich protein 1B (comifin)	10.46	12.75
	409601	AF237621	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	10.41	25.49
	420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	9.20	8.63
50	420033	A1659838	Hs.99923	tectin, galactoside-binding, soluble, 7	8.11	11.14
50	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	7.90	8.92
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	7.14	22.14
	427666	A1791495	Hs.180142	calmodulin-like skin protein (CLSP)	7.03	8.90
	430686	NM_001942	Hs.2633	desmoglein 1	6.88	5.39
55	431369	BE184455	Hs.251754	secretory teukocyte protease inhibitor (	6.60	12.79
55	456525	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	6.44	6.19
	437191	NM_006846	Hs.331555	serine protease inhibitor, Kazal type, 5	6.34	7.77
	422166	W72424	Hs.112405	S100 calcium-binding protein A9 (calgran	6.15	8.91
	418067	AJ127958	Hs.83393	cystatin E/M	6.08	9.24
60	408536	AW381532	Hs.135188	ESTs	6.04	17.40
UU	402075	A11301332	113.133100	ENSP00000251056*:Plasma membrane calcium	5.96	8.41
	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	5.46	3.32
	410001	AB041036	Hs.57771	kalikrein 11	5.38	5.36
	421100	AW351839	Hs.124660	Homo sapiens cDNA: FLJ21763 fis, clone C	5.32	3.84
65	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	5.19	5.30
05	419329	AY007220	Hs.288998	S100-type calcium binding protein A14	5.03	7.94
	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3) (NGAL)	4.86	5.22
	421773	W69233	Hs.112457	ESTs	4.82	12.41
	442577	AA292998	Hs.163900	ESTs	4.82	4.40
70	401760	AA232330	115.105500	Target Exon	4.60	11.03
70	401700	AJ541214	Hs.46320	Small proline-rich protein SPRK [human,	4.50	11.35
	417515	1.24203	Hs.82237	ataxia-telangiectasia group D-associated	4.47	12.43
	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	4.45	2.99
	446989	AK001898	Hs.16740	hypothetical protein FLJ11036	4.39	4.23
75	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibito	4.38	4.55
15	418663	AK001100	Hs.41690	desmocollin 3	4.36	5.16
		AA101043	Hs.151254	kallikrein 7 (chymotryptic, stratum com	4.29	5.19
	424620	AATOTOAS	ns.131234	Homo sapiens keratin 17 (KRT17)	4.28	5.41
	401747	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	4.24	2.30
80	414807 411274	NM_002776		kalikrein 10	4.22	4.82
ου		BE616501	Hs.32343	Homo sapiens, Similar to RIKEN cDNA 1110	4.21	8.26
	439496 420039	NM_004605		suffotransferase family, cytosolic, 2B,	4.18	4.73
	429538	BE182592	Hs.139322	small proline-rich protein 2A	4,16	7.30
	423030	DE 102392	13.133322	Account to the second of the s		

					4.49	4.00
	418686	Z36830	Hs.87268	annexin A8	4.12	4.09 2.13
	407366	AF026942	Hs.17518	gb:Homo sapiens cig33 mRNA, partial sequ	4.08	
	421733	AL119671	Hs.1420	fibroblast growth factor receptor 3 (ach	4.08	4.38
_	416091	AF295370	Hs.283082	defensin, beta 3	4.05	5.38
5	442757	A1739528	Hs.28345	ESTs	3.94	4.28
	427318	AF186081	Hs.175783	zinc transporter	3.92	3.07
	453309	AI791809	Hs.32949	defensin, beta 1	3.90	4.30
	422192	AA305159	Hs.113019	Rs485	3.88	2.81
10	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	3.86	5.03
10	429365	AA451798	Hs.99249	ESTs	3.76	4.05
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	3.72	6.35
	425580	L11144	Hs.1907	galanin	3.68	3.65
	448966	AW372914	Hs.86149	phosphoinosital 3-phosphate-binding prot	3.68	2.75
4 -	444946	AW139205	Hs.156457	hypothetical protein FLJ22408	3.59	5.72
15	408591	AF015224	Hs.46452	mammaglobin 1	3.58	4.73
	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	3.58	2.62
	438501	Z44110	Hs.86149	phosphoinositol 3-phosphate-binding prot	3.56	2.61
	421574	AJ000152	Hs.105924	defensin, beta 2	3.56	4.04
	402294			Target Exon	3.48	4.38
20	428666	AL080190	Hs.189242	Homo sapiens mRNA; cDNA DKFZp434A202 (fr	3.44	2.95
	401785			NM_002275":Homo sapiens keratin 15 (KRT1	3.42	4.92
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	3.36	4.24
	418394	AF132818	Hs.84728	Kruppel-like factor 5 (intestinal)	3.31	5.42
	452392	L20815	Hs.507	comeodesmosin	3.30	8.56
25	445183	AB007877	Hs.12385	KIAA0417 gene product	3.30	2.35
	433124	U51712	Hs.13775	hypothetical protein SMAP31	3.26	2.15
	419098	AA234041	Hs.87271	ESTs	3.25	4.34
	421978	AJ243562	Hs.110196	NICE-1 protein	3.17	5.86
	445493	AI915771		metallothionein 1E (functional)	3.16	2.98
30	448111	AA053486	Hs.20315	interferon-induced protein with tetratri	3.14	2.07
50	445745	AB007924	Hs.13245	KIAA0455 gene product	3.10	2.39
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	3.06	2.71
	407839	AA045144	Hs.161566	ESTs	3.06	3.54
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	3.04	4.64
35	439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	3.04	2.78
33	452240	AI591147	Hs.61232	ESTs	3.00	4.79
	409190	AU076536	Hs.50984	sarcoma amplified sequence	2.96	3.05
	408015	AW136771	Hs.244349	epidermal differentiation complex protei	2.94	10.53
	420798	W93774	Hs.99936	keratin 10 (epidermolytic hyperkeratosis	2.91	3.01
40	406954	M21305	113.33350	FGENES predicted novel secreted protein	2.90	5.34
40		BE279383	Hs.26557	plakophilin 3	2.69	6.64
	451541		Hs.21527	Human DNA sequence from clone GS1-115M3	2.86	2.81
	454027	R40192			2.84	1.76
	414737	A1160386	Hs.125087	ESTs	2.82	1.83
45	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	2.80	2.77
40	405542	45443030	11- 150053	Target Exon	2.78	5.17
	442503	AF147078	Hs.150853	p53-responsive gene 5	2.78	3.37
	402970	T00057		C200008861:gij9280563jgbjAAF86472.1] (AF	2.76	2.76
	416730	T99937	040000	gb:ye72d04.r1 Soares fetal liver spleen	2.75	2.76
50	433435	BE545277	Hs.340959	Ts translation elongation factor, mitoch	2.72	2.86
50	447164	AF026941	Hs.17518	vipirin; similar to inflammatory respon	2.72	6.68
	409453	AJ885516	Hs.95612	ESTs		2.75
	428824	W23624	Hs.173059	ESTs	2.67	3.07
	437233	D81448	Hs.339352	Homo sapiens brother of CDO (BOC) mRNA,	2.65	
E E	430630	AW269920	Hs.2621	cystatin A (stefin A)	2.63	2.38 2.44
55	433339	AF019226	Hs.8036	glioblastoma overexpressed	2.61	
	444670	H58373	Hs.332938	hypothetical protein MGC5370	2.57	1,74 3.66
	414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	2.54	2.93
	400995			C11000295*:gi]12737279[ref]XP_012163.1[	2.54	
<b>6</b> 0	423515	AA327017	Hs.176594	ESTs	2.53	7.36
60	41735 <del>9</del>	T99264	Hs.191117	ESTs	2.53	2.54
	432426	AW973152	Hs.31050	ESTs	2.52	2.15
	413822	R08950	Hs.272044	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.52	3.05
	414987	AA524394	Hs.294022	hypothetical protein FLJ14950	2.52	3.85
	407748	AL079409	Hs.38176	KIAA0606 protein; SCN Circadian Oscillat	2.48	1.76
65	426990	AL044315	Hs.173094	Homo sapiens mRNA for KIAA1750 protein,	2.47	1.92
	· 413392	AW021404	Hs.13021	ESTs	2.47	2.56
	442762	AF035119	Hs.8700	deleted in liver cancer 1	2.46	1.90
	444781	NM_014400		GPI-anchored metastasis-associated prote	2.46	7.90
	424364	AW383226	Hs.163834	ESTs, Wealthy similar to G01763 atrophin-	2.46	2.66
70	420568	F09247	Hs.247735	protocadherin alpha 10	2.46	3.01
	405885			Target Exon	2.46	2.82
	412633	AF001691	Hs.74304	periplakin	2.45	5.01
	429852	AB010445	Hs.225948	small inducible cytokine subfamily A (Cy	2.45	3.35
	429624	AA458648	Hs.99476	ESTs, Weakly similar to 13131848 alpha1	2.44	2.33
75	407325	AA291180	Hs.328476	ESTs, Weakly similar to alternatively sp	2.44	2.11
	431441	U81961	Hs.2794	sodium channel, nonvoltage-gated 1 alpha	2.43	3.66
	432543	AA552690	Hs.152423	Homo sapiens cDNA: FLJ21274 fis, clone C	2.42	3.12
	430168	AW968343	Hs.145582	DKFZP434I1735 protein	2.41	2.75
	408000	L11690	Hs.198689	bullous pemphigoid antigen 1 (230/240kD)	2.40	3.67
80	404049			NM_018937":Homo sapiens protocadherin be	2.39	1.89
	433576	BE080715	Hs.161091	ESTs	2.39	1.59
	444083	Al123195		gb:co17a10.x1 Soares_NSF_F8_9W_OT_PA_P_S	2.38	2.59
	408208	BE018717		ESTs	2.37	2.12

					2.36	2.23
	431842		Hs.271473	epithetial protein up-regulated in carci	2.34	1.99
	453931	AL121278	Hs.25144 Hs.61297	ESTs ESTs	2.31	3.82
	452308 431048	A1167560 R50253	Hs.249129	cell death-inducing DFFA-like effector a	2.31	2.18
5	403752	140200	, <b></b>	NM 002753*:Homo sapiens mitogen-activate	2.30	2.38
•	402525			NM_002699*:Homo sapiens POU domain, clas	2.30 2.30	2.36 1.73
	420223	N27807		ribosomal protein L4	2.29	4.54
	452023	AB032999	Hs.27566 Hs.199061	KIAA1173 protein p300/CBP-associated factor	2.28	2.02
10	443172 439979	AW662964 AW600291	Hs.6823	hypothetical protein FLJ10430	2.28	1.71
10	414004	AA737033	Hs.7155	ESTs, Moderately similar to 2115357A TYK	2.27	1.81
	429554	NM_012275	Hs.207224	interleukin 1, delta	2.26 2.26	2.17 2.51
	436895	AF037335	Hs.5338	carbonic anhydrase XII NM_018936*:Homo sapiens protocadherin be	2.26	2.19
15	404029	40014634	Hs.138380	KIAA0624 protein	2.26	2.99
15	424049 442423	AB014524 BE326264	Hs.246842	ESTs	2.26	1.75
	408452	AA054683	Hs.192455	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.26	2.29
	428471	X57348	Hs.184510	stratifin	2.25	2.40 2.46
	410541	AA065003	Hs.64179	syntenin-2 protein	2.24 2.22	1.64
20	415539	AI733881	Hs.72472	BMP-R1B Human clone 137308 mRNA, partial cds	2.22	3.04
	425701	AA361850	Hs.240443 Hs.136574	arachidonate 12-lipoxygenase, 12R type	2.22	3.24
	423973 409178	AF038461 BE393948	Hs.50915	kalikrein 5	2.19	4.74
	433091	Y12642	Hs.3185	lymphocyte antigen 6 comptex, locus D	2.19	7.96
25	430171	AF086289	Hs.234766	skin-specific protein	2.17	3.56 3.34
	401994			Target Exon	2.14 2.11	5.52
	449228	AJ403107	Hs.148590	protein related with psoriasis  Rh type C glycoprotein	2.11	5.78
	446292	AF081497	Hs.279682 Hs.167218	Bart-like homeobox 2	2.05	2.96
30	426150 452554	NM_003658 AW452434	Hs.58006	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.04	4.17
50	443162	T49951	Hs.9029	DKFZP434G032 protein	1.98	3.20
	400304	AF005082	Hs.113261	Homo sapiens skin-specific protein (xp33	1.94 1.92	3.20 3.24
	407395	AF005082		gb:Homo sapiens skin-specific protein (x	1.92	3.06
25	412507	L36645	Hs.73964	EphA4 coagulation factor III (thromboplastin.	1.90	3.18
35	410310	J02931 M13903	Hs.62192 Hs.157091	involucin	1.89	5.26
	425415 417324	AW265494	113.131031	ESTs	1,88	3.82
	412446	AI768015		ESTs	1.88	3.36
	451092	AI207256	Hs.13766	Homo sapiens mRNA for FLJ00074 protein,	1.87 1.86	3,75 4,11
40	444726	NM_006147		interferon regulatory factor 6	1.85	4.20
	424399	A!905687		Al905687:IL-BT095-190199-019 BT095 Homo ESTs	1.84	3.08
	434346 446051	AA630445 BE048061	Hs.37054	ephrin-A3	1.83	3.44
	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	1.78	3.45
45	413859	AW992356	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	1.76	2.99 3.60
	411908	L27943	Hs.72924	cytidine deaminase	1.74 1.71	3.56
	445656	W22050	Hs.21299	ESTs, Weakly similar to AF 151840 1 CGI-8 ESTs, Moderately similar to A53959 throm	1.71	3.38
	413966	AA133935 AF027866	Hs.173704 Hs.138202	serine (or cysteine) proteinase inhibito	1.70	3.92
50	424046 425650	NM_001944		desmoglein 3 (pemphigus vulgaris antigen	· 1.68	3.25
50	429299	AI620463	Hs.347408	hypothetical protein MGC13102	1.67	2.92
	429002	AW248439	Hs.2340	junction plakoglobin	1.66 1.66	3.35 4.31
	421335		Hs.103505	ARS component B RAB25 RAB25, member RAS oncogene family	1.65	3.55
55	433662		Hs.150826 Hs.198249	gap junction protein, beta 5 (connexin 3	1.64	4.04
رر	429211 414214		Hs.75819	glycoprotein M6A	1.64	3.59
	437897		Hs.146170	hypothetical protein FLJ22969	1.62	3.13
	426350			transglutaminase 3 (E polypeptide, prote	1.62 1,57	2.92 3.09
<b>~</b>	413163		Hs.75216	protein tyrosine phosphalase, receptor t	1.57	3.39
60	422106		Hs.111732	Fc fragment of IgG binding protein	1.52	3.53
	427751 416881		Hs.141358	conserved gene amplitted in osteosarcoma ESTs	1.52	3.06
	435013		Hs.110024	NM_020142:Homo sapiens NADH:ubiquinone o	1.49	2.91
	434574		Hs.33470	ESTs	1.48	3.05
65	454478			superoxide dismutase 2, mitochondrial	1.48 1.46	3.54 4.48
	44733			ladinin 1	1.40	2.99
	41458			proline arginine-rich end leucine-rich r Homo sapiens cDNA: FLJ23538 fis, clone L	1.40	3.71
	43364 42746			hypothetical protein MGC13010	1.36	2.98
70	43020			carbonic anhydrase XIV	1.36	3.14
, ,	45079			envoptakin	1,34	3.74
	40739	4 AF005081		gb:Homo sapiens skin-specific protein (x	1.30 1.28	3.26 3.26
	43051	3 AJ012008		G6C protein	1.28 1.22	3.64
76	41138		Hs.69752	desmocollin 1 ESTs, Weakly similar to unknown protein	1.14	3.71
75	43108 44410		Hs.10319	UDP divoosyltransferase 2 family, polype	1.00	3.20
	44367			butyrobetaine (gamma), 2-oxoglutarate di	1.00	3.26

TABLE 528:
Pkey:
CAT number:
Accession:

Unique Eos probeset identifier number Gene cluster number Genbank accession numbers

	Pkey	CAT Number	Accession	
5	412636	1438_1	J05211 BG698 BF149266 BES	04415 AF139055 BG681115 BG740377 BI712964 BG000656 AA128470 BI438324 H27408 BE931630 BE167165 AW370827 AW370813 8865 BG740734 BG680618 BG739778 BI765807 BM353403 BM353248 AW177784 AW205789 AW951576 AW848592 BE182164 940187 BI060445 BI060444 BF350983 BE720095 BE720069 BE715154 BE082584 BE082576 BE004047 AA857316 BI039774 BE713818 H770253 BE160433 BI039775 AW886475 BM462504 BE931734 BF149264 AA340777 BF381183 BG621737 AU127260 AW364859
,			BF993352 BG BE819069 BE AW995615 BE	223489 BE819009 BF381184 BE715956 R58704 AA852212 AW366566 BI090358 BF087707 BE819046 BE819005 AA377127 BE073467 B19048 BI035306 BG990973 BI040954 BF919911 AU140155 AI951766 A434518 AW804674 BF752596 BE837009 BE925808 BF149265 B14264 BI039782 AU140407 BE144243 BE709863 BF985642 BE001923 BF933310 AW265328 BG436319 BE182166 AW365175 B18280 AW177933 BF873679 AW178000 BE082526 BF476866 BF085994 BF592276 BE082507 BE082514 BE082505 BF873693
10			AW068840 AV BE698470 BE BE865341 AW BE696084 AW	9847678 BE 604153 AW365157 BE813930 BE002303 AW365153 BE184941 BE749421 BE184920 BF839562 BE184931 BF842254 931048 BF999889 BF368816 BE184924 BE159646 BE714632 BE184948 BG986845 AA131128 AA099931 W39488 C04715 BF096124 //99304 AL603116 BE149760 BE705967 BE705966 BE705988 AW364723 AW376699 AW376817 AW376697 BG005097 BF751115 //848371 AW376782 AW848789 AW849074 AW3614743 BF927725 BF094211 AW997139 BE856474 BE185187 BE156621 BE715089 //13298 BE179915 AW799309 BF872345 BF088676 BE705939 AW752599 BG005197 BF350086 BE715196 BE715155 BF752396
15			BF093817 BF AI190590 AI5 AI142882 AAC	713298 BE179313 AW793303 BE703483 BE7034833 BF094748 BF094583 AW377599 AW607238 BE082519 AW377700 BF349467 S41190 BF752409 BE006561 BG395922 BF094833 BF094748 BF094583 AW377599 AW607238 BE082519 AW377700 BF349467 S4403 Al392926 AU158477 BI467252 AU159919 AI760816 BF082516 AI439101 AA451923 AI340326 AI590975 BI791553 AI700963 I39975 AA946936 AA644381 BM314884 AA702424 AI417612 AW190555 AI220573 AI304772 AIZ70345 AA652300 AJ911702 346078 W95070 AA149191 AA026864 AI830049 AW780435 AI078449 AI819828 BI468588 AI866684 AI025932 AA026047 559154 AA515500 AW192085 AA918281 T77881 AI927207 AI205263 BF082491 AW021347 AI568096 BE939862 AA088866 D12062
20			AA056527 AA BG681425 BE AW799118 BI AISSGSSS AIS	58154 AASISSON AWT9605 AWT5003 AA022701 T87181 H44405 AI910434 BF082513 AI494069 AI270027 AI655878 AA128330 7706078 R20904 BG680059 BG676647 BF764409 AA026654 AV745530 BI762796 BG287391 AW798780 BE706045 BE926470 7687996 BE002273 AW879451 AI571075 BE067786 AV721320 AI022862 N29754 C03378 N84767 AA131077 H30146 BE714290 86892 AI915596 AW105614 AI887258 AI538577 BE926474 BE067737 BG319486 AA247685 AW788883 AW103521 BF989173 E939707 BE185750 BE714064 BE713903 BE713868 BE713763 BG950164 BE713810 AW365151 BG955489 BE005272 BF915937
25			AW365148 AI BI089483 BE BG961498 BG BG949393 BE	2539707 BE18573 BE71304 BE71305 BE71305 BE57305 BE57305 BE57305 BE57305 BE57305 BE7305 BE7305 BE7305 BE7305 BE595210 B95527 BF5952780 AW853812 BG954443 BI77053 BG679406 BG740832 BG681087 BG698430 AAA55100 T87267 BE695209 BE695210 B05273 BE872225 AW391912 BE925515 BG677012 BG741970 AA026480 BE705999 BG677157 BE009090 BG681378 BE712291 S678984 BI040941 AA337270 AW384371 AW9847442 BI058653 BE813665 W95048 W25458 AW177786 AA025851 BE931733 BF154837 E714441 AW996245 BE711801 AI284090 BE064323 BE719300 BE940148 BG991212 BF375714 BF349522 BG996267 T48793 BI013292 W355166 AW365154 AW606653 BF763109 BE931637 BE167181 BE713879 BF354008 BF678726 H90899 AW365145 W38382 A4498487
30	445493	423456_1		809938 AI808768 AI240593 AI915771
20	416730	1988296_1	H80564 T999	
	444083	10908_12	BI836699 AI1	23195 /439843 AW172765 BE018717 BE464329 BE302285 H96902 BF477981 BE674508 BE670755 H95980 T15387
	408208 420223	642734_1 191648_1		ASSIST AWITZ 105 BED 10 11 BE 404329 BE 30 2205 H30502 BF 41 150 1 BE 51 4300 BE 51 01 35 11 35 300 1 1 300 1
35	417324	292720_1	BG775668 B	G680336 AW991605 AA455904 AW265494 AW265432 BF911380 AA456370 BF911379 AA195677 BF914311 BF913866 BG775059
			RC951874 A	572169
	412446	63467_1	REGROSSO A	569212 AL 120184 AI769949 BE701002 BE184363 BE819031 BG702238 BF090049 BF963318 BF961912 BF943013 AA934514 AA151245 4987907 Z41449 BF908059 BF908053 BF908049 BE699424 BF908060 BF962832 BF952020 BF963134 BI035538 BF908052 BF908057 4943158 AI632924 BF512340 BF952021 BF960776 BF943437 BF942847 AI768015 F09778 F04816 F02721 AA102645 AI633838
40			AA617929 RI	F947001 RI03544R RE935876 AW890837 AW898604 BE957405 BE963433 BG704815
	444726	3503_2	BG285809 B	E940673 BGA32524 BE157554 BG676980 AU144284 AI745383 AU159045 AI693500 AW293668 AW371408 BE856107 AI338042 I698246 BE673290 AW297653 AA156532 AI017342 AI916754 AI190644 AI184302 AA857671 BE857018 AI307420 AI318157 AW204327
			AW188320 A	1698246 BE673290 AW297633 AA136532 AU17/32 AI916734 A194644 A164332 A4637617 BE657016 A6677426 A2676187 A16274 W274339 AA582788 AI345741 AW301433 AI873468 AW137388 BF718731 BF718413 AA877495 BF001575 AI824693 AW849604
			A COOPCOVA	W849396 AW849173 BE673179 AI611327 AA705753 BE715478 AW849414 AW849399 AI085759 A1140849 T67412 AI889885 AW104647
45			AIQ124Q5 AII	RRORTA AITAADA1 RE717113 RE717108 RE715564 AIR72527 AAN29457 C00338 AI469558 BE715577 AAD45413 BF843813
	424399	2196_1	NM 058173	AFA14NR7 W72R37 RF742R09 AW070916 RE092421 AI905687 AA340069 BE074512 AI905623 AI905633 BG202312 W72838 AI139456
			BG218084 B	E926938 BE186013 AW176044 AW291950 BG185269 BG197186 BG192597 BG183176 BG207535 Al127172 BE815819 Al905624
	12/2/5	1011004 14		02313 AI905837 BE815853 1924216 AI660493 AI984141 AI991272 AA593860 AI983793 AI346155 AIZ74929 AI281211 AI821178 BC020841 BF352476 BF843140
50	434346	MH1094_14	RE917041 W	180832 AA630A45 RE350167 RE162052 BE931808 AI572329 BG536379
	427751	15028_1	BE875818 A AW410526 E	W751975 W39241 BF808798 W22600 BF082190 AAG31290 R42801 H98235 H17925 AIG31236 AI933786 H42736 AF000152 AU123911 BM354207 BF800492 BM142340 BE019322 AL597008 AW327818 BI041915 AW504825 AW504941 BF987969 NM_005730 U81555 BM354078 AA147822 AAR73109 AI082344 A1360868 AW168024 AI819848 AA811327 A1355616 AA281629 A1880578 AL274316 AW014622
			ALCERGED AL	270283 AA171981 A1349410 AA402469 A1421985 A1004864 A1423497 A1361503 A1363096 AW805345 AL539979 AA553967 AW502264
55			A1290698 N	22420 A1281054 A1500699 AW342095 C75122 AW504577 A1130811 A1423567 R79086 A1860451 BE222885 A1697830 A1279575 BF438693 BE218210 A1952376 AA506609 A1147566 A1391690 AA991622 A1696368 A1784664 AA741555 A1002681 AW474554 AW474508 D25623
			A DCDCDNIA	3 170800 W73566 AW411368 AA147971 AA088581 RFR04510 AU145809 AU148108 AA223219 AU157840 AW169757 AI537862 N42341
			A1128667 AL	u327853 AA713015 W15255 W56743 AA058322 H81878 AA723464 N27523 R37745 AA613566 AL526353 AI905211 BF802713 N40338
<b>60</b>			A A 240207 D	IC752020 DC250441 H64761 DCR52011 HR1877 H9608R A1 576453 W73585 H39990 AW438965 BF899684 AI040299 AL561879 AA253821
60			H27760 BC	)18922 ALS33396 BES13580 BF432649 A1884985 AA404264 AW024396 AW167863 AW027036 AL302177 A1660487 AW026086 BF432564 L193156 AA744623 A1859510 B1063081 B1061541 AA777036 BG058486 B1063555 Al349411 BF874521 AW139801 AL268585 AA401267
			AIGNS 200 PI	64276 N72043 AF022231 RI256540 AU134437 BG826972 BE298386 AW134499 AW206089 BF846730 AW500331 BF849336 BI041697
			AIR57745 A	W19284D AWA10527 A1697435 AW006631 AW504124 AL048926 A1085476 AW327855 AA459344 AW207516 AW204875 BM142514
			REARKSO A	AGGGGRD AW2A2GGG RID123G3 AW837102 RE703126 RE814612 RE837981 RE703141 RF343101 R47375 AA031413 N40264 BG02/7363
65			BF526360 B	E391263 AA280192 BE294042 BE250630 AU147734 AU146610 AA196787 N59465 AW575791 H16738 H96089 H64762 AW006603 U719393 AU155418 BG770385 AA339673 BG337748 H42694 BE834346 AA090896 BE619985 BM006968 R46008 BF304621 AA172280
			AW957721	BF304885 BF933455 BF809973 BG386280 AW079808 T51091 AL520569 BE694350 T06360 BF347780 BE560703 BE296629
	454478	4273_16	AW796921	AW798102 AW805749 AW805872 BF985060 AW794380 BF380449 AW794466 AW794538
70	407394	27110_2	AF005081 E	
70	431089	125941_2	BG940189	AW063489 AA715980 BF001091 BF880066 AA666102 AA621946 AA491826
	TABLE S	32C:		
	Pkey:	l tr	ique number co	responding to an Eos probeset
75	Ref:	Se	quence source.	The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA
75	C+			n chromosome 22" Dunham, et al. (1999) <u>Nature</u> 402:489-495. nd from which exons were predicted.
	Strand: Nt_posit			na nom which exons were predicted. e positions of predicted exons.
00	Pkey	Ref	Strand	Nt_position
80	401781 401780	7249190 7249190	Minus Minus	83215-83435,83531-83656,83740-83901,8423 28397-28617,28920-29045,29135-29296,2941
	401760	8117407	Pkus	121907-122035,122804-122921,124019-12416
	401760		Plus	83126-83250,85320-85540,94719-95287

PCT/US02/29560 WO 03/025138

	401747	9789672	Minus	118596-118816,119119-119244,119609-11976
	402294	2282012	Minus	2575-3000
	401785	7249190	Minus	165776-165996,166189-166314,166408-16656
	405542	9857564	Plus	71331-72183
5	402970	9650703	Minus	124891-125049
•	400995	8099094	Plus	141186-141601
	405885	7677703	Minus	42574-42998
	404049	3688074	Minus	75765-78155
	403752	7678857	Plus	33704-33828
10	402525	9800048	Minus	19748-20683
• •	404029	7671252	Plus	108716-111112
	401994	4153858	Minus	42904-43124,43211-43336,44607-44763,4519

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TABLE 53A: ABOUT 298 GENES UPREGULATED IN MELANOMA METASTASES RELATIVE TO PRIMARY MELANOMAS

Table 53A lists about 298 genes upregulated in melanoma metastases relative to primary melanomas. Genes were selected from 59680 probesets on the Eos/Alfymetrix Hu03

Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. Unique Eos probeset identifier number
Exemplar Accession number, Genbank accession number
Unigene number
Unigene number
Unigene gene title
90th percentile of melanoma metastasis Als divided by the 90th percentile of primary melanoma Als
90th percentile of melanoma metastasis Als divided by the 90th percentile of primary melanoma Als, where the 15th percentile of normal tissue Als was subtracted from both the numerator and denominator

Pkey: ExAccn: UnigenelD:

20

Unigene Title: R1

25

R2

	Pkey	ExAcco	UnigenelD	Unigene Tide	R1	R2
	407245	X90568		<b>titin</b>	10.56	11.32
	412228	AW503785	Hs.73792	complement component (3d/Epstein Barr vi	9.22	6.14
30	426752	X69490	Hs.172004	titin	8.78	- 10.44
•	418310	AA814100	Hs.86693	ESTs	8.65	6.49
	414522	AW518944	Hs.76325	Immunoglobulin J chain	8.37	4.39
	433447	U29195	Hs.3281	neuronal pentraxin II	8.27	7.25
	456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A	7.78	6.70
35	425545	N98529	Hs.158295	Homo sapiens, clone MGC:12401, mRNA, com	7.49	9.02
55	428087	AA100573	Hs.182421	troponin C2, fast	7.45	7.65
	436485	X59135	Hs.156110	immunoglobulin kappa constant	7.35	6.18
	414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	6.97	5.75
	412519	AA196241	Hs.73980	troponin T1, skeletal, slow	6.15	6.33
40	430280	AA361258	Hs.237868	interleukin 7 receptor	6.07	3.11
	449078	AK001256	Hs.22975	KIAA1576 protein	6.05	8.55
	437952	D63209	Hs.5944	solute carrier family 11 (proton-coupled	6.03	5.36
	412561	NM_002286	Hs.74011	lymphocyte-activation gene 3	5.85	5.57
	431574	AW572659	Hs.261373	hypothetical protein dJ434014.3	5.74	6.40
45	458079	AI796870	Hs.54277	DNA segment on chromosome X (unique) 992	5.72	4.76
73	417880	BE241595	Hs.82848	selectin L (lymphocyte adhesion molecule	5.71	5.00
	429412	NM_006235	Hs.2407	POU domain, class 2, associating factor	5.69	3.84
	420338	AA825595	Hs.88269	Homo sapiens, clone MGC:17339, mRNA, com	5.37	4.12
	430580	AA806105	Hs.300697	immunoglobulin heavy constant gamma 3 (G	5.31	6.02
50	428804	AK000713	Hs.193736	hypothetical protein FLJ20706	5.29	7.97
50	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	5.26	2.93
	445784	AI253155	Hs.146065	ESTs	5.12	3.10
	409461	AA382169	Hs.54483	N-myc (and STAT) interactor	5.05	3.41
	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	4.59	4.00
55	420301	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	4.47	3.92
23	453857	AL080235	Hs.35861	DKFZP586E1621 protein	4.46	3.61
	428242	H55709	Hs.2250	leukernia inhibitory factor (cholinergic	4.37	3.22
	414829	AA321568	Hs.77436	pleckstrin	4.35	3.35
	417878	U90916	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	4.35	2.68
60	422603	BE242587	Hs.118651	hematopoietically expressed homeobox	4.27	2.67
UU	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	4.27	3.67
	441623	AA315805	1.0.2000	desmoglein 2	4.24	3.66
	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	4.22	3.60
	417022	NM_014737		Ras association (RalGOS/AF-6) domain fam	4.20	2.58
65	426317	AA312350	Hs.169294	transcription factor 7 (T-cell specific,	4.16	5.82
UJ	430770	AA765694	Hs.123296		4.15	5.10
	420931	AF044197	Hs.100431		4.12	5.06
	406707	S73840	Hs.931	myosin, heavy polypeptide 2, skeletal mu	4.11	3.82
	444863	AW384082	Hs.104879		4.10	2.68
70	432306	Y18207	Hs.303090		4.04	4.10
, 0	417105	X60992	Hs.81226	CD6 antigen	4.03	4.51
	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	4.02	3.72
	432485	N90866	Hs.276770		3.99	4.87
	415165			complement component ?	3.97	3.98
75	421181				3.96	3.19
,,	421712		Hs.107139		3.95	7.34
	408380		Hs.44532	diubiquitin	3.94	2.45
	422423		Hs.11648		3.93	3.29
	408989			KIAA0746 protein	3.90	3.02
80	424321		Hs.1765	tymphocyte-specific protein tyrosine kin	3.84	3.40
00	420137		Hs.95327	CD3D antigen, delta polypeptide (TiT3 co	3.84	4.84
	424922		Hs.21711		3.78	3.04
	400440		Hs.83870		3.77	4.89
	4004.4					

	418870	AF 147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	3.74	3.91
	450293	N36754	Hs.171118	hypothetical protein FLJ00026	3.74	2.89
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	3.72	2.65
5	408548 429490	AA055449	Hs.63187 Hs.23889	ESTs, Wealthy similar to ALUC_HUMAN !!!! ESTs, Wealthy similar to ALU7_HUMAN ALU S	3.72 3.71	2.43 2.23
,	414821	AI971131 M63835	Hs.77424	Fc fragment of IgG, high affinity ta, re	3.70	2.36
	419749	X73608	Hs.93029	sparc/osteonectin, cwcv and kazal-like d	3.67	3.30
	410016	AA297977	Hs.57907	small inducible cytokine subfamily A (Cy	3.67	6.72
10	433658 424153	L03678	Hs.156110	immunoglobulin kappa constant	3.66 3.64	2.49 2.65
10	424155	AA451737 AL035250	Hs.141496 Hs.1408	MAGE-like 2 endothelin 3	3.64	5.92
	417696	BE241624	Hs.82401	CD69 antigen (p60, early T-cell activati	3.61	2.69
	429732	U20158	Hs.2488	lymphocyte cytosotic protein 2 (SH2 doma	3.60	1.95
15	422173	BE385828	Hs.250619	phorbolin-like protein MDS019 (CEM15)	3.59	3.08
13	413778 442379	AA090235 NM_004613	Hs.75535 Hs.8265	myosin, light polypeptide 2, regulatory, transglutaminase 2 (C polypeptide, prote	3.57 3.56	11.26 4.91
	439859	AW292872	Hs.124554	ESTs	3.53	4.15
	453064	R40334	Hs.89463	potassium targe conductance calcium-acti	3.51	2.88
20	411252	AB018549	Hs.69328	MD-2 protein	3.46	1.82
20	414324 420286	Y14768 AI796395	Hs.890 Hs.111377	lymphotoxin bela (TNF superfamily, membe ESTs	3.45 3.42	4.65 2.47
	413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	3.42	3.09
	442104	L20971	Hs.188	phosphodiesterase 4B, cAMP-specific (dun	3.41	2.22
25	405545			Target Exon	3.40	2.46
25	416373	AA195845 AF063020	LL 02110	ESTs, Weakly similar to \$12658 cysteine-	3.40 3.37	5.64 4.27
	417410 418522	AA605038	Hs.82110 Hs.7149	PC4 and SFRS1 interacting protein 1 Homo sapiens cDNA: FLJ21950 fis, clone H	3.33	2.37
	433470	AW960564	110.1110	transmembrane 4 superfamily member 1	3.33	3.13
20	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	3.32	2.51
30	442149	AB014550	Hs.8118	KIAA0650 protein	3.30 3.29	2.29 3.85
	411852 447023	AA528140 AA356764	Hs.107515 Hs.17109	ESTs, Weakly similar to T00329 hypotheti integral membrane protein 2A	3.29 3.24	2.79
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	3.23	1.78
~ ~	414176	BE140638	Hs.75794	EDG-2 (endothelial differentiation, lys	3.22	2.90
35	447513	AW955776	Hs.313500	ESTs, Moderately similar to ALU7_HUMAN A	3.18	4.16
	421893 424148	NM_001078 BE242274	Hs.109225 Hs.1741	vascular cell adhesion molecule 1 integrin, beta 7	3.17 3.14	3.59 2.29
	406648	AA563730	Hs.277477	major histocompatibility complex, class	3.13	3.05
40	429505	AW820035	Hs.278679	a disintegrin and metalloproteinase doma	3.13	2.36
40	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	3.12	2.55
	406704 443885	M21665 H91806	Hs.929 Hs.15284	myosin, heavy polypeptide 7, cardiac mus ESTs	3.12 3.08	5.54 3.55
	418203	X54942	Hs.83758	CDC28 protein kinase 2	3.08	2.20
	417640	D30857	Hs.82353	protein C receptor, endothetial (EPCR)	3.06	3.21
45	447232	AW499834	Hs.327	interleukin 10 receptor, alpha	3.05	3.36
	409103	AF251237	Hs.112208	XAGE-1 protein	3.04 3.04	2.07 2.24
	413719 421834	BE439580 BE543205	Hs.75498 Hs.288771	smatt inducible cytokine subfamily A (Cy DKFZP586A0522 protein	3.03	1.91
	444666	BE293347	Hs.11638	long-chain fatty acid coenzyme A ligase	3.01	3.43
50	425295	AA431366	Hs.37251	ESTs	3.01	3.07
	429109	AL008637	Hs.196352	neutrophil cytosofic factor 4 (40kD)	2.99	2.55 5.98
	420340 418968	NM_000734 NM_000078	Hs.97087 Hs.89538	CD3Z antigen, zeta polypeptide (TiT3 com cholesteryl ester transfer protein, plas	2.98 2.97	2.68
	438914	N93892	Hs.10727	ESTs	2.97	2.19
55	418391	NM_003281	Hs.84673	troponin I, skeletal, slow	2.96	2.68
	419056	M89957	Hs.89575	CD79B antigen (immunoglobulin-associated	2.96	3.94
	449523	NM_000579	Hs.54443 Hs.25590	chemokine (C-C motif) receptor 5 stanniocalcin 1	2.96 2.96	4.02 3.24
	450847 418460	NM_003155 M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	2.95	2.73
60	426711	AA383471	Hs.343800	conserved gene amplified in osteosarcoma	2.94	2.36
	426559	AB001914	Hs.170414	paired basic amino acid cleaving system	2.93	2.17
	424528	AW073971	Hs.238954	ESTs, Weakly similar to KIAA1204 protein PRO2000 protein	2.93 2.92	2.70 2.16
	408633 443195	AW963372 BE148235	Hs.46677 Hs.193063	Homo sapiens cDNA FLJ14201 fis, clone NT	2.92	2.92
65	425234	AW152225	Hs.165909	ESTs, Wealty similar to 138022 hypotheti	2.90	2.09
	437802	AJ475995	Hs.122910		2.90	3.71
	417771	AA804698	Hs.82547	retinoic acid receptor responder (lazaro	2.90	3.56 2.60
	438000	AJ825880 N98569	Hs.5985 Hs.76422	non-kinase Cdc42 effector protein SPEC2 phospholipase A2, group ItA (platelets,	2.90 2.87	2.07
70	414555 421958	AA357185	Hs.109918		2.87	3.48
. •	420224	M84371	Hs.96023	CD19 antigen	2.86	4.77
	434883	AW381538	Hs.19807	hypothetical protein MGC12959	2.85	5.44
	452852	AK001972 AIR00057	Hs.30822	hypothetical protein FLJ11110 immunoglobulin heavy constant mu	2.84 2.84	2.55 4.16
75	427527 446231	AI809057 NM_002163	Hs.153261 Hs.14453	interferon consensus sequence binding pr	2.83	2.97
	408838	A1669535	Hs.40369	ESTs	2.82	1.82
	429124	AW505086	Hs.196914		2.82	4.21
	425023	AW956889	Hs.154210		2.79	4.00 2.28
80	425388 414 <b>2</b> 90	AA329384 AI568801	Hs.156110 Hs.71721	immunoglobulin kappa constant ESTs	2.79 2.78	3.19
-	418255	AW135405	Hs.37251	ESTs	2.76	3.27
	451952	AL120173	Hs.301663	ĘSTs	2.75	1.74
	424865	AF011333	Hs.153563	lymphocyte antigen 75	2.75	3.10

					0.74	242
	409245	AA361037		tRNA isopentenylpyrophosphate transferas	2.74 2.74	2.12 3.08
	453920	AI133148	Hs.36602	I factor (complement)	2.74	2.34
	443968	AA287702	Hs.10031	KIAA0955 protein hypothetical protein PRO2013	2.73	1.67
5	434094 436476	AA305599 AA326108	Hs.238205 Hs.33829	bHLH protein DEC2	2.72	1.70
,	428398	AI249368	Hs.98558	ESTs	2.72	2.06
	417141	U22662	113.30330	nuclear receptor subfamily 1, group H, m	2.70	2.55
	427080	AW068287	Hs.301175	ras-related C3 botulinum toxin substrate	2.69	3.15
	442485	BE092285	Hs.29724	hypothetical protein FLJ13187	2.69	1.99
10	429317	AA831552	Hs.268016	Homo sapiens cDNA: FLJ21243 fis, clone C	2.69	1.70
	443998	AI620661	Hs.296276	ESTs .	2.69	2.30
	417542	J04129	Hs.82269	progestagen-associated endometrial prote	2.68	3.23
	414291	AI289619	Hs.13040	G protein-coupled receptor 86	2.68	3.01
1.5	448861	AL049951	Hs.22370	Homo sapiens mRNA; cDNA DKFZp56400122 (f	2.66	2.51
15	432435	BE218886	Hs.282070	ESTs	2.65 2.65	3.28 3.04
	430132	AA204686	Hs.234149	hypothetical protein FLJ20647	2.64	3.82
	427792	M63928	Hs.180841	tumor necrosis factor receptor superfami	2.64	1.94
	414696	AF002020	Hs.76918 Hs.287379	Niemann-Pick disease, type C1 Homo sapiens mRNA for FLJ00111 protein,	2.64	251
20	420991 401566	AW504814	NS.20/3/3	NM_005159:Homo sapiens actin, alpha, car	2.63	3.74
20	444119	R41231	Hs.184261	ESTs, Weakly similar to T26686 hypotheti	2.63	2.13
	425231	AA527161	113.104201	ESTs	261	2.95
	417427	M90391	Hs.82127	interleukin 16 (lymphocyte chemoattracta	2.61	1.90
	437669	AI358105	Hs.123164	ESTs, Weakly similar to match to ESTs AA	2.60	4.45
25	413856	D13639	Hs.75586	cyclin D2	2.60	5.71
	407928	NM_002262	Hs.41682	killer cell lectin-like receptor subfami	2.59	2.68
	443247	BE614387	Hs.333893	c-Myc target JPO1	2.58	2.77
	447131	NM_004585	Hs.17466	retinoic acid receptor responder (tazaro	2.58	9.28
••	443021	AA368546	Hs.8904	tg superfamily protein	2.58	4.49
30	424779	AL046851	Hs.153053	CD37 antigen	2.58 2.57	3.88 2.09
	425235	AA353113	Hs.112497	Homo sapiens cDNA: FLJ22743 fis, clone H	2.57	3.57
	424265	AF173901	Hs.144287	hairy/enhancer-of-split related with YRP	2.57	1.86
	426780	BE242284	Hs.172199	adenylate cyclase 7 solute carrier family 37 (glycerol-3-pho	2.56	2.90
35	452721 442904	AJ269529 AW575008	Hs.301871 Hs.11355	thymopoletin	2.56	3.39
	433646	AA603319	Hs.155195	ESTs	2.54	2.19
	417289	D86962	Hs.81875	growth factor receptor-bound protein 10	2.53	4.56
	422640	M37984	Hs.118845	troponin C, slow	2.53	5.38
	448413	AI745379	Hs.42911	ESTs	2.53	2.08
40	429536	AA873016	Hs.206097	oncogene TC21	2.52	2.49
	446272	BE268912	Hs.14601	hematopoietic cell-specific Lyn substrat	2.52	3.46
	424378	W28020	Hs.167988	neural cell adhesion molecule 1	2.52	2.91
	410257	BE244044	Hs.61469	hypothetical protein	2.51	3.67
40	427609	AKQ00436	Hs.179791	hypothetical protein FLJ20429	2.51	3.11
45	424868	AI568170	Hs.96886	ESTs	2.51	2.30 2.64
	418945	BE246762	Hs.89499	arachidonate 5-lipoxygenase	2.50 2.50	3.04
	420899	NM_001629	Hs.100194		2.49 2.49	2.37
	413441	AI929374	Hs.75367	Src-like-adapter	2.49	1.82
50	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	2.49	2.40
20	429493	AL134708 AW188117	Hs.145998	ESTs popeye protein 3	2.48	1.85
	419631 437175	AW968078	Hs.87773	protein kinase, cAMP-dependent, catalyti	2.48	2.32
	421552	AF026692	Hs.105700		2.47	4.17
	420158	AI791905	Hs.95549	hypothetical protein	2.47	2.62
55	453987	AA323750	Hs.235026		2.47	2.49
	429640	U83508	Hs.2463	angiopoletin 1	2.47	2.57
	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	2.46	2.42
	426969	AI936504		CDC-like kinase 1	2.46	2.41
	427674	NM_003528	Hs.2178	H2B histone family, member Q	246	2.17
60	405547			NM_018833*:Homo sapiens transporter 2, A	2.46	2.84
	406678	U77534		gb:Human clone 1A11 immunoglobulin varia	2.45 2.45	2.89 3.40
	407013		Hs.83870	gb:Human nebulin mRNA, partial cds	2.43	6.25
	428746	AW503820	Hs.192861		2.39	4.01
65	453953		Hs.36972	CD7 antigen (p41) perforin 1 (pore forming protein)	2.39	4.56
0.5	427759		Hs.2200	complement component 1, q subcomponent,	2.39	3.31
	443071 437211		Hs.8986 Hs.5509	ecotropic viral integration site 2B	2.38	3.15
	440596		Hs.103378		2.37	3.68
	452651		Hs.30209		2.36	4.08
70	421563				2.34	3.25
	421924		Hs.10960		2.33	3.38
	449092			alpha2,8-sialyttransferase	2.32	3.53
	425367		Hs.15597	5 protein tyrosine phosphatase, receptor t	2.32	7.02
	418117	AJ922013	Hs.83496		2.30	3.56
75	425795	AJ000479	Hs.15954		2.26	3.42
	428111		Hs.2243	B lymphoid tyrosine kinase	2.25	3.69
	439981		Hs.12467		2.25	4.05
	425722		Hs.97031		2.25 2.24	3.44 3.23
00	436648		Ue 20022	ESTs	2.23	3.23
80	452250		Hs.28607		2.23	3.30
	441715		Hs.34265 8 Hs.1652	chemokine (C-C motif) receptor 7	2.22	3.25
	423397 449626		Hs.30163		2.21	3.14
	443020	, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	3.00.00	. eve mån komm ann		

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	440076	T70070	11- 75406	at a facility of the state of t	210	2.41
	412975 418739	170956 AA310064	Hs.75106 Hs.88012	clusterin (complement lysis inhibitor, S	2.18 2.15	3.41 3.62
	418185	AA310964 AW958272	Hs.347326	SHP2 interacting transmembrane adaptor Intercellular adhesion molecule 2 (ICAM	2.09	5.21
	435420	AA443966	Hs.31595	ESTs	2.07	3.81
5	418174	L20688	Hs.83656	Rho GDP dissociation inhibitor (GDI) bet	2.05	3.14
	420626	AF043722	Hs.99491	RAS guanyl releasing protein 2 (calcium	2.01	4.42
	428289	M26301	Hs.2253	complement component 2	2.00	3.33
	429683	AF148213	Hs.211604	a disintegrin-like and metalloprotease (	2.00	3.75
10	421445	AA913059	Hs.104433	Homo sapiens, clone IMAGE:4054868, mRNA	1.96 1.91	3.68 4.84
10	450300 416445	AL041440 AL043004	Hs.58210 Hs.79337	ESTs, Highly similar to ITH4_HUMAN INTER KIAA0135 protein	1.91	3.41
	409817	BE295464	Hs.56607	Williams-Beuren syndrome chromosome regi	1.87	3.53
	416967	BE616731	Hs.80645	interferon regulatory factor 1	1.86	3.55
	437740	AA810265	Hs.122915	ESTs	1.86	3.79
15	437938	A1950087		gb:wq05c02.x1 NCI_CGAP_Kid12 Homo sapien	1.83	3.42
	425240	AA306495	Hs.1869	phosphoglucomutase 1	1.83	3.75
	406972	M32053	N- 2555	gb:Human H19 RNA gene, complete cds. tumor necrosis factor receptor superfami	1.80 1.78	4.03 3.53
	430378 437470	Z29572 AL390147	Hs.2556 Hs.134742	hypothetical protein DKFZp547D065	1.78	3.39
20	416350	AF188625	Hs.189507	phospholipase A2, group IID .	1.78	5.48
	417852	AJ250562	Hs.82749	transmembrane 4 superfamily member 2	1.78	4.88
	414682	AL021154	Hs.76884	inhibitor of DNA binding 3, dominant neg	1.77	5.79
	444090	S69115	Hs.10306	natural killer cell group 7 sequence	1.74	3.41
25	427278	AL031428	Hs.174174	KIAA0601 protein	. 1.74	3.80
25	418618	U66097	Hs.86724	GTP cyclohydrolase 1 (dopa-responsive dy	1.73 1.73	4.21 3.21
	420397 418678	NM_007018 NM_001327	Hs.97437 Hs.167379	centrosomal protein 1 cancertestis antigen (NY-ESO-1)	1.73	3.77
	459245	BE242623	Hs.31939	manic fringe (Drosophila) homolog	1.72	3.12
	425356	BE244879	Hs.155939	inositol polyphosphate-5-phosphatase, 14	1.71	3.55
30	423984	AF163825	Hs.136713	pre-B lymphocyte gene 3	1.70	7.70
	422355	AW403724	Hs.300697	coagulation factor VII (serum prothrombi	1.70	3.10
	451579	AW607731	Hs.26670	Human PAC clone RP3-515N1 from 22q11.2-q	1.68	4.19
	451287 416819	AK002158 U77735	Hs.26194 Hs.80205	likely homolog of mouse immunity-associa pim-2 oncogene	1.68 1.67	5.76 3.17
35	409896	AW205479	Hs.279780	NY-REN-18 entigen	1.67	3.74
	447532	AK000614	Hs.18791	hypothetical protein FLJ20607	1.66	3.62
	426666	AW500131	Hs.171763	CD22 antigen	1.65	4.67
	412265	AA101325	Hs.86154	hypothetical protein FLJ12457	1.65	3.43
40	416971	R34657	Hs.80658	uncoupling protein 2 (mitochondrial, pro	1.64	3.66
40	430449	AA352723	Hs.241471	RNB6	1.62	3.09
	424661	M29551	Hs.151531	protein phosphatase 3 (formerly 28), cat	1.61 1.61	3.37 11.60
	453027 410068	A1879341 A1633888	Hs.539 Hs.58435	ribosomal protein S29 FYN-binding protein (FYB-120/130)	1.60	3.28
	440446	NM_013385	Hs.7189	pleckstrin homology, Sec7 and coiled/coi	1.59	3.14
45	453657	W23237	Hs.296162	AD037 protein	1.59	3.12
	418102	RS8958	Hs.26608	hypothetical protein MGC15880	1.58	3.55
	424614	X54486	Hs.151242	serine (or cysteine) proteinase inhibito	1.58	3.07
	406791	AI220684	Hs.347939	hemoglobin, alpha 2	1.55	5.06
50	421703	AI936513	Hs.1416 Hs.108947	Fc fragment of IgE, low affinity II, rec	1.53 1.52	3.59 3.41
50	421859 416783	AA356620 AA206186	Hs.79889	KIAA0050 gene product monocyte to macrophage differentiation-a	1.52	3.28
	456086	AL161999	Hs.77324	eukaryotic translation termination facto	1.47	3.34
	425783	AJ026740	Hs.1948	ribosomal protein S21	1.46	4.95
	407682	AL035858	Hs.3807	FXYD domain-containing ion transport reg	1.46	3.48
55	409169	F00991	Hs.50889	(clone PWHLC2-24) myosin light chain 2	1.45	3.25
	435624	AF218942	Hs.24889	formin 2	1.45	3.11 3.33
	413969	X14034	Hs.75648	phospholipase C, gamma 2 (phosphatidylin complement component 4A	1.45 1.44	4.27
	426530 425928	U24578 S55736	Hs.278625 Hs.238852	ESTs, Weakly similar to hypothetical pro	1,44	3.65
60	418219	AA731836	Hs.137319	ESTs	1.43	4.01
• •	429071	AW794126	Hs.195453	ribosomal protein S27 (metallopanstimuli	1,41	4.23
	418473	AA243335	Hs.309943	nuclear body protein Sp140	1.41	3.29
	423766	AA303799	Hs.300141	ribosomal protein L39	1.40	3.22
65	430150	L05148	Hs.234569		1.39	3.29
65	416370	N90470	Hs.203697		1.36 1.32	3.08 3.29
	406758 448610	AA552326 NM_006157	Hs.77039 Hs.21602	ATP synthase, H transporting, mitochondr nel (chicken)-like 1	1.32	3.85
	444674	8E562200	Hs.244	amino-terminal enhancer of split	1.30	3.10
	407694	U77594	Hs.37682	retinoic acid receptor responder (tazaro	1.30	3.91
70	427349	AA360154	Hs.177415		1.28	3.59
-	419032	W81330	Hs.99877	ESTs, Highly similar to JAK3B [H.sapiens	1.28	3.21
	436553	AW407157	Hs.8997	immunoglobulin lambda locus	1.27	4.00
	415138	C18356	Hs.295944		1.24	3.25
75	406623	X69392 AB014568	Un 6000	ribosomal protein L26 KIAA0668 protein	1.24 1.21	3.31 3.33
15	437895 421143	AB014508 AB024536	Hs.5898 Hs.102171		1.18	3.35
	721170	-10424400		and the second s		3.00

TABLE 538:
Picay:
CAT number:
Accession:
Unique Eos probeset identifier number
Gene cluster number
Genbank accession numbers 80

Pkey CAT Number Accession

5	441623	3362_1	BC022413 BE395396 BF754175 AA506621 BE706665 BE706678 AA723159 BE153169 BE706729 BE706558 BE153312 BE706706 AW371853 AW371849 BE153241 BC017410 A337912 A1090244 AW090300 BE219837 AI623661 BE501576 BE501734 A1742222 A1023964 A458424 AA975373 A1288904 A1984583 AA890325 N32562 A1388102 AW241694 A103848 A672071 A1018389 AA576391 AA977874 AW189392 W37448 AA612894 A1277548 H89551 A1659774 H89365 AA315806 AW978168 BC014584 BC014581 AW780125 A1672414 BE328145 AW600919 BF031306 AW172758 A1277548 H89551 A1659775 BE875779 H28241 H25318 BF540913 BG179688 BF110202 AA528775 W37573 BE041644 AW366504 BM129522 BM129822 BE708322 AA345675 BE875779 H28241 H25318 BF540913 BG179688 BF110202 AA528775 W37573 BE041644 AW366504 BM129522 BM129822
5			A1122760 BE718200 AW887496 A4149420 BE706307 BE539395 BE748765 AI3/3653 K/5904 BF3/9165 BF03/353 BIO35353 BIO35455 BIO36406
10	416373	3442_1	BC495559 BF28373 BC494607 AK056582 AW755252 AL596757 BF827376 BF827373 BF827375 BF827369 BF826900 F01252 BC022888 BI850312 AA195845 BF825671 BF574821 ZZ16565 F32854 AA211780 F21563 AI288453 AI803678 AA180309 AI074627 AA192950 AA661688 F36698 F32290 F28773 F22692 AA424993 AW340328 AA192247 BF672229 BF575143 BF673106 BF693623
10	433470	6624_1	X75684 AL573167 AL445461 AL453743 A1983655 AI564644 AA977180 AI694111 AI591358 AW071625 AIG78712 AI7 20331 A1927769 BEC439786 AI963432 AA292956 AW192593 AI865838 AI696905 AL424384 A1161312 AI911921 AI597801 BI494959 AI240988 AI492554 AW262737 BEO44033 AW008570 AW625950 BI494958 AA088439 AA706057 BF222820 BF593608 BE501957 AA524526 BE044134 AW572531 AW015724 BE349186 AA32471 BE201974 AI79884 AA32675 AI671727 AI477033 BEA45195 AW777775 AA903050 AA14728 AA404570 AI075878 W38161 AI972739
15			AW575152 AA723200 C06123 BF057147 AA827686 AA157944 A1990245 AA662517 T32487 A1800106 A1333170 A1859160 W45410 A1990827 AW575152 AA723200 C06123 BF057147 AA827686 AA157944 A1990245 AA662517 T32487 A1800106 A1333170 A1859160 W45410 A1990827 AW275048 AA182640 AAA78328 A1258935 AW85158 AW471421 AW103470 AW300456 AW191997 A1823466 AA962397 AA135655 A1251817 AW339104 AA724739 AA411100 AA191349 AA757735 AA037669 A1769516 AW772283 AA010631 A1692466 A1061065 H80983 R79933 A1950693 AW3393104 AA724739 AA411100 AA191349 AA757735 AA03766 A1769516 AW772283 AA010631 A169286 A1063065 A186286 A1978523 A1872628 A1978523 A1878628 A1978523 A1878628 A1978523 A1878628 A1978523 A197
20			A189356 AW338678 A1261359 A1500576 B1-477/35 A1032509 A197299 A1983535 Z26771 A135838678 A1261359 A1500576 B1-477/35 A1032509 A197299 A1983535 Z26771 A135836 BE811418 BE811415 BE811400 BE811398 BE811340 BE811352 BE773405 BE773494 BE773478 BE773478 BE773470 BE773478 BE811350 BE811379 BF593847 BG055071 BE811388 BE811352 BE773501 BE773494 BE773478 BE773478 BE773470 BE773478 BE811350 BE811379 BF593847 BG055071 AW675302 BF603086 AA719173 BE811348 A1582462 A1686240 BE773500 A124845 A1565439 A1918453 A1472527 A1446740 AA035576 AA191414 AW675302 BF603086 AA719173 BE811348 A1582462 A1686240 BE773500 A124845 A1565439 A1918453 A1472527 A1446740 AA035576 AA191414 AW675302 BF603086 AA719173 BE811348 A1582462 A1686240 BE7737500 A124845 A156459 A1918453 A1472527 A146740 AA035576 AA191414 AW675302 BF603086 AA719173 BE811348 A1582462 A1686240 BE773750 A126746 A1918453 A1472527 A146740 AA035576 AA191414 AW675302 BF603086 AA719173 BE811348 A1582462 A1686240 BE773470 BF603076 A1918463 A1472527 A146740 AA035576 AA191414 AW675302 BF603086 AA719173 BE811348 A168645 AL576810 BG496381 A1928364 BE879732 AA479834 AA479712 C17732 BW691258 BF843901 AW820230 C17476 BE327120 A129574 A136645 AL576810 BG496381 A1928364 BE879732 AA479834 AA479712 C17732 BW691258 BF843901 AW820230 C17476 BE327120 A129574 A16645
25			AL578810 BC498331 AU24336 BE3792 AA43983 AA43972 CT732 BM3723 B BE37340 BE573498 BEB11401 BE773484 BEB11437 BE811380 BF843900 AW806193 AA502832 AA649494 AL568520 AL547960 BE705937 BE811360 BE773498 BE811401 BE773484 BE811437 BE811380 BE811399 BF997171 BF757734 BE926037 A377596 C06111 AW089968 BE811404 BE811472 AI865912 AI925607 AI871950 AI093510 BE905927 BE811435 AA191387 AW772000 BE811433 BE514379 BF844522 BID4896 A1744233 AW984527 C17504 BF843883 AI248307 BE773483 AI567995 W60075 BF941183 AI738844 BE811458 BE773481 AI252390 AA948565 BE706942 BE156356 T65026 AW742958 AW197954 BE905184 AA722206 AI344943 AI348877 AI334860 BE621857 BE156280 AA454099 AA037722 BF843897 AW806183 AA043216 BG482896 AA182734 AA877242
30			ANJA4943 ALJA8877 ALJASABO BECK 108 JE 135260 VANJASABS JACK 1083 ALJASABS ALJASABS BITS5027 BG505731 BC008442 AW372926 H27252 R38114 BF851858 BE156214 AA190427 T91762 AA033067 AA837326 T10930 BF906587 BI755027 BG505731 BC008442 BC010166 AL550134 AL553096 AL548700 AL550751 AL547978 AL545286 AL540643 AU118627 AL 601379 BI259821 BG741786 BI868522 AU135866 BI552770 BI259210 BI256520 BI255569 BG485098 BI258228 BC498501 BM044512 AU133984 AL556586 BE745111 BI222633 AU133931 BG288151 BI260715 BI550550 BG500773 BI551761 BG707601 BI818593 BF691383 BG7211729 BG541578 BE906666 BG751088 BI224135 BG440746 BG478065 BE790436 AW080238 AU137549 BG428896 BE392486 AW961686 BG721056 BE908365 BE546656 BG541235 AW689335 BG588290 BI260895
35			AW651691 BM048974 BM043805 BG142185 AA315188 AI446615 C06300 BC497644 AA088544 AB15997 BG328651 BE519162 AW259165 AW062910 AW062902 AA347236 F11933 AA488005 AA301631 AA376800 D56120 AA343532 AA308636 F00242 AA376086 AA316968 AA343799 BI870221 BE910282 BC538748 AW960564 AV732879 D16854 AA192519 BF922148 AA216013 BG624091 BE544387 BG507008 AW176446
40	409245	3199_2	AF030234 BC017455 BC008526 AW505550 BM460141 N47324 AA361037 AA321632 M55016 AV5293 AV5073715 AA25903 AV507467
45			N41605 AA478519 AA463875 AI858260 AA463379 AI292305 BE045947 AA971089 AI125820 BG940947 AU680245 AA864994 AI125702 A392494 AA931835 AI358631 AW439905 AI027833 AI399648 AI014533 AA347851 AA738261 N67374 N69081 AI768667 AA948472 AI819214 AA293133 AI186725 AA889214 AI222635 BI495143 N29605 N48812 AA769041 AI492769 D56771 AA095911 BE222062 D56772 AW372265 BM054985 D12465 BG534562 AW003511 H87486 H42880 AW190293 BF594697 BF377611 H22043 BI255749 BI492848 H16217 H21980 H22651 H88179 H87354 H44052
50	417141	9517_1	H25165 H44126 A391712 U22662 NM_005693 AW166878 BF339795 AI970974 AI521157 AI336082 AW339789 AI288682 BF477594 BF477593 AI703008 AI290961 AI049684 AW770753 AI208561 AI699406 F33996 AA630563 AI985346 AI927058 AA533982 AW204589 AI206938 AW590068 AI263769 AA991550 AI192005 AL58946 AL524337 AL516239 AL590848 AL580659 AI719135 AW026500 AI698217 AI872977 AI670983 AI654870 AA493407 AA548525 AI016420 AA843563 W15576 H61726 AA913245 BF438146 AL524338 BI762380 AU136488 BI759892 AV655930 T78977 BI524075 BE538944 AA527161 BC211784 AA527065 AA505489 AW512550
55	425231 419631	235504_ 2743_1	BC022323 AF204171 NM_022361 BM264431 BE670789 AW188117 AI025298 AA861832 H84897 AI38ZZ94 AA6628/4 AW993380 BE813/42 H84300
	426969	12113_1	MISBUTY NZUBAZ 100-329 MISBUTY NZUBAZ 100-329 MISBUTY NZUBAZ 100-320 MISBUTY NZUBAZ 100-320
60			AISS1093 AWS13819 AAQ42856 AAZ-2509 AAV35176 AUZ8102 AISS1857 AISS
65			AA373395 BE710347 AL564154 AI708332 AA729530 N92729 AI573015 T29655 H89333 H85847 AI886473 AW18990 H02905 AIB 11960 AU 157755 W86829 AA020844 AU158204 AA057356 AA283466 AA405504 AA017027 W94754 AA226498 W72391 H66461 C00442 H01925 BI912232
	406678 449092		U77534 U77537 AK056270 AV706896 AI692935 AI681140 AW162481 AW087114 AW157019 AI689795 AW251085 AW206911 BF438207 AW134945 BE041668 BF111425 U91641 NM_013305 BF968902 U55966 AU130750 BE174853 AI929731 AW161524 R43753 BE779688
70	436648		AJ002788 AL118666 AJ381600 BE672862 AW500520 BF223709 AW593740 AA262174 AA810597 AA810596 AA310596 F03382 BF376590 AN790002  AA262288 BF931698 AW968014 R18656 BM459356 AW794189 BF954184 Z42558 BF891641 BF963380 Z45874 F05187 X93079 BF742651 BF742649  R51324 D80031 BI457883 F06613 Z43128 F12243 BF950830 H19040 BF950829 F06439 R14947 F06702 R61037 R52173 R14953 R12174 R13610
75	437938	66997_	1 U71456 AA482911 W78802 AW856538 BF737212 N36809 N35320 AA282915 AW505512 Al653832 W87891 Al961530 T85904 H59397 R97278 W01059 Al820532 T82391 Al820501 T63226 R66056 R67840 AW961101 AA337499 W37181 AA180009 AW205862 AA388777 AA856975 BF172457 BG751124 A1741346 Al950344 Al68902 Al872193 AW102898 AW173586 A1763273 Al890387 AW150329 A1762688 AA488892 Al356394 Al539642 AA642789 Al950087 BF589902 N70208 AA283144 AA488964 H60052 R97040 BF886630 AW967677 AW971573 AW967671 Al308119 AA251875 AA908598 Al819225 Al564289 AA308741 AA293273 AA969759 AW276905 AA044209 H83488 T92487
80	406623	3 0_0	X69392 T24055
00	TABLE Pkey:	53C:	Unique number corresponding to an Eos probeset

PCT/US02/29560 WO 03/025138

Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 27 Dunham, et al. (1999) Nature 402-489-495. Ref:

Indicates DNA strand from which exons were predicted. Strand: Nt_position: Indicates nucleotide positions of predicted exons.

5 NL_position Ref Strand

405545 1054740 118677-118807,119091-119296,121626-12182 Plus

96277-96420,96979-97160 124361-124520,124914-125050 401566 8469090 405547 1054740 Ptus 10

> TABLE 54A: ABOUT 151 GENES UPREGULATED IN PRIMARY MELANOMAS FROM TUMORS THAT LATER METASTASIZED RELATIVE TO PRIMARY MELANOMAS THAT DID NOT METASTASIZE LATER

Table 54A lists about 161 genes upregulated in primary metanomas from tumors that later metastasized relative to primary metanomas that did not metastasize later. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average 15 intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey: Unique Eos probeset identifier number

Exemplar Accession number, Genbank accession number ExAcon:

UnigenetD: Unigene Title: Unigene number Unigene gene title 20

90th percentile of Als for primary melanomas that later metastasized divided by the 90th percentile of Als for primary melanomas that did not metastasize later 90th percentile of Als for primary melanomas that did not metastasize later, where the 15th percentile of normal tissue Als was subtracted from both the numerator and denominator R1: R2:

25	Pkey	ExAcon	UnigenelD	Unigena Title	R1	R2
	448966	AW372914	Hs.86149	phosphoinosital 3-phosphate-binding prot	7.15	3.41
	413916	N49813	Hs.75615	apolipoprotein C-II	5.93	6.55
	414807	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	5.64	2.98
	415668	AW957684	Hs.306814	hypothetical protein FLJ21889	5.03	4.56
30	440274	R24595	Hs.7122	scrapie responsive protein 1	4.98	4.83
	417542	J04129	Hs.82269	progestagen-essociated endometrial prote	4.96	7.07
	427882	AA640987	Hs.193767	ESTs	4.68	4.68
	452744	AI267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	4.29	3.06
	407907	AI752235	Hs.41270	procollagen-lysine, 2-oxoglutarate 5-dio	3.94	3.86
35	424410	W79027	Hs.271762	ESTs .	3.67	3.19
-	429083	Y09397	Hs.227817	BCL2-related protein A1	3.46	2.49
	407951	W77762	Hs.79015	antigen identified by monoctonal antibod	3.31	3.06
	428330	1.22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	3.27	2.12
	440099	AL080058	Hs.6909	DKFZP564G202 protein	3.22	2.69
40	428001	H97428	Hs.219907	ESTs, Moderately similar to Transforming	3.20	1.85
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	3.18	4.61
	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	3.13	2.11
	430643	AW970065	Hs.287425	MEGF10 protein	3.10	3.31
	412262	W26406		seven in absentia (Drosophila) homolog 1	3.06	3.94
45	438328	Al492261	Hs.32450	ESTs	3.05	3.09
73	409760	AA302840	113.32.700	gb:EST10534 Adipose fissue, white I Horno	3.01	2.65
	453912	AL121031		SWI/SNF related, matrix associated, acti	2.94	1.86
	416426	AA180256	Hs.210473	Homo sapiens cDNA FLJ14872 fis, clone PL	2.91	3.70
	407744	AB020629	Hs.38095	ATP-binding cassette, sub-family A (ABC1	2.88	2.53
50	453935	AI633770	Hs.42572	ESTs	2.88	2.00
50	452689	F33868	Hs.284176	transferrin	2.84	6.47
	449550	AA353125	Hs.184721	ESTs	2.83	4.74
	409417	AA156247	Hs.104879	serine (or cysteine) proteinase inhibito	2.82	2.43
	438898	AI819863	Hs.106243	ESTs	2.81	2.08
55	430191	Al149880	Hs.188809	ESTs	2.80	2.69
55	408418	AW963897	Hs.44743	KIAA1435 protein	2.79	1.75
	450157	AW961576	Hs.60178	ESTs	2.77	3.40
	420380	AA640891	Hs.102406	ESTs	2.77	4.28
	443172	AW662964	Hs.199061	p300/CBP-associated factor	2.75	2.88
60	456629	AW891965	NS.133001	histone deacetylase 3	2.72	2.24
OO	407857	A1928445	Hs.92254	synaptotagmin-like 2	2.72	1.93
	421097	AI280112	Hs.125232	Homo sapiens cDNA FLJ13266 fis, clone OV	2.68	2.59
	436280	AIS90734	NS.123232	Homo sapiens cDNA: FLJ22562 fis, clone H	2.67	2.79
	436260	Y10515		gb:H.sapiens mRNA for CD58 T7 protein.	2.65	1.98
65	427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	2.64	1.76
05	427899	AA829286	Hs.332053	serum amyloid A1	2.59	3.01
		AI017798	15.332033	ESTs, Weakly similar to TI47_HUMAN CARGO	2.58	1.60
	442793	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	2.57	1.91
	446619		Hs.283713	ESTs, Weakly similar to S64054 hypotheti	2.57	2.13
70	444381	BE387335		ESTs, Weakly similar to 30-054 hypotheti	2.56	2.61
70	458247	R14439	Hs.209194 Hs.326444	cartilage acidic protein 1	2.52	2.74
	451668	Z43948 AA137152	Hs.286049	phosphoserine aminotransferase	2.51	1.88
	433980	AW016610	Hs.816	ESTs	2.50	1.68
	412719			KIAA0871 protein	2.50	3.11
75	441789	D52059	Hs.7972	Target Exon	2.50	3.15
13	405885	41004044	11- 20000		2.48	3.33
	453464	AI884911	Hs.32989	receptor (catcitonin) activity modifying protein tyrosine kinase 9	2.48	1.66
	417821	BE245149	Hs.82643		2.47	2.79
	450202	AW969756	Hs.34145	ESTs, Weakly similar to B49647 GTP-bindi	2.47	2.75
80	436825	AW341123	Hs.120275	ESTs	2.42	2.33
δÚ	424762	AL119442	Hs.183684	eukaryotic translation initiation factor	2.42	1.76
	432426	AW973152	Hs.31050	ESTs	2.42 2.41	2.41
	409095 403752	AW337272	Hs.293656	ESTs, Moderately similar to S72481 proba NM_002753*:Homo sapiens mitogen-activate	2.41	2.87

	404489 411690	AA669253		Target Exon RNA, U2 small nuclear	2.39 2.37	1.97 2.54
	439195	H89360		gb:yw28d08.s1 Morton Fetal Cochlea Homo	2.37	2.27
	453582	AW854339	Hs.33476	hypothetical protein FLJ11937	2.36	2.81
5	438461	AW075485	Hs.286049	phosphoserine aminotransferase	2.35	2.91
	432878	BE386490	Hs.279663	Pirin	2.35	2.28
	416647	BE297139	Hs.79411	replication protein A2 (32kD)	2.33	1.97
	428666	AL080190	Hs.189242	Homo sapiens mRNA; cDNA DKFZp434A202 (fr	2.32	2.92
10	413645	AA130992	115 40700	gb:zo15e02.s1 Stratagene colon (937204)	2.31	2.63
10	421282	AA286914	Hs.40782	ESTs	2.31 2.31	1.85 2.21
	434418 413204	AF134707 BE071603	Hs.278679	a disintegrin and metalloproteinase doma gb:QV3-BT0510-161299-032-f03 BT0510 Homo	2.31	1.49
	449720	AA311152	Hs.288708	hypothetical protein FLJ21562	2.30	1.78
	451838	AW005866	Hs.193969	ESTs	2.28	2.05
15	410943	AW968322	Hs.11156	low molecular mass ubiquinone-binding pr	2.28	2.39
	459711	BE386801	Hs.21858	trinucleotide repeat containing 3	2.27	2.39
	429489	AF008203	Hs.204039	aristaless-like homeobox 3	2.26	1.97
	429493	AL134708	Hs.145998	ESTs Committee of the C	2.26	2.77
20	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	2.26	1.78
20	441989	AA306207	Hs.286241	protein kinase, cAMP-dependent, regulato	2.26 2.25	1.84 1.47
	419352 427393	A1675008 AB029018	Hs.199493 Hs.177635	ESTs KIAA1095 protein	2.25	1.83
	418522	AA605038	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	2.24	2.42
	433468	AA832055	Hs.172843	ESTs, Wealthy similar to ALU1_HUMAN ALU S	2.24	1.76
25	452782	AA028166	Hs.17733	ESTs	2.24	2.34
	443910	AW051711	Hs.132440	ESTs	2.24	1.79
	408832	AW085690	Hs.63428	ESTs, Weakly similar to Z195_HUMAN ZINC	2.22	1.52
	407283	T51008		gb:yb55e08.s1 Stratagene ovary (937217)	2.22	1.31
20	437376	AA749400	Hs.257890	ESTs	2.22 2.22	2.44 1.62
30	450712	AI732130	Hs.270496	ESTs, Weakly similar to ALU8_HUMAN !!!! hypothetical protein FLJ20043	2.22	2.36
	421362 445183	AK000050 AB007877	Hs.103853 Hs.12385	KIAA0417 gene product	2.20	1.84
	438501	Z44110	Hs.86149	phospholnositol 3-phosphate-binding prot	2.20	1.76
	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-li	2.19	1.59
35	414900	AW452420	Hs.248678	ESTs	2.18	1.89
,	427704	AW971063	Hs.292882	ESTs	2.17	1.86
	404942			splicing factor, arginine/serine-rich 9	2.17	1.86
	448019	AW947164	Hs.195641	ESTs, Moderately similar to 138022 hypot	2.17	1.64
40	459254	AA694386	Hs.290914	ESTs	2.16	1.61
40	418965	A1002238	Hs.11482	splicing factor, arginine/serine-rich 11	2.16 2.16	1.79 2.32
	443357 412432	AW016773 AA126311	Hs.9879	tow motecular mass ubiquinone-binding pr ESTs	2.15	2.73
	449567	A1990790	Hs.188614	ESTs	2.08	2.85
	433179	AW362945	Hs.162459	ESTs	2.07	4,77
45	408243	Y00787	Hs.624	interleukin 8	2.05	3.12
	435294	T84084	Hs.196008	Homo sapiens cDNA FLJ11723 fis, clone HE	1.97	2.89
	449656	AA002008	Hs.188633	ESTs	1.94	3.60
	412649	NM_002206	Hs.74369	integrin, alpha 7	1.93	2.76
50	445162	AB011131	Hs.12376	piccoto (presynaptic cytomatrix protein)	1.93	2.66 3.39
20	419356 424263	AI656166	Hs.7331	hypothetical protein FLJ22316 L1 cell adhesion molecule (hydrocephalus	1.92 1.89	3.10
	414694	M77640 NM_015362	Hs.1757 Hs.76907	HSPC002 protein	1.88	4.25
	415825	Y18024	Hs.78877	inositol 1,4,5-trisphosphate 3-kinase B	1.87	2.66
	409105	AW467539	Hs.255877	ESTs	1.87	2.96
55	444784	D12485	Hs.11951	ectonucleofide pyrophosphatase/phosphodi	1.85	2.80
	404149			C6002509*:gi 5031885pef NP_005568.1  li	1.84	2.93
	406387			Target Exon	1.82	2.96
	420871	AA702972	Hs.65300	ESTs	1.76	3.12
60	455797 418751	BE091833		gb:IL2-870731-260400-076-F04 8T0731 Homo phosphoinositide-3-kinase, regulatory su	1.75 1.70	3.12 3.20
00	412347	BE389014 AW970026	Hs.73818	ubiquinol-cytochrome c reductase hinge p	1.67	3.65
	413211	AW967107	Hs.109274	hypothetical protein MGC4365	1.66	2.89
	459317	BRCA16	1.0.1002.1	Eos Control	1.61	7.34
	425525	AA358883	Hs.23871	ESTs	1.59	2.67
65	436823	AW749865	Hs.117077	ESTs, Weakly similar to I38022 hypotheti	1.56	2.76
	433669	AL047879	Hs.194251	ESTs, Weakly similar to ALU2_HUMAN ALU S	1.55	2.76
	424389	AA339786		lymphocyte-specific protein 1	1.53	2.95
	426672	AW270555	Hs.171774	hypothetical protein	1.51 1.47	3.39 2.65
70	415977 404780	AL037622	Hs.78935	methionine aminopeptidase; efF-2-associa Target Exon	1.43	2.77
70	436476	AA326108	, Hs.33829	bHLH protein DEC2	1.41	3.04
	428284	AA535762	Hs.183435	NM 004545:Homo sapiens NADH dehydrogenas	1.38	2.94
	448571	AA486794	Hs.66915	ESTs, Weakly similar to 16.7Kd protein [	1.37	2.80
~ -	428156	BE269388	Hs.182698	mitochondrial ribosomal protein L20	1.36	3.29
75	447752	M73700	Hs.105938	lactotransferrin	1.35	2.70
	447455	H38335	Hs.6750	Homo sapiens mRNA for FLJ00058 protein,	1.35	3.03
	453281	W46280	Hs.55940	ESTs, Wealdy similar to A25704 synapsin	1.34	2.69
	413142	M81740	Hs.75212	omithine decarboxylase 1 gb:af54a01.s1 Soares_total_fetus_Nb2HF8_	1.33 1.32	2.96 2.70
80	407194 444107	AA621644 T46839	Hs.10319	UDP glycosyltransferase 2 family, polype	1.26	3.27
30	406797	AJ432224		ribosomal protein L6	1.26	2.72
	406711	N25514	Hs.77385	myosin, light polypeptide 6, alkali, smo	1.25	7.10
	414608	BE396215	Hs.76572	ATP synthase, H transporting, mitochondr	1.24	2.72

	401846			NM_000988*:Homo sapiens ribosomal protei	1.24	2.82
	432982	AA531058	Hs.182248	truncated calcium binding protein	1.23	3.10
	428578	BE391797	Hs.343588	ribosomal protein S12	1.23	2.74
_	400199			Eas Control	1.21	3.58
5	400079			Eos Control	1.20	2.99
	412623	R28898	Hs.74170	metallothionein 1E (functional)	1.19 1.19	2.63 4.15
	406713 406712	U02629 M31212	Hs.77385 Hs.77385	myosin, light polypeptide 6, alkali, smo myosin, light polypeptide 6, alkali, smo	1.18	4.75
	442492	AA528489	Hs.234518	ribosomal protein L23	1.17	2.74
10	431526	Y10129	Hs.258742	myosin-binding protein C, cardiac	1.17	3.15
10	436398	H87136	Hs.5174	ribosomal protein S17	1.16	3.22
	432205	AIB06583	Hs.125291	ESTs	1.15	2.76
	406859	AI581134	Hs.181357	taminin receptor 1 (67kD, ribosomal prot	1.09	2.66
	401254			Target Exon	1.00	3.08
15	405752			Target Exon	1.00	2.87
	445772	AI733941	Hs.145493	ESTs, Weakly similar to ALU7_HUMAN ALU S	1.00	2.70
	452916	AA642831	Hs.31016	putative DNA binding protein	1.00 1.00	2.62 2.64
	451411	AA017492	Hs.135655	EST	1.00	2.62
20	415658 448610	BE501921 NM_006157	Hs.270471 Hs.21602	ESTs nel (chicken)-like 1	1.00	3.30
20	440010	MM_000137	NS.21002	Hei (Claukei)/Hike 1	1.00	
	TABLE 54	<b>8</b> :				
	Pkey:	Uni	que Eos probesel ide	ntifier number		
0.5	CAT numb		ne cluster number			
25	Accession	: Ger	nbank accession num	bers		
	D	C4T41				
	Pkey	CAT Numbe	r Accession	250 A1501124 A11145124 A1802200 AAG17225 AAG226	KI REROSINSA	AJ304442 AJ167464 AJ284188 AA054272 AA829262 AJ351910
	412262	4362_1	TOPOGO A PRESON	LIZONSE ALIT 19916 REAA6537 RESO3207 RESO2849	A1698102 AA25	8553 AV718529 AV719917 BF724133 BI438668 AI804000
30			RE349103 AI912	294 BE645117 AA227954 AA446520 AA879147 AA28	1770 AW13687	2 AA807907 AI435989 AI339626 AI383274 AA418512 BE771804
-			BF894509 AA455	i093 Al379061 Al150855 BF769906 R17298 AU13874	0 BF808607 BE	674633 AV700132 AA227789 AA253099 AW975199 AA935418
			T74315 F12666 A	A022923 T89028 AA258606 W26406 BE838620 AV7	00706 AA10132	21 R41382 H14479 AA253044 R54810 R42784 R44804 R41278
	409760	865166_1	AA302840 T9301	6 T92950 AU184997 AA077551		
~ ~	453912	32562_3	BM472224 B1966	849 B1966735 AW973032 B1962894 B1963048 AA548	765 AI926504 A	A041551 AW043754 A1086702 AW008105 AA974849 AW614893
35				5996 AW262982 AI580991 BF726843 AV693312 W35	325 AA039927	BG460936 AW388482 AW388420 BF374777 W01360 N94710
	455500	007.00	H87967	1740 DE000030 D45550 DE477523 AMIO03530 AMIO	16343 AI34616	7 T07082 AW805679 W96278 AA135796 W32615 AW995418
	456629	207_22	AW891905 AW60	JA749 BEUBUB72 K13339 BE177023 AW30332U AW3 2022 AW001621 AW206721 AW395742 AW395714 A	13343 MZ40 IO WENA757 W87	409 AW604738 AW385757 AW580796 AW801247 BE003239
						791 AW604759 AW866589 AW604758 N44337 Al378548
40			AWROAAR AAAA	7172 AI288683 AA229639 AA091945 AW945454 AA0	63629 AA7025	04 AW861938 AW894816 AW580841 AA094372 T06399
••			AW885686 BE24	4086 BE005035 AW861913 AA551773 AW858460 AV	V370926 AW75	4352 AW889695 AW384408 AI907428 BE067491 AW861939
			AA248197 AW38	1373 AW177325 AW806879 AA935217 BE067498 BE	083742 BE067	470 AW894935 BE082529 AI248811 BE179917 BE002200
			AW607506 AW3	92889 AW894560 AW381360 AI904206 AW863533 CX	0609 AW3813	72 BE082530 AW898120 BE075323 AW392799 AW601420
			AI695314 BE083	790 AW858568 AW945550 BE177153 AW970506 BE	350419 Al9069	19 AW360794 AI906917 AW885979 AW794240 AW945566
45			A1688683 A16886	94 AW009660 AW601421 AW360793 BE066524 BE0	83901 AW3698	47 AW381871 AW935435 AW664582 AW877775 AW838449
•			BE180466 AW85	8501 BE180464 AI371163 AA778231 AI174991 BE01	1720 AW87777	6 AW877800 AW877795 T19900 AW866365 AW898099
			BE011715 BE16	7842 BE011718 BE011724 AW363639 AW878658 AW	1878662 AW89	4887 BE082356 AW389211 AW804286 AW610312 AI904717
			AW610318 AW9	95909 AW610296 AW901923 AW880003 AI/621/1 AV	NU02382 AW30 307438 BE0086	58713 AW062593 AW176663 AW842064 AW842089 AW842095 186 BE172115 BE077030 AW608556 AW835577 Al909628
50			ALZ43049 AVY90	20/4 AWUG2332 AW 1/0004 AW731032 DEU0//U3 AU 20/41 DE077553 DE160370 DE160388 AW835666 AW	1606765 AW60	6770 AW835678 AW606758 AW606778 AI907484 BE 172821
50			AWEGETER AWG	99517 AWR44165 RF 171738 AW751683 AW610493 R	E177484 BE17	7487 AA090510 AW844117 BE173367 AW999878 AI124870
			RF163472 AW84	1823 AW379762 AW893297 AI290296 BE089132 AA	610287 AW176	676 AW607622 BE172639 AW893232 AA329629 BE089008
			BE178350 BE17	8214 BE063291 AW820236 AW999653 BE089486 BE	173126 BE171	775 BE185787 AA558280 AI174840 AW999112 BE218391
			RF172734 BF17	8021 BE 172738 BE 173324 AW603494 AL036722 R38	1192 R60905 H	53721 H41052 AL037917 R37795 AW998972 AA767189
55			AW044272 H506	89 AA768399 AA767764 Al087888 H44202 BE22279	2 N90597 W81	396 N90615 AJ935353 BE501168 F10945 AW118215 AJ970480
					1 N69276 BE46	7722 AW392780 BE172467 H92861 AI524921 F02989 Z39328
			F02705 F01414	T88678 AI215165 H87220 AW374781	104 D30000 A14	PC1C70 AI0170C0 DC044272 AA2224E9 AA097027 AA29ERG0
	436280	36296_1	AKU26215 AI201	248 BE6/1206 AA860436 AA/30/6/ AA83450/ U/S:	NA 0/3000 AV	/961628 A1017068 BE044373 AA322458 AA987927 AA385869 0734 R79189 A1536900 AW589301 A1128434 BE838011 BE837891
60	•		BFB94555 H954		W101013 MUS	1/3 (1/3 (03 M300300 M1100300 1 M120-0-1 0-0000 1 1 0-001 00 1
00	442793	417820_2		1022 AI017798 AI953594 AW445065 AI245087		
	411690	53926_1	AK027091 BF51	4593 BF768430 BI037830 BE175161 BG000114 BG8	97171 AA7453	91 AA669569 AA669253 BI049453 BE304449 BG010136
	411000		BG830874 BF09	1358 BF762561 T56173 BC003629 BF091330 BE697	323 BF091340	BE843330 AA744150 AA745471 W26276 BI037837
	439195	21979_1	AF086037 H893			
65	413645	1234345_1		69537 AA503835		
	413204	1494523_1		1613 BE071603 BE071587 BE071607 BE071615 BE0		
	443357	427117_1		54600 AI052778 BG057892 AW016773 AI452937 AW0	285293	
	455797	1511159_1		91874 BE091871	7741600 AWAE	0447 AA843698 AW188066 AW007171 AW007027 AI075008
70	418751	21393_1	BF09U141 BE13	19300 A1937 JI I AU 13 1230 A1734 1342 A17274231 A17 19002 AWI 15 1842 AAE22181 A1272854 A1005661 AA26	1504F AAR77RG	9 AW473512 AW296620 AA872899 Al094216 Al025188 AA25699
70			AL320331 AAGU	192 A1289493 A1040740 RF167841 AW151374 RF167	754 RF036108	AA299181 N23237 T62967 W96060 AA574412 AW606697
			W96059 R5130	3 R09158 R59113 T48473 T59023 AA122066 AW6066	343 R38386 R0	6567
	424389	1059_4	BG190758 AW9	61118 W77994 AA339877 AW845121 AW845129 BG	181820 BE716	719 AI125483 AI161017 W73951 AI250771 AA912611 AA339786
			BE838286 BE83	38282 BE716636 AA777158 W94063 BE716628 BE71	6625 BE83837	1 BF371044 BE716631 BE716402
75	406797	0_0		76890 A1499346 AA937014 AA653573 A1318525 A1246		
		_				
	TABLE			day to an Eas amband		
	Pkey:	ň	nique number corresi	conding to an Eos probeset	(CI) susseen	"Dunham, et al." refers to the publication entitled "The DNA
80	Ref:	5	equence source. The	o 7 digit numbers in this column are Genoant Identifier romosome 22° Dunham, et al. (1999) <u>Nature</u> 402:489-	(G) (W)( <b>10</b> 27 <b>5.</b> 195.	Seattletin, Ct or. Tellera to the promotion character the offer
30	Strand:			rom which exons were predicted.		
	Nt_posit			sitions of predicted exons.		

PCT/US02/29560 WO 03/025138

	Pkey	Ref	Strand	Nt_position
	405885	7677703	Minus	42574-42998
	403752	7678857	Plus	33704-33828
	404489	8113772	Plus	98183-98480
5	404942	7382153	Plus	92095-92252
-	404149	7534008	Plus	121831-121951,124044-124150
	406387	9256180	Plus	116229-116371,117512-117651
	404780	9887810	Minus	175708-175871
	401846	7712190	Minus	82775-82823,82912-83022
10	401254	9796309	Plus	152209-152383
	405752	9212305	Plus	91392-91528

TABLE 55A: ABOUT 201 GENES UPREGULATED IN PRIMARY MELANOMAS FROM TUMORS THAT DID NOT METASTASIZE RELATIVE TO PRIMARY MELANOMAS THAT LATER METASTASIZED 15

LATER METASTASIZED

Table 55A lists about 201 genes upregulated in primary melanomas from tumors that did not metastasize relative to primary melanomas that metastasized later. Genes were selected from 59880 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey: Unique Eos probeset identifier number

ExAcon: Exemplar Accession number, Genbank accession number

20

UnigenelD:

Unigene Title:

25

Unigene number
Unigene gene title
90th percentile of Als for primary metanomas that did not metastasize divided by the 90th percentile of Als from primary metanomas that metastasized later
90th percentile of Als for primary metanomas that did not metastasize divided by the 90th percentile of Als from primary metanomas that metastasized later,
where the 15th percentile of normal tissue Als was subtracted from both the numerator and denominator R1: R2:

	Pkey	ExAcon	UnigenelD	Unigene Title	Rí	R2
	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	8.08	5.48
	404854	70015140		Target Exon	5.18	8.18
30	406636	L12064		gb:Horno sapiens (clone WR4.12VL) anti-th	4.89	4.95
	433435	BE545277	Hs.340959	Ts translation elongation factor, mitoch	4.83	4.86
	408471	NM_012317	Hs.45231	teucine zipper, down-regulated in cancer	4.71	4.70
	433658	L03678	Hs.156110	immunoglobulin kappa constant	4.71	3.85 4.01
·	412802	U41518	Hs.74602	aquaporin 1 (channel-forming integral pr	3.98 3.92	3.35
35	415801	R24219	Hs.278443	Fc fragment of IgG, low affinity Itb, re	3.83	2.78
	400417	X72475		Target	3.67	2.29
	419870	AW403911	Hs.266175	phosphoprotein associated with GEMs	3.62	3.68
	409190	AU076536	Hs.50984	sarcoma amplified sequence dipeptidylpeptidase VI	3.61	3.89
40	408692	AL040127	Hs.34074 Hs.249159	adrenergic, alpha-2A-, receptor	3.56	3.61
40	423619	T48691 AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447	3.55	2.85
	442117 445745	A8007924	Hs.13245	KIAA0455 gene product	3.38	2.55
	406663	U24683	115.13243	immunoglobulin heavy constant mu	3.34	6.16
	414522	AW518944	Hs.76325	tmmunoglobulin J chain	3.32	2.75
45	419235	AW470411	Hs.288433	neurotrimin	3.32	2.74
43	441598	AI733219	Hs.58262	ESTs	3.31	3.71
	402294		1.2.00	Target Exon	3.24	2.35
	402737			Target Exon	3.22	2.87
	414135	NM_004419	Hs.2128	dual specificity phosphatase 5	3.20	3.04
50	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	3.18	2.81 4.62
	427335	AA448542	Hs.251677	G antigen 7B	3.17 3.13	4.62 2.34
	404995			ENSP00000251890":Monocytic leukemia zinc	3.13 3.12	2.21
	430540	AW245422		Homo sapiens cDNA: FLJ22105 fis, clone H	3.12	1.93
E E	430015	AW768399		ESTs	3.09	2.87
55	414340	AI022656	Hs.296272	ESTs Eos Control	3.08	3.16
	400072	4544470	Hs.118407	glypican 6	3.06	2.73
	422567	AF111178	ns.110407	Target Exon	3.04	2.56
	401284 455839	BE145814		ob:MR0-HT0208-101299-202-a04 HT0208 Homo	3.02	2.76
60	454027	R40192	Hs.21527	Human DNA sequence from clone GS1-115M3	3.00	3.15
00	437258	AL041243	Hs.174104	ESTs	2.99	2.44
	445612	N94126	Hs.12969	hypothetical protein ·	2.98	2.40
	417777	AI823763	Hs.7055	ESTs, Wealthy similar to 178885 serine/th	2.97	2.13
	437723	AI572731	Hs.13256	ESTs	2.95	2.46
65	439668	AI091277	Hs.302634	frizzled (Drosophila) homolog 8	2.95	2.77 2.68
	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	2.94 2.92	2.68 3.81
	424761	AA534528	Hs.152944	loss of heterozygosity, 11, chromosomal	2.92	3.00
	405757			Target Exon	2.92	6.71
70	406621	X57809	Hs.8997	immunoglobufin lambda locus	2.86	2.16
70	409060	AI815867 R26584	Hs.50130 Hs.267993	necdin (mouse) homolog hypothetical protein FLJ10143	2.82	2.50
	431712	AI929374	Hs.75367	Src-like-adapter	2.82	2.48
	413441 452651	AI218918	Hs.30209	KIAA0854 protein	2.82	1.13
	422386	AF105374	Hs.115830	heparan sutfate (glucosamine) 3-0-sulfot	2.78	2.77
75	439778	AL109729	Hs.99364	gutative transmembrane protein	2.77	1.92
,,	434293	NM_00444		Eph86	2.75	2.89
	406642	AJ245210		gb:Homo sapiens mRNA for immunoglobulin	2.70	2.03
	406638	M13861		gb:Human T-cell receptor active beta-cha	2.69	2.67
	432331	W37862	Hs.274368	MSTP032 protein	2.68	3.08
80	408989	AW361666	Hs.49500	KIAA0746 protein	2.68 2.68	2.58 2.53
	401731			NM_017990*:Homo sapiens hypothetical pro	2.68	3.42
	401979			C17000767:gi]11990770[emb[CAC19651.1] (A	2.68	2.51
	415539	AJ733881	Hs.72472	BMP-R18	2.00	2.01
				550		

					2.67	2.13
	425032	NM_001186	Hs.154276	BTB and CNC homology 1, basic leucine zi	2.67	3.25
	406837	R70292	Hs.156110	immunoglobulin kappa constant	2.66	2.74
	422550	BE297626	Hs.296049	microfibrillar-associated protein 4	2.66	
_	425100	AF051850	Hs.154567	supervillin	2.65	2.80
5	452933	AW391423	Hs.288555	Homo sapiens cDNA: FLJ22425 fis, clone H	2.65	2.63
	439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	2.64	1.84
	447232	AW499834	Hs.327	interleukin 10 receptor, alpha	2.63	2.63
	425580	L11144	Hs.1907	galanin	2.62	2.00
	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	2.61	1.80
10	412482	A1499930	Hs.334885	mitochondrial GTP binding protein	2.61	1.82
10	433470	AW960564	1.5.55 1000	transmembrane 4 superfamily member 1	2.60	2.44
	419138	U48508	Hs.89631	ryanodine receptor 1 (skeletal)	2.60	2.47
		040000	113.03031	NM_024997":Horno sapiens hypothetical pro	2.60	2.58
	401112	A A 722204			2.59	2.32
15	411802	AA733204	11- 000430	nuclear transcription factor Y, gamma	2.59	1.88
15	407856	AA045281	Hs.266175	phosphoprotein associated with GEMs	2.58	2.81
	425209	AL049761	Hs.155140	casein kinase 2, alpha 1 polypeptide		2.10
	417165	R80137	Hs.302738	Homo sapiens cDNA: FLJ21425 fis, clone C	2.56	
	442560	AA365042	Hs.325531	ESTs, Wealdy similar to 2004399A chromos	2.55	3.97
	408491	A1088063	Hs.7882	ESTs	2.54	2.74
20	420223	N27807		ribosomal protein L4	2.54	2.02
	444467	AI150368	Hs.143844	ESTs	2.54	2.59
	436729	BE621807		transmembrane 4 superfamily member 1	2.53	2.29
	449217	AA278536	Hs.23262	ribonuctease, RNase A family, k6	2.53	1.80
	453507	AF083217	Hs.33085	WD repeat domain 3	2.52	1.99
25	420315	NM_006299	Hs.96448	zinc finger protein 193	2.52	2.50
	443060	D78874	Hs.8944	procellagen C-endopeptidase enhancer 2	2.50	2.35
	453500	AI478427	Hs.43125	esophageal cancer related gene 4 protein	2.50	2.44
	402692	MINIONEI	16.43123	Target Exon	2.50	1.73
		1402020	Un 100041	turnor necrosis factor receptor superfami	2.50	4.55
30	427792	M63928	Hs.180841		2.49	2.95
30	440065	W03476	Hs.266331	hypothetical protein MGC4595	2.49	3.55
	420568	F09247	Hs.247735	protocadherin alpha 10		
	444115	AW954585	Hs.271920	ESTs. Weakly similar to Z195_HUMAN ZINC	2.49	2.52
	404049			NM_018937*:Homo sapiens protocadherin be	2.48	2.67
	417694	R09486	Hs.193118	ESTs	2.48	2.09
35	420600	BE011657	Hs.165695	ESTs. Weakly similar to unnamed protein	2.48	2.00
	429922	297630	Hs.226117	H1 histone family, member 0	2.47	2.01
	404752			NM_024778:Homo sapiens hypothetical prot	2.47	3.07
	421429	NM_014922	Hs.104305	death effector filament-forming Ced-4-li	2.47	2.46
	436378	AJ227874	Hs.99244	ESTs	2.46	1.88
40	429852	AB010445	Hs.225948	small inducible cytokine subfamily A (Cy	2.44	2.98
40	431190	AL134172	Hs.120852	ESTs	2.44	2.48
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	2.44	2.96
			Hs.192371	down syndrome critical region protein DS	2.44	3.16
	436608	AA628980			2.43	3.33
AS	445547	D86181	Hs.273	galactosylceramidase (Krabbe disease)	2.43	2.07
45	443030	R68048	Hs.9238	hypothetical protein FLJ23516	243	3.36
	416908	AA333990	Hs.80424	coagulation factor XIII, A1 polypeptide	2.40	3.38
	406782	AA430373		gb:zw20f11.s1 Soares ovary tumor NbHOT H		3.78
	407260	L09095		gb:Homo sapiens mRNA fragment.	2.38	
	419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	2.36	3.56
50	431365	AA504080	Hs.191958	immunoglobulin superfamily receptor tran	2.34	2.84
	414555	N98569	Hs.76422	phospholipase A2, group IIA (platelets,	2.33	3.21
	436485	X59135	Hs.156110	immunoglobulin kappa constant	2.31	2.94
	403632			Target Exon	2.27	2.80
	434232	AW297064	Hs.131862	ESTs	2.24	2.98
55	428114	AJ821548	Hs.98363	ESTs, Wealty similar to I38022 hypotheti	2.23	2.81
	403294			Target Exon	2.19	2.81
	429249	X81479	Hs.2375	egf-like module containing, mucin-like,	2.16	3.13
	403295	,	1.0.2070	Target Exon	2.15	2.95
	427817	AA503373	Hs.186678	ESTs	2.13	2.80
60	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	2.08	3.28
00		AI696081	Hs.223770	ESTs	2.04	3.50
	443176	M030001	ns.223770	C17001739*:gij2327052 gb AAC48759.1  (U9	2.04	5.39
	401770	500450		gb:yf18a07.s1 Soares fetal liver spleen	2.03	2.95
	407124	R08160			2.03	2.97
15	456060	C14904	Hs.45184	Homo sapiens cONA FLJ12284 fis, clone MA	2.01	3.42
65	413053	AW963263	Hs.65377	ESTs, Moderately similar to KIAA1399 pro		
	426653	AA530892	Hs.171695	dual specificity phosphatase 1	2.01	3.05
	410677	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein	2.01	3.58
	401673			C15001416*:gi 12743112 ref XP_010131.2	1.99	4.99
	420983	W95228	Hs.100764	cathepsin G	1,95	5.47
70	413624	BE177019	Hs.75445	SPARC-like 1 (mast9, hevin)	1.94	4.58
	433554	AW957666	Hs.8108	disabled (Drosophila) homolog 1	1.93	2.82
	405121			mitogen-activated protein kinase 8 inter	1.92	2.82
	436456	AW292677	Hs.248122	G protein-coupled receptor 24	1.92	2.80
	450852		Hs.7740	oxysterol binding protein-like 1	1.91	5.08
75	432902			histone deacetylase 3	1.90	2.84
, ,			Hs.111554	ADP-ribosylation factor-like 7	1.89	3.04
	422100		Hs.95577	cycfin-dependent kinase 4	1.87	2.85
	420162		Hs.146393	homocysteine-inducible, endoplasmic reti	1.85	3.71
	424398		Hs.79630	CO79A antigen (immunoglobulin-associated	1.85	3.38
80	416714			selenoprotein P, plasma, 1	1.85	3.57
٥U	433455		Hs.3314		· 1.82	6.17
	447990		Hs.20144	small inducible cytokine sublamily A (Cy	1.80	3.50
	421563			granutysin	1.78	2.87
	453804	AA300204	Hs.35276	KIAA0852 protein	1.10	2.07

	429412 437866	NM_006235 AA156781	Hs.2407	POU domain, class 2, associating factor metallothionein 1E (functional)	1.78 1.77	3.54 2.97 6.89	
	427751	AF000152		conserved gene amplified in osteosarcoma	1.75 1.74	3.60	
5	400442	NIM 004020	Hs.155597	DKFZP586G1722 protein D component of complement (adipsin)	1.74	3.45	
5	456898 414477	NM_001928 U41635	Hs.76228	amplified in osleosarcoma	1.71	4.99	
	432870	AW974124	110.17 0220	gb:EST386227 MAGE resequences, MAGM Homo	1.68	2.86	
	456642	AW451623	Hs.109752	putative c-Myc-responsive	1.68	3.0 <del>9</del> 2.83	
10	456694	AW016382	Hs.105642	Homo sapiens cDNA: FLJ23271 fis, clone H	1.66 1.65	2.84	
10	430449	AA352723	Hs.241471	RNB6	1.65	2.88	
	401029			v-myc avian myelocytomatosis viral relat NM_002508:Homo sapiens nidogen (enactin)	1.64	3.37	
	402742 402559			Rho GTPase activating protein 1	1.63	3.07	
	418271	NM_000919	Hs.83920	peptidylglycine alpha-amidating monooxyg	1.62	3.11	
15	406851	AA609784		major histocompatibility complex, class	1.62	2.86	
	450912	AW939251	Hs.25647	v-fos FBJ murine osteosarcoma viral onco	1.60 1.60	3.94 3.75	
	447029	AL137281	Hs.17110	Homo sapiens mRNA; cDNA DKFZp434C2016 (f gb:HSC1QB121 normalized infant brain cDN	1.59	2.96	
	417739	Z43995 AA428123	Hs.302766	tyrosine 3-monooxygenase/tryptophan 5-mo	1.58	2.95	
20	452950 427461	AA531527	Hs.332040	hypothetical protein MGC13010	1.58	4.11	
20	444182	AW160432	Hs.296460	craniofacial development protein 1	1.57	2.98	
	407815	AW373860	Hs.183860	hypothetical protein FLJ20277	1.57	3.88 2.88	
	452887	AI702223	Hs.107253	hypothetical protein OKFZp761F241	1.56 1.56	3.59	
25	416819	U77735	Hs.80205	pim-2 oncogena proline arginine-rich end leucine-rich r	1.56	4.38	
25	414583	AA362907 AI204418	Hs.76494 Hs.190080	ESTs	1.55	3.47	
	426104 441591	AF055992	Hs.183	Duffy blood group	1.52	4.28	
	446406	AI553681	1,0.120	Arg/Abl-interacting protein ArgBP2	1.49	2.87	
	427343	AI880044	Hs.176977	protein kinase C binding protein 2	1.49	2.88	
30	415550	L13720	Hs.78501	growth arrest-specific 6	1.47 1.46	· 4.82	
	411961	AJ478432	Hs.72956	hypermethylated in cancer 1	1.40	3.19	
	406213			ENSP00000246202*:DJ63M2.2 (similar to AC NM_003105*:Homo sapiens sortilin-related	1.41	2.97	
	400847			NM_021965°:Homo sapiens phosphoglucomuta	1.40	3.02	
35	404642 452650	AW270150	Hs.254516	ESTs	1.40	2.86	
	432894	AW167668	Hs.279772	brain specific protein	1.37	5.52	
	404030			NM_015669°:Homo sapiens protocadherin be	1.37	3.03 3.15	
	422033	AW245805	Hs.110903	daudin 5 (transmembrane protein deleted	1.35 1.34	3.13	
40	413762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	1.32		
40	425367	BE271188	Hs.155975	protein tyrosine phosphatase, receptor t natural killer cell transcript 4	1.32		
	415198	AW009480 Z25437	Hs.943	gb:H.sapiens protein-tyrosine kinase gen	1.31		
	406908 423959	AA333025		gb:EST37122 Embryo, 8 week I Homo sapien	1.31		
	408135	AA317248	Hs.42957	methyttransferase-like 1	1.29		
45	427523	BE242779	Hs.179526	upregulated by 1,25-dihydroxyvitamin D-3	1.29		
	415512	Y16270	Hs.78482	paralemmin	1.29 1.28		
	413531	AL036958	Hs.75416	DAZ associated protein 2 transmembrane 9 superfamily member 1	1.27		
	419608 424614	AL037237 X54486	Hs.91586 Hs.151242	serine (or cysteine) proteinase inhibito	1.26		
50	422934	BE244189	Hs.122492	hypothetical protein	1.25		
-	450935	BE514743		turnor suppressor deleted in oral cancer-	1.25		
	416630		Hs.174051	small nuclear ribonucleoprotein 70kD pol	1.24		
	416950		Hs.80552	dermatopontin	1.23 1.21		
55	412558	AW962019		gb:EST374092 MAGE resequences, MAGG Homo ESTs	1.19		
33	419593 403470		Hs.58282	Target Exon	1.14		
	402230			Fgenesh predicted: CYTOCHROME P450 4F5 (	1.13		
	400559			Target Exon	1.0		
<b>60</b>	412695			gb:PM3-HN0011-220300-002-c05 HN0011 Homo	1.0 1.0		
60	427072		Hs.293981	ESTs DKFZP434B061 protein	1.0		
	430439 418183		2 Hs.83731	CD33 antigen (gp67)	1.0		
	410102	, MM_001//	2 113.00701	Coop amage. (Spec)			
	TABLE	55B:					
65	Pkey:			t identifier number			
	CAT na		ene cluster numbe				
	Access	sion: G	enbank accession	numbers			
	Pkey	CAT Numb	ber Accession				
70	40663		1400041400	83 L12065 L12075 L12066 L12085 L12072 L12082 L12081	L12062 L12080		
	43054		DC017171 D	COLOLOG NIM DOZIOG AFIDOZSO AL 137377 770768 RM474	865 RG754BD6 AU12	4376 BG7572	03 BG764420 BG775028 BG624410
			BM045810 A	10120387 BG770238 BG686740 BG913323 BI759980 BG39 196861 BE856897 AA463876 AI375927 AA648810 AA9481	15998 BM048875 BE8	810/0 BE313	689 8E879144 BM309634 AVV243647
			AI770171 BF	196861 BE856897 AA463876 AI375927 AA648810 AA5481 N337984 AW026150 BE466591 BE674599 AI818438 AA77	193 AA49U9 10 A14390 2107 AIRS1927 AW15	1143 RI19882	5 BG819083 BM458764 BE903567
75			00723746.0	unizano econoses econozos RF731097 RF390023 RG87	15784 REGGGANG REG	88930 BM475	542 AVV246213 BE3U (897 BE9U30 IV
13			DESC1520 D	CECAE37 DEDA3793 RE732947 RI227204 RG761305 RF262	7642 RF391848 BE38	2475 BG0082	29 RI241231 RI422022 RE231231 DE522450
			DE200400 A	WOAEA22 ALA220A7 AIQ14618 HRD534 RE301004 AI 53179	1 AM35581 RF793112	2 AL577303 A	A373265 BE /46965 BF /43630 BE8/9290
			A1250402 DI	UN18508 AIGROSEN AWN7245N F20201 AW151405 AW5175	72 AA773468 BG259	694 BE <i>3</i> 9116.	3 BG621529 AI421/28 BG/6/231 BM462333
00			BG340524 V	V52648 AA113434 BE785431 BI041981 BG832385 BG2531 5690 BG958989 AI205206 H19721 W17051 W77958 BI262	58 8G759470 BF369	329 BF981333 42 W72214 M	2 85404 86734033 86464041056 N14012 85404 86734033 86464000 44031060
80			C12C4C D41	201 AMD25759 DC180077 RE340455 AAR12018 AA740241	A1027722 A1150356 A	4A886395 AW	977627 BE220225 AA884082 AW518114
			1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	394 AKU25758 BG180977 BE349433 AA612016 AK740241 A809493 AA481029 AA825718 AI347866 AI431670 AA8144	36 AI251109 R07704	AA765606 AA	A724593 AI918399 AI537550 AA491103
			, = , 100m N				

			AW003188 R07703 AA989120 AA746235 AW028983 AA789102 AU185751 AW971465 AA489581 AW971893 AW612086 BE077936 BI860809
5	430015	713_2	BE002760 BG746251 BE962912 BM454584 AL134894 BF104082 H80591 BC017171 BC012195 NM, 007126 AF100752 AL137377 Z70768 BM474665 BG754806 AU124376 BG757203 BG764420 BG775026 BG824418 BM045810 AU120387 BG770238 BG68674 BG913323 BI759980 BG395998 BM048875 BE881070 BE313689 BE879144 BM309834 AW245847 AI770171 BF196861 BE856897 AA463876 AJ375927 AA648810 AA948193 AA490916 AJ459893 AJ458188 AJ240408 AJ191843 AJ131029 AW768399 AJ365196 AW337984 AW026150 BE466591 BE674599 AJ818438 AA772197 AJ651927 AW151143 BJ198825 BG819083 BM458764 BE903567 BE732715 BM043200 BE900263 BE900706 BE731097 BE390023 BG875384 BF996406 BF988930 BM475542 AW246215 BE501897 BE903510 BE561530 BE560537 BE903782 BE732947 BJ227204 BG761305 BE262642 BE391848 BE382475 BG008258 BJ547991 BJ459099 BE391391 BE259420
10			BE298109 AW245422 A422847 A4914618 H80534 BE301004 AL531791 A1435581 BF793112 AL577303 AA373265 BE746965 BF743630 BE879296 A1359493 BM018598 A1689260 AW072450 F20201 AW151405 AW517572 AA773468 BG258594 BE393168 BG251529 A4421728 BG767231 BM462953 BG340524 W52648 AA113434 BE785431 BI041981 BG632385 BG253168 BG759470 BF369398 BP381332 BE259418 BE785738 B1091658 N72512 W58732 W85690 BG958989 A1205206 H19721 W17051 W77958 B1262010 AA844319 W74143 W72214 NB5194 BE734033 BG164099 AA931069 F13645 R41394 AX025758 BG180977 BE349455 AA812018 AA740241 A1027722 A1150356 AA86395 AW977627 BE220225 AA884082 AW518114 A1243844 AA809493 AA481029 AA825718 A1347866 A1431670 AA814436 A1251109 R07704 AA765606 AA724533 AP918399 A1537550 AA491103
15	455839 406642	1518842_1 0_0	AW008188 R07703 AA389120 AA746235 AW028983 AA789102 AU185751 AW971465 AA489681 AW971893 AW612086 BE077936 BI860809 BE002760 BG746251 BE962912 BM454584 AL134894 BF104082 H80591 BE145823 BE145830 BE145884 BE145814 BE145905 BE145833 BE145834 BE145883 BE145889 AJ245210 AJ245212 AJ245211 AJ245213
20	406638 433470	0_0 6624_1	M13861 X758A AL573167 AI445461 AI453743 AI983655 AI564644 AA977180 AI694111 AI591358 AW071625 AI678712 AI720939 AI927769 BE439796 AI963432 AA292956 AW192593 AI865838 AI696905 AI424384 AI161312 AI911921 AI597801 BI494959 AI240988 AI492554 AW762737 BE044033 AW008570 AW629505 BI494958 AA088439 AA706057 BF222820 BF593608 BE501957 AA524526 BE044134 AW572531 AW015724 BE349186 AA043217 BE219784 AI799814 AA129575 AI671727 AI470033 BE646195 AW779725 AA903050 AA147228 AA404570 AI075878 W38161 AI972739 AW673152 AA723200 C06123 BF057147 AA627686 AA157944 AI990245 AA662517 T32487 AI800106 AI333170 AI859160 W45410 AI990827
25			AW275048 AA182640 AA478328 A1298935 AW085158 AW471421 AW103470 AW300456 AW191997 AI823466 AA962297 AA136698 A1251817 AW339104 AA724739 AA411100 AA191349 AA757735 AA037696 A1769516 AW772283 AA010631 A1692846 AI061065 H80983 R79933 AI950693 AI245632 AI349390 AA148284 A1798502 AA487893 AI621320 AW194272 C06365 AA953883 BE858936 AI918523 AI872628 AI927217 AI453453 AI180366 AW336738 AI261369 AI570676 RF477735 AI013766 AI977899 AI985583 Z28771 AI363829 AI693030 AA603386 BE773888 AW339331
30			BE773462 BE773462 BE773495 AI650338 BE773499 AI745717 BE811475 BE811470 BE811464 BE811418 BE811415 BE811400 BE811398 BE811388 BE811352 BE773501 BE773494 BE773494 BE773474 BE773473 BE773470 BE773461 BE811350 BE811337 BF593847 BG055071 AW675302 BF003068 AA719173 BE811348 AI582462 AI686240 BE773500 AI244845 AI565439 AI918453 AI472527 AI446740 AA035576 AA191414 AW674145 CO5782 AI589264 D67558 AI688237 AI432033 AA989662 R21752 BF002457 AA988297 AL574095 AL576200 AL571074 AL574525 AL578810 BG498381 AI928364 BE879732 AA479834 AA479712 C17732 BM091258 BF683901 AW820230 C17476 BE327120 AA129574 AA136645 BF6843900 AW8061933 AA502832 AA649494 AL568520 AL57850 BE706937 BE811360 BE773498 BE811401 BE773484 BE811437 BE811380
35			BE811399 BF997171 BF757734 BE926037 AI377596 C06111 AW088968 BE811404 BE811472 AI865912 AI925607 AI871950 AI093510 BE905927 BE811435 AA191387 AW772000 BE811453 BE614379 BF844522 BI044896 AI744233 AW984527 C17504 BF843883 AI248307 BE773483 AI567995 W60075 BF941183 AI738844 BE811458 BE773481 AI262930 AA948565 BE706942 BE156360 BF94249598 AW197954 BE905184 AA722206 AI344943 AI348877 AI334860 BE621857 BE156280 AA454099 AA037722 BF843887 AW886183 AA043216 BG482896 AA182734 AA877242 AN372936 H77852 B78114 BE951858 BE156280 AA45099 AA037722 BF843887 AW886183 AA043216 BG482896 AA182734 AA877242
40			BC010166 AL550134 AL553096 AL548700 AL550751 AL547978 AL545286 AL540643 AU118627 AL601379 BL259821 BG741786 BI886522 AU1139866 BL552770 Bl259210 Bl256520 Bl255569 BG485098 Bl258228 BG498501 BM044512 AU133984 AL556586 BC745111 Bl222633 AU133917 BG288151 Bl260715 BI550550 BG500773 BI551761 BG707601 BI818593 BF691383 BG721129 BG541578 BE906666 BG751098 Bl224135 BG400746 BG478065 BE790436 AW080238 AU137549 BG429896 BE392486 AW961568 BG721056 BE908365 BE546656 BG571038 Bl224135 BG528290 Bl260895 AW651601 BU048774 BW043396 BC142185 AA315188 AU46615 CD6300 BC497644 AA088544 AU815987 BG528631 BE619182 AW239185
45	411802	609_6	AW062910 AW062902 AA347236 F11933 AA488005 AA301631 AA376800 D56120 AA343532 AA308636 F00242 AA376086 AA316968 AA343799 BI870221 BE910282 BG538748 AW960564 AV732879 D16854 AA192519 BF922148 AA216013 BG624091 BE544387 BG507008 AW176446 BF790033 BE088925 BE088854 AA921353 R21800 AA011222 T97525 BF345917 AL549635 BI040919 AA733204 AA232382 T34425 T32000 BF906697 Z42382 BI544863 AL548378 AW816536 AW816719 BE152340
50		_	BF375392 AW816716 BE152336 BF375367
50	420223 436729	191648_1 6624_1	N27807 AA256634 BE276324 X75684 AL573167 AI445461 AI453743 AI983655 AI564644 AA977180 AI694111 AI591358 AW071625 AI678712 AI720939 AI927769 BE439796 AI963432 AA292956 AW192593 AI865838 AI696905 AI424384 AI161312 AI911921 AI597801 BI494959 AI240988 AI492554 AW262737 BE044033 AW008570 AW629505 BI494958 AA088439 AA706057 BF222820 BF593608 BE501957 AA524526 BE044134 AW572531 AW015724 BE349186 AA043217 BE219784 AI799814 AA129575 AI671727 AI470033 BE646195 AW779725 AA903050 AA147228 AA404570 AI075878 W33161 AI972739
55			AW573152 AA723200 C06123 BF057147 AA627686 AA157944 A1990245 AA662517 T32487 A1800106 A1333170 A1859160 W45410 A1990827 AW275048 AA182640 AA478328 A1298935 AW085158 AW471421 AW103470 AW300456 AW191997 A1823466 AA962397 AA136658 A1251817 AW339104 AA724739 AA411100 AA191349 AA757735 AA037695 A1769516 AW772283 AA010631 A1692846 A1061065 H80983 R79933 A1950693 A1245632 A1349390 AA148284 A1798502 AA487893 A1621320 AW194272 C06365 AA953883 BE656936 A1918523 A1875628 A19277217 A1453453 A1189366 AW338678 A1261359 A1500576 BF477735 A1032569 A1972899 A1985583 Z28771 A1363829 A1693030 AA603585 BE773488 AW339301
60	•		BE773489 BE773469 E773495 AIGS0338 BE773499 AI745717 BE811475 BE811470 BE811464 BE811418 BE811415 BE811400 BE811398 BE811388 BE811352 BE773495 AIGS0338 BE773499 AI745717 BE811477 BE873473 BE773470 BE773476 BE811390 BE811337 BF593847 BG055071 AV675302 BF003068 AA719173 BE811348 AIS82462 AI686240 BE773470 BE773470 BE773470 BE773470 BE811377 BF593847 BG055071 AV675302 BF003068 AA719173 BE811348 AIS82462 AI686240 BE773500 AI244845 AI56439 AI918453 AI472527 AI445740 AA013576 AA191414 AW674145 C05782 AI689264 D57558 AI468237 AI432033 AA9893662 R21752 BF002457 AA988297 AL574095 AL576200 AL571074 AL574525 AL578810 BG498381 AI928364 BE879732 AA479834 AA479712 C17732 BM091258 BF843901 AW820230 C17476 BE327120 AA129574 AA136645
65			BF843900 AW806193 AA502832 AA649494 AL568520 AL547950 BE705937 BE811350 BE773498 BE811401 BE773484 BE811437 BE811380 BE811399 BF997171 BF757734 BE926037 AL377596 CO6111 AW088968 BE811404 BE811472 AL865912 AU925607 AL871950 AU933510 BE905927 BE811435 AA191387 AW772000 BE811453 BE614379 BF844522 BID44896 AI744233 AW984527 C17504 BF843883 AL248307 BE773483 AL557995 W60075 BF941183 AI738844 BE811458 BE773481 AL562930 AA948565 BE706942 BE1563360 T65026 AW42958 AW197954 BE905184 AA7722206 AL344943 AL348877 AU3248600 BE621857 BE156230 AA45099 AA037722 BF843897 AW806183 AA043216 BG482896 AA182734 AA877242
70			AW372926 H27252 R38114 BF651859 BE155214 AA190427 T91762 AA035067 AA837326 T10930 BF906587 BI755027 BG506731 BC008442 BC010166 AL550134 AL553096 AL548700 AL550751 AL547978 AL545286 AL540643 AU118627 AL601379 BL259821 BG741786 B1868522 AU135866 BI552770 BI759210 BI256520 BI255569 BC485098 BI258228 BG498501 BM044512 AU133984 AL556586 BE745111 BI222633 AU133917 BG288151 BI260715 BI550550 BG500773 BI551761 BG707601 BI818593 BF69133 BG721129 BG541578 BE906666 BG751098 BI224133 BG400746 BC478065 BE790436 AW080238 AU137549 BC429896 BE392486 AW981686 BG721056 BE908365 BE546566 BG541235 AW580738 BG528290 BI260895
75		•	AW651691 BM048974 BM043805 BG142185 AA315188 AI446615 C06300 BC497644 AA088544 A815987 BC528631 BE619182 AW239185 AW062910 AW062902 AA347236 F11933 AA488005 AA301631 AA376800 DE6120 AA343532 AA308636 F00242 AA376086 AA316888 AA343799 BB70221 BE910282 BC538748 AW960564 AV732879 D16854 AA192519 BF922148 AA216013 BC624091 BE544387 BC507008 AW176446 BF790033 BE088925 BE088854 AA921353 R21800 AA011222 T97525
80	406782 432902		AA430373 AAS88771 U75697 AI362269 AW575181 AL035820 AF039703 NM_003883 U66914 BE513355 BE302938 BE302938 BE302018 AA094475 F08725 R98879 R18769 BE019412 AA045846 AL120913 BE168807 BE168812 R21136 BE168915 H71247 N59055 AA533007 AW938705 BE260952 BE313803 AA307436 AW951917 AW581926 AW277164 AI439049 AW581905 AI744899 AW804572 BE004443 AA335928 AA486355 AA115468 AA312123 R77086 AA595186 AW166991 AI952071 AW593311 AW571813 AI749734 AI674761 AI560970 AI480266 AA534470 AA737815 BE300597 AW022818
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				911621 A1074678 BE300694 A1187018 R98969 AA456572 A1032111 A1830414 AA045874 AA932352 A1871262 T78896 AA714518 7250 R76914 AW317029 H71248 AA931900 AA282808 A1032140 A1208512 A1244759 A1420456 A128085 A1283758 A1369297 R46731
5			W78118 R430	91 241762 AW135694 AW263376 AA115046 134171 134071 N53974 W79902 DESTAIN BESTSTON THE STATE OF T
3	437866	34267_1		
			A1/766630 AW	MERAMA AWAERONO AAR11830 AAER1806 A1866686 AIS/2124 AA68/333 UZUTOU AA612463 AU 103240 AU 103000 AA 13010 1 A18670 AU
				171893 AAD40926 BF507639 AAD43777 AW874142 BEB32523 BE163972 BI022546 BI021204 1751975 W39241 BF808798 W22600 BF082190 AAD31290 R42801 H98235 H17925 AIG51236 AI933786 H42736 AF000152 AU123911
10	427751	15028_1		
10				
				154008 AA14/822 AA4/3109 AA0/3469 AI421985 AI004864 AI423497 AI361503 AI363096 AW805345 AL539979 AA553967 AW502264 70283 AA171931 AI349410 AA402469 AI421985 AI004864 AI423497 AI361503 AI363096 AW805345 AL539979 AA553967 AW502264 7420 AI281054 AI500699 AW342095 C75122 AW504577 AI130811 AI423567 R79086 AI8674 ND0621 AW474569 AW474569 D7623
15				I MARAA IAMBEECE AMIALAGEO A A LATOTL A ARESEST DERIMENTA ATTAMEN ATTAMENTATION DAZZOZES AUTOLOGO ANTIGOLOGO ANGOLOGO INTEGRA
			*******	1798UU W73993 W411395 W15255 W56743 AA058322 H81878 AA723464 H27523 R31745 AA613566 AL526353 A1905211 BF802713 N40338 327853 AA713915 W15255 W56743 AA058322 H81878 AA723464 H27523 R31745 AA613566 AL526353 A1905211 BF802713 N40338 327853 AA713915 W15255 W56743 AA058322 H81878 AA723821 H81877 H96088 AL576453 W73595 H39990 AW438955 BF899564 AU00299 AL576787 AU002906 BF437578 BF437578 AA723821 BF80278 AU002990 AW438956 BF899564 AU00299 AAV38281 BF89564 AU0029 AAV3881 AU0029 AAV381 AU0029 AAV381 AU0029 AAV381 AU0029 AAV381 AU0029 AAV381 AU0029 AAV381 AU0029 AU0029 AAV
				1004C0 4 4944C00 410C0C40 DIOCORGA DIOCASAL & A 777/1786 BICENNANN HUB.(5555 BUSANG)   DEG/4024 MYT100001 PAGODOV POPPAGA
20			*****************************	193150 AA/44623 N8059510 BUSG540 AU134437 BG926972 BE298386 AW134499 AW206089 BF846730 AW500331 BF849336 BI041697 4276 N72034 AF022231 BI256540 AU134437 BG926972 BE298386 AW134499 AW206089 BF846730 AW500331 BF849336 BI041697 192840 AW410527 AI697435 AW006631 AW504124 AL048926 AI085476 AW327855 AAA59344 AW207516 AW20475 BM142514 192840 AW410527 AI697435 AW006631 AW504124 AL048926 AI085476 AW327855 AAA59344 AW207516 AW204735 BM142514
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25	432870	1238170_1	AW957721 B	F304885 BF933455 BF809973 BG366280 AW075006 131097 AC22003 BC337604 10005 BC377604 10005 BC37760 BC3776 BC3776
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TABLE 56A: ABOUT 277 GENES UPREGULATED IN MELANOMA METASTASES RELATIVE TO BENIGN NEVI
Table 56A lists about 277 genes upregulated in melanoma metastases relative to benign nevi. Genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip
array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA

expression. Pkey: ExAcon: Unique Eos probeset identifier number Exemplar Accession number, Genbank accession number Unigene number 5

UnigeneID: Unigene Title:

Unigene gene file
Toth percentile of melanoma metastasis Als divided by the maximum of benign nevi Als
Toth percentile of melanoma metastasis Als divided by the maximum of benign nevi Als, where the 15th percentile of normal tissue Als was subtracted from both
the numerator and denominator R1: R2: 10

		5.5				
	Pkey	ExAcca	UnigenelD	Unigene Title	R1	R2
	422424	AI186431	Hs.296638	prostate differentiation factor	13.73	17.18
15	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	11.67	13.25
	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wil	9.35	8.75 6.22
	444381	BE387335	Hs.283713	ESTs. Weakly similar to S64054 hypotheti	8.63 8.21	8.65
	417880 424321	BE241595 W74048	Hs.82848 Hs.1765	selectin t. (lymphocyte adhesion motecule tymphocyte-specific protein tyrosine kin	7.13	5.04
20	447210	AF035269	Hs.17752	phosphatidylserine-specific phospholipas	6.79	7.12
20	417693	AW959741	Hs.40368	adaptor-related protein complex 1, sigma	6.55	5.94
	429500	X78565	Hs.289114	hexabraction (tenascin C, cytotactin)	6.43	3.46
	414812	X72755	Hs.77367	monokine induced by gamma interferon	6.43	5.44
	451736	AW080356	Hs.23889	ESTs, Wealty similar to ALU7_HUMAN ALU S	6.31	6.08
25	418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	6.20	6.04
	428291	AA534009	Hs.183487	interferon stimulated gene (20kD)	6.03	4.72
	417308	H60720	Hs.81892	KIAA0101 gene product	6.01	7.07
	448569	BE382657	Hs.21486	signal transducer and activator of trans	5.99	8.88
20	439310	AF086120	Hs.102793	ESTs	5.95	6.63
30	452838	U65011	Hs.30743	preferentially expressed antigen in mela	5.95 5.76	3.77 6.37
	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	5.76	3.14
	442379	NM_004613	Hs.8265 Hs.52644	transglutaminase 2 (C polypeptide, prote SKAPSS homologue	5.65	5.01
	409274 442739	NM_003930 NM_007274	Hs.8679	cytosolic acyl coenzyme A thioester hydr	5.58	3.50
35	442711	AF151073	Hs.8645	hypothetical protein	5.45	5.84
55	425118	AU076611	Hs.154672	methylene tetrahydrofolate dehydrogenase	5.42	5.75
	412918	BE563957	12.101012	activated RNA polymerase II transcriptio	5.35	4.94
	428125	AA393071	Hs.182579	leucine aminopeptidase	5.33	5.34
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	5.33	4.98
40	431183	NM_006855	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	5.30	6.25
	414219	W20010	Hs.75823	ALL1-fused gene from chromosome 1q	5.16	5.33
	426600	NM_003378	Hs.171014	VGF nerve growth factor inducible	5.05	8.77
	415444	BE247295	Hs.78452	solute carrier family 20 (phosphate tran	5.03	5.17
45	436701	AW959032		ESTs, Moderately similar to 178885 serin	5.03 4.99	4.17 5.08
45	406648	AA563730	Hs.277477	major histocompatibility complex, class	4.98	4.71
	410850	AW362867	Hs.302738	Homo sapiens cDNA: FLJ21425 fis, clone C	4.98	4.08
	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly CGI-100 protein	4.97	4.70
	432469 404854	AL080084		Target Exon	4.85	4.07
50	415701	NM_003878	Hs.78619	gamma-glutamyl hydrolase (conjugase, fol	4.82	4.90
20	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	4.81	3.45
	408958	T99607	Hs.49346	signal recognition particle 54kD	4.78	2.34
	453949	AU077146	Hs.36927	heat shock 105kD	4.78	6.32
	458079	AJ796870	Hs.54277	DNA segment on chromosome X (unique) 992	4.77	6.57
55	440245	AK001913	Hs.7100	hypothetical protein	4.74	3.83
	412228	AW503785	Hs.73792	complement component (3d/Epstein Barr vi	4.74	5.53
	417834	BE172058	Hs.82689	tumor rejection antigen (gp96) 1	4.73	4.35 4.60
	451003	AF058696	Hs.25812	Nijmegen breakage syndrome 1 (nibrin)	4.67 4.62	3.50
60	424571	BE379766	003550	polymerase (RNA) II (DNA directed) polyp	4.61	5.67
OU	434203	BE262677	Hs.283558 Hs.28777	hypothetical protein PRO1855 H2A histone family, member L	4.60	3.79
	452268 421311	NM_003512 N71848	Hs.283609	hypothetical protein PRO2032	4.60	3.58
	410491	AA465131	Hs.64001	Homo sapiens clone 25218 mRNA sequence	4.60	4.68
	425706	AW406678	Hs.122559		4.59	3.83
65	450293	N36754	Hs.171118		4.57	5.40
	406836	AW514501	Hs.156110	immunoglobulin kappa constant	4.57	6.33
	413441	AI929374	Hs.75367	Src-like-adapter	4.53	4.77
	431129	AL137751	Hs.263671	Homo sapiens mRNA; cDNA DKFZp434I0812 (f	4.48	4.89
-	418506	AA084248	Hs.85339	G protein-coupled receptor 39	4,47	4.17
70	411060	NM_006074	Hs.318501		4,47	4.33 3.32
	417501	AL041219	Hs.82222	sema domain, immunoglobulin domain (lg).	4.45 4.43	3.32 4.43
	437763	AA459369	Hs.5831	tissue inhibitor of metalloproteinase 1	4.42	3.91
	448883	BE614989	Hs.7503	hypothetical protein FLJ14153	4.41	4.09
75	417274	N92036 D31887	Hs.81848 Hs.89868	RAD21 (S. pombe) homolog KIAA0062 protein	4.40	3.56
13	419285 418321	D63477	Hs.84087	KIAA0143 protein	4.38	3.00
	418321	AW583058	Hs.234726		4.37	4.26
	428450	NM_014791			4.36	4.90
	428297	AA236291	Hs.183583		4.36	3.57
80	447232	AW499834	Hs.327	interleukin 10 receptor, alpha	4.36	4.07
	409598	NM_014018		mitochondrial ribosomal protein \$28	4.35	3.29
	442432	8E093589	Hs.38178	hypothetical protein FLJ23468	4.34	5.80
	407047	X65965		gb:H.sapiens SOO-2 gene for manganese su	4.33	3.51
				564		

					4.92	4.23
	443991			potassium intermediate/small conductance	4.33 4.32	4.23 2.68
	452322	BE566343		glutaredoxin (thioltransferase)	4.32	4.54
	420991	AW504814		Horno sapiens mRNA for FLJ00111 protein, cyclin B1	4.31	3.73
5	449722 408380	BE280074 AF123050		diubiquitin	4,30	5.74
,	427127	AW802282		pyruvate dehydrogenase phosphatase	4.28	4.80
	417933	X02308	Hs.82962	thymidylate synthetase	4.28	3.59
	432828	AB042326		chondroitin 4-sulfotransferase	4.25 4.24	4.15 3.15
10	450306	AL080080	Hs.24766	thioredoxin domain-containing	4.23	4.12
10	440266	AA088809	Hs.19525	hypothetical protein FLJ22794 antigen identified by monoclonal antibod	4.22	4.64
	407951 427337	W77762 Z46223	Hs.79015 Hs.176663	Fc fragment of tgG, low affinity Ilib, r	4.20	4.62
	408989	AW361666	Hs.49500	KIAA0746 protein	4.20	4.92
	449626	AA774247	Hs.301637	zinc finger protein 258	4.19	3.17
15	422846	BE513934	Hs.1583	neutrophil cytosolic factor 1 (47kD, chr	4.18 4.16	8.91 4.21
	415726	T89844	Hs.78712	aminolevulinate, delta-, synthase 1	4.16	1.89
	444207	A1565004	U- 00004	cathepsin D (lysosomal aspartyl protease high-mobility group (nonhistone chromoso	4,14	3.30
	416980 438718	AA381133 AL040058	Hs.80684 Hs.6375	uncharacterized hypothalamus protein HTO	4.14	3.04
20	437802	A1475995	Hs.122910	ESTs	4.12	5.13
20	446392	AF142419	Hs.15020	homolog of mouse quaking QKI (KH domain	4.12	3.87
	409461	AA382169	Hs.54483	N-myc (and STAT) interactor	4.11 4.11	4.96 6.37
	427247	AW504221	Hs.174103	integrin, alpha L (antigen CD11A (p180),	4.10	4.16
25	414359	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob Homo sapiens cDNA FLJ11174 fis, clone PL	4.10	2.35
25	450071 452882	AA018283 AW972990	Hs.24359 Hs.196270	folate transporter/carrier	4.10	4.50
	414522	AW518944	Hs.76325	Immunoglobulin J chain	4.09	6.07
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	4.09	5.03
	405506			Target Exon	4.08 4.07	3.71 . 8.61
30	417497	AW402482	Hs.82212	CD53 antigen Homo sapiens cDNA: FLJ22139 fis, clone H	4.06	4.05
	413715	AW851121	Hs.75497	absent in melanoma 2	4.05	4.61
	421508	NM_004833 AF055581	Hs.105115 Hs.13131	lymphocyte adaptor protein	4.02	4.56
	445701 443071	AL080021	Hs.8986	complement component 1, q subcomponent,	4.00	8.91
35	417615	BE548641	Hs.82314	hypoxanthine phosphoribosyltransferase 1	3.99	4.15
	444371	BE540274	Hs.239	forkhead box M1	3.86 3.85	4.58 4.26
	450515	AW304226		biphenyl hydrolase-like (serine hydrolas	3.81	4.06
	446506	AI123118	Hs.15159	chemokine-like factor, alternatively spl	3.80	6.84
40	410668	BE379794	Hs.159651 Hs.9691	hypothetical protein Homo sapiens cDNA: FLJ23249 fis, clone C	3.77	4.46
40	443710 406837	AI928136 R70292	Hs.156110	immunoglobulin kappa constant	3.77	6.44
	419381	AB023420	Hs.90093	heat shock 70kD protein 4	3.76	4.00
	402474			NM_004079:Homo sapiens cathepsin S (CTSS	3.76	4.67 6.22
	454080	AI199711	Hs.576	fucosidase, alpha-L- 1, tissue	3.74 3.69	4.36
45	409264	NM_014937		KIAA0966 protein	3.68	5.18
	428398	A1249368	Hs.98558 Hs.24143	ESTs Wiskott-Aldrich syndrome protein interac	3.67	4.12
	423494 414829	AW504365 AA321568	Hs.77436	pleckstrin	3.65	4.45
	437239	AW503395	Hs.5541	ATPase, Ca transporting, ubiquitous	3.63	4.84
50	433867	AK000596	Hs.3618	hippocalcin-like 1	3.59	4.49 5.31
	432485	N90866	Hs.276770		3.54 3.49	4.57
	418310	AA814100	Hs.86693	ESTs	3.48	4.33
	406868	AA505445	Hs.300697 Hs.1B4727		3.47	6.87
55	438746 427527	AI885815 AI809057	Hs. 153261		3.44	10.42
55	442485		Hs.29724	hypothetical protein FLJ13187	3.41	4.60
	432606			granzyme K (serine protease, granzyme 3;	3.40	4.50 4.22
	435080		Hs.15511	hypothetical protein FLJ14428	3.40 3.40	5.03
<b>60</b>	436810		Hs.5321	ARP3 (actin-related protein 3, yeast) ho	3.39	7.32
60	422545	44400077	Hs.28782		3.36	4.47
	409142 434826		Hs.50758 Hs.22265		3.34	5.02
	416975			granzyme B (granzyme 2, cytotoxic T-lymp	3.34	4.24
	448410			hypothetical protein FLJ20220	3.33	4.2 <del>9</del> 4.48
65	432642		Hs.3069	heat shock 70kD protein 9B (mortatin-2)	3.32 3.24	4.40
	425234			9 ESTs, Weakly similar to 138022 hypotheti	3.23	13.58
	443623			complement component 1, q subcomponent, anyl hydrocarbon receptor	3.23	4.20
	426490				3.16	5.05
70	443956 407862				3.15	4.04
, 0	41257		Hs.74076	CD163 antigen	3.14	5.32
	41405		66 Hs.75724		3.13	4.65 4.34
	44290				3.13 3.12	4.99
76	42163				3.12	5.47
75	41393					4,30
	42879 40851				3.10	4.03
	40944			48 cytochrome c	3.07	4.00
	45637	3 BE24770	6 Hs.8975	1 membrane-spanning 4-domains, subfamily A	3.04	4.38 5.53
80					3.04 3.03	5.55 4.97
	41852				3.03	4.87
	45213 43047			· · · · · · · · · · · · · · · · · · ·	2.98	4,44
	43017	U 14M_U14V	,,, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	es aperprendiction of		

	439237	AW408158	Hs.318893	ESTs, Wealthy similar to A47582 B-cell gr	2.95	7.45 8.49
	406782 450455	AA430373 AL117424	Hs.25035	gb:zw2011.s1 Soares ovary tumor NbHOT H chlorida intracellular channel 4	2.93 2.90	5.08
	422530	AW972300	Hs.118110	bone marrow stromal cell antigen 2	2.87	7.07
5	429490	AI971131	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.87	4.29
	410231	AA314163	Hs.61153	proteasome (prosome, macropain) 26S subu	2.82	5.53 4.26
	419956 416511	AL137939 NM_006762	Hs.40096 Hs.79356	cadherin 19, type 2 Lysosomal-associated multispanning membr	2.80 2.79	4.20 5.55
	421712	AK000140	Hs.107139	hypothetical protein	2.79	6.29
10	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	2.78	4.74
	448517	AA082750	Hs.42194	hypothetical protein FLJ22649 similar to	. 2.78	4.69
	427792 446272	M63928 BE268912	Hs.180841 Hs.14601	tumor necrosis factor receptor superfami hematopoietic cell-specific Lyn substrat	2.77 2.75	5.18 4.90
	422173	BE385828	Hs.250619	phorbolin-like protein MDS019 (CEM15)	2.75	4.33
15	446566	H95741	Hs.17914	membrane-spanning 4-domains, subfamily A	2.72	4.19
	429402	AF116571	Hs.201671	SRY (sex determining region Y)-box 13	2.72	5.15
	421360 425762	AA297012 BE244076	Hs.103839 Hs.159578	erythrocyte membrane protein band 4.1-li AT-hook transcription factor AKNA	2.71 2.71	4.82 4.61
	429412	NM_006235	Hs.2407	POU domain, class 2, associating factor	2.69	4.45
20	409202	AA236881	Hs.51043	hexosaminidase 8 (beta polypeptide)	2.68	4.89
	426124	AI268389	Hs.250697	phosphatidyfinositol glycan, class F	2.68	4.25
	422672	X12784	Hs.119129	collagen, type IV, alpha 1	2.67 2.65	5.00 9.54
	417389 445784	BE260964 A1253155	Hs.82045 Hs.146065	midkine (neurite growth-promoting factor ESTs	2.65	4.11
25	410341	AW499985	Hs.42915	ARP2 (actin-related protein 2, yeast) ho	2.64	4.50
	422603	BE242587	Hs.118651	hematopoietically expressed homeobox	2.63	4.17
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	2.62 2.61	5.80 5.57
	410016 424779	AA297977 AL046851	Hs.57907 Hs.153053	small inducible cytokine subfamily A (Cy CD37 antigen	2.60	5.72
30	420224	M84371	Hs.96023	CD19 antigen	2.60	4.02
	421924	BE514514	Hs.109606	coronin, actin-binding protein, 1A	2.57	4.83
	426143	BE379836	Lie 100000	proteasome (prosome, macropain) subunit,	2.56 2.56	4.50 5.35
	421563 425593	NM_006433 AA278921	Hs.105806 Hs.1908	granulysin proteoglycan 1, secretory granule	2.55	4.32
35	428169	AI928984	Hs.182793	golgi phosphoprotein 2	2.54	5.78
	417022	NM_014737	Hs.80905	Ras association (RalGDS/AF-6) domain fam	2.54	4.09
	414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	2.53 2.50	4.41 5.68
	429800 407241	AA333375 M34516	Hs.223014	antizyme inhibitor gb:Human omega light chain protein 14.1	2.50	4.69
40	421739	AB004550	Hs.107526	UDP-Gal:betaGlcNAc beta 1,4- galactosyli	2.45	4.35
	412819	T25829	Hs.24048	FK506 binding protein precursor	2.45	4.66
	435523	T62849	Hs.11090	membrane-spanning 4-domains, subfamily A	2.44 2.41	4.91 4.80
	434883 420340	AW381538 NM_000734	Hs.19807 Hs.97087	hypothetical protein MGC12959 CD3Z antigen, zeta polypeptide (TIT3 com	2,41	4.00
45	449296	AL137257	Hs.23458	Homo sapiens cDNA: FLJ23015 fis, clone L	2.41	4.77
	417370	T28651	Hs.82030	tryptophanyl-tRNA synthetase	2.41	4.04
	400223		000000	Eos Control	2.39 2.38	5.47 7.67
	431629 414622	AU077025 AI752666	Hs.265827 Hs.76669	interferon, alpha-inducible protein (clo nicotinamide N-methyltransferase	2.38	5.32
50	415149	X12451	Hs.78056	cathepsin L	2.37	8.07
	435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	2.37	5.23
	454390	AB020713	Hs.56966	KIAA0906 protein	2.35	4.57 5.48
	427407 449029	BE268649 N28989	Hs.177766 Hs.22891	ADP-ribosyttransferase (NAD; poly (ADP-r solute carrier family 7 (cationic arnino	2.31 2.24	4.08
55	438956	W00847	Hs.135056	Human DNA sequence from clone RP5-850E9	2.23	4.02
	423397	NM_001838		chemokine (C-C motif) receptor 7	2.23	4.90
	416232	AW502678	Hs.79090	exportin 1 (CRM1, yeast, homolog)	2.18	4.97
	436692	AW243158 AI083668	Hs.5297 Hs.50601	DKFZP564A2416 protein hypothetical protein MGC10986	2.17 2.14	4.13 5.14
60	420842 428227	AA321649	Hs.2248	small inducible cytokine subfamily 8 (Cy	2.13	4.43
-	429642	X68264	Hs.211579	melanoma cell adhesion molecule (MCAM) (	2.11	5.42
	416448	L13210	Hs.79339	tectin, galactoside-binding, soluble, 3	2.10	6.36 4.06
	416714	AF283770	Hs.79630 Hs.51233	CD79A antigen (immunoglobulin-associated tumor necrosis factor receptor superfami	2.10 2.09	4.67
65	409220 414045	BE243323 NM_002951		ribophorin II	2.07	4.32
05	422451	AA310753	Hs.42491	ESTs, Wealthy similar to \$65657 alpha-1C-	2.07	4.24
	441211	AW946155	Hs.7750	hypothetical protein AL133206	2.06	4.64
	434692	H06586	Hs.94	DnaJ (Hsp40) homolog, subfamily A, membe	2.05 2.04	4.33 13.36
70	452363 438393	AI582743 AA351815	Hs.94953 Hs.50740	Homo sapiens, Similar to complement comp Homo sapiens cDNA: FLJ22272 fis, clone H	2.03	4.52
70	413313	NM_002047			2.02	4.11
	452700	AI859390	Hs.288940	five-span transmembrane protein M83	2.00	4.04
	406621	X57809	Hs.8997	immunoglobulin lambda locus	1.99	4.35 4.52
75	424415	NM_001975 BE409861	5 Hs.146580 Hs.202833		1.98 1.95	4.52 5.60
15	429451 416967	BE616731	Hs.80645	interferon regulatory factor 1	1.95	5.38
	414945	BE076358	Hs.77667	lymphocyte antigen 6 comptax, locus E	1.93	4.69
	418917	XD2994	Hs.1217	adenosine dearninase	1.91	4.32
80	445411	AL137255	Hs.12646	hypothetical protein FLJ22693	1.91 1.90	4.48 6.03
οU	413945 429119		1 Hs.75627 Hs.196437	CD14 antigen hypothetical protein FLJ10788	1.90	4.08
	413317		Hs.75283	sorting nexin 1	1.89	4.06
	427239			ubiquitin carrier protein	1.87	5.98

					4.07	6.33
	450440			tyrosine 3-monooxygenase/tryptophan 5-mo	1.87 1.85	4.21
	413142	M81740	Hs.75212	omithine decarboxylase 1	1.84	5.07
	447131	NM_004585	Hs.17466	retinoic acid receptor responder (tazaro pM5 protein	1.83	5.57
5	430040	AW503115	Hs.227823 Hs.80205	pim-2 oncogene	1.83	4.12
5	416819 425356	U77735 BE244879	Hs.155939	inositol polyphosphate-5-phosphatase, 14	1.82	5.71
	414570	Y00285	Hs.76473	insulin-like growth factor 2 receptor	1.81	4.73
	443639	BE269042	Hs.9661	proteasome (prosome, macropain) subunit,	1.80	4.71
	418707	U97502	Hs.87497	butyrophilin, subfamily 3, member A2	1.78	5.16 7.00
10	425367	BE271188	Hs.155975	protein tyrosine phosphatase, receptor t	1.78 1.74	5.10
	409154	U72882	Hs.50842	interferon-induced protein 35	1.74	5.15
	444954	AW247076	Hs.12163	eukaryotic translation initiation factor	1.70	4.43
	424825	AF207069	Hs.153357	procollagen-lysine, 2-oxoglutarate 5-dio outative Rab5-interacting protein	1,69	4.06
15	428385	AF112213 BE515037	Hs.184062 Hs.177556	melanoma antigen, family D, 1	1.67	5.68
13	427378 413322	AA380158	Hs.75290	ADP-ribosylation factor 4	1.67	4.56
	442414	BE408758	Hs.8297	ribonuclease 6 precursor	1.65	4.40
	410129	BE244074	Hs.58831	regulator of Fas-induced apoptosis	1.64	4.02
	452472	AW957300	Hs.294142	ESTs, Weakly similar to C55663 oligodend	1.63	4.49
20	446143	BE245342	Hs.306079	sec61 homolog	1.62	4.73 4.19
	413511	AJ627178	Hs.75412	arginine-rich, mutated in early stage tu	1.60 1.60	4.61
	415017	F06434	Hs.77805	ATPase, H transporting, lysosomal (vacuo	1.59	4.26
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon- FYN-binding protein (FYB-120/130)	1.56	4.10
25	410068	AI633888	Hs.58435 Hs.90693	replication initiation region protein (6	1.55	4.30
25	419489	AW411280 BE621702	Hs.29076	hypothetical protein FLJ21841	1.55	6.54
	439627	L19711	Hs.76111	dystroglycan 1 (dystrophin-associated gl	1.53	4.00
	416971	R34657	Hs.80658	uncoupling protein 2 (mitochondrial, pro	1.53	4.79
	426059	BE292842	Hs.166120	interferon regulatory factor 7	1.51	4.12 .
30	418879	AW162087	Hs.5437	Tax1 (human T-cell leukernia virus type !	1.50	4.93
• •	433271	BE621697	Hs.14317	nucleolar protein family A, member 3 (H/	1.45 1.45	4.15 4.03
	422481	AL050163	Hs.117339	DNAX-activation protein 10	1.43	4.11
	432805	X94630	Hs.3107	CD97 antigen	1.43	4.08
25	447150	AI439011	Hs.86386	myeloid cell leukemia sequence 1 (BCL2-r hypothetical protein FLI11856	1.41	4.36
35	421975	AW961017	Hs.6459 Hs.29283	ESTs, Weakty similar to LKHU proteoglyca	1.41	4.10
•	427458 412968	BE208364 AW500508	Hs.75102	alanyl-tRNA synthetase	1.40	4.25
	428511	AA019912	Hs.184693		1.38	4.91
	413825	BE299181	Hs.75564	CD151 antigen	1.37	4.46
40	427496	D21260	Hs.178710		1.30	4.04
	407143	C14076	Hs.332329	EST	1.29	4.37
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	TABLE 5 Pkey:	i68: Uni	que Eos probe	eset identifier number		
45	TABLE 5 Pkey: CAT nun	Uni nber: Ger	ne cluster num			
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45 50	Pkey: CAT nun Accession Pkey	Uni nber: Ger on: Ger CAT Numbe	ne cluster num nbank accession er Accession BE784583 AA946555	ber on numbers B AL519009 AV755430 AV756363 AV711927 BI52343 S AA723580 AA512925 BG105326 BG532618 AW513	994 AW602165 AI3734467 62 AW304207 RF9393617	AW795569 BG210592 AW795644 BE939358 AW102886
	Pkey: CAT nun Accession Pkey	Uni nber: Ger on: Ger CAT Numbe	re cluster num nbank accession BE784583 AA946555 BE774875 BE065977	ber on numbers AL519009 AV755430 AV755363 AV711927 BI52343 5 AA723580 AA512925 BG105326 BG532618 AV513 5 BG190378 AA483698 BE066066 BE066067 BE0666 7 BG182971 197042 D58090 BI046351 H81248 AI75	994 AW602165 AI3734467 162 AW304207 BE9393617 0112 AW372079 C05492 D	AW795569 BG210592 AW795644 BE939358 AW102886
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50	Pkey: CAT nun Accession Pkey	Uni nber: Ger on: Ger CAT Numbe	er Accession BE784583 AA946555 BE774875 BE065977 AW36846	ber on numbers J. ALS19009 AV755430 AV755363 AV711927 BI52343 5 AA723580 AA512925 BG105326 BG532618 AW513 6 BG190378 AA483698 BE066066 BE066067 BE066 7 BG182971 H97042 D58090 BI046351 H81248 A175 7 BG495535 BGS33177 BI087962 BE541579 BF1301	994 AW602165 AI373446 / 162 AW304207 BE939361 / 0112 AW372079 C05492 D 153 AR42206 AA418925 AI478	WY795569 BG210592 AW795644 BE339358 AW102886 58287 D57835 AA935095 BF700910 BG215802 BG195459 552 AI400067 AI360304 AA418828 AW301673 BE218952
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30	TABLE 56	C:					•				
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	Ref:	Se se	iquence source. ] quence of human	The 7 digit numbers in this column an chromosome 22" Dunham, et al. (19)	e Genbank Identiner (GI) nur 99) Nature 402:489-495.	nbers. "Dunnam, et al." re	ners to the puroncation entitled	ine ONA			
25	Strand:	tno	ficates DNA stran	d from which exons were predicted.							
35	Nt_position	n: the	ficates nucleotide	positions of predicted exons.			•				
	Pkey	Ref	Strand	Nt_position							
	404854 405506	7143420 6466489	Plus Plus	14260-14537 80014-80401,80593-81125							
40	402474	7547175	Minus	53526-53628,55755-55920,57530-9	57757						
45	Table 57A array. Ge expression Pkey: ExAccn:	Hists about 30 ne expression n. Un Ex	04 genes upregul: n data for each pr nique Eos probes xemplar Accessio	GULATED IN MELANOMA METAST ated in melanoma metastases relative obeset obtained from this analysis wa et identifier number n number, Genbank accession numb	e to normal skin. Genes wer is expressed as average inte	e selected from 59680 pro	besets on the Eos/Affymetrix Hi alue reflecting the relative level o	u03 Genechip of mRNA			
50	Unigenel ( Unigene 1		nigene number nigene gene title								
20	R1:	Q	Ith necessite of m	netanoma metastasis Ats divided by t	ne 90th percentile of normal	skin Als	m	and the same of the same			
	R2:		Ith percentile of mother than the numerator	nelanoma metastasis Als divided by the	ne 90th percentile of normal	skin Als, where the 15th p	ercentile of normal dssue Als Wi	as subtracted from			
		_				<b>5</b> 4	R2				
55	Pksy 422424	ExAccn Al186431	UnigenelD Hs.296638		r	R1 18.94	25.00				
	438549	BE386801	Hs.21858	trinucleotide repeat containi	ng 3	17.45	18.47				
	417880	BE241595		selectin L (lymphocyte adhe		14.05 13.91	11.15 15.41				
60	452838 446619	U65011 AU076643	Hs.30743 Hs.313	preferentially expressed ant secreted phosphoprotein 1		13.41	9.73				
00	426555	NM_0003		tyrosinase (oculocutaneous		12.24	7.33				
	439310	AF086120	Hs.10279			10.12	10.80				
	414020	NM_0029				9.74 9.43	10.16 11.69				
65	447210 414812	AF035269 X72755	Hs.17752 Hs.77367			9.28	10.97				
•	430377	NM_0019				9.07	7.96				
	426600	NM_0033			<b>Jucible</b>	9.06	19.93				
	453857 418310	AL080235 AAB14100				8.66 8.65	5.87 6.62				
70	433447	U29195	Hs.3281	neuronal pentraxin ()		8.27	4.68				
	430280	AA361256	3 Hs.23786	8 interteukin 7 receptor		8.01	6.37				
	430822	AJ005371				7.80 7.78	6.10 7.60				
	456373 415752	BE247706 BE314524				7.68	5.41				
75	419628	H67546	Hs.49768			7.66	8.96				
	417355	D13168	Hs.82002	endothelin receptor type B		7.56	4.59				
	424321	W74048 AW50378	Hs.1765 S Hs.73792	lymphocyte-specific protein complement component (3)		7.48 7.43	5.77 4.93				
	412228 438485	X59135	13 Hs.15611			7.35	7.98				
80	414646	AA35377	6 Hs.901	CD48 antigen (B-cell mem)	orane protein)	6.97	5.06				
	422241	Y00062	Hs.17012			6.83 6.67	5.20 3.77				
	429170 417542	NM_0013 J04129	94 Hs.2359 Hs.82269	dual specificity phosphatas progestagen-associated en		6.67	15.22				
	411.542	-07143	· 10.04.403			<i></i>					

						• • •
	428398	AI249368	Hs.98558	ESTs	6.57	3.60
	408989	AW361666	Hs.49500	KIAA0746 protein	6.48 6.38	4.93 3.65
	417022	NM_014737	Hs.80905	Ras association (RalGDS/AF-6) domain fam	6.35	5.84
5	449644 412326	AW960707 R07566	Hs.148324	ESTs small inducible cytokine A3 (homologous	6.30	7.18
,	457211	AW972565	Hs.73817 Hs.32399	ESTs, Weakly similar to S51797 vasodilat	6.25	7.21
	420991	AW504814	Hs.287379	Homo sapiens mRNA for FLJ00111 protein,	6.25	5.36
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	6.18	6.01
	432828	AB042326	Hs.287402	chondroitin 4-sulfotransferase	6.12	6.51
10	449078	AK001256	Hs.22975	KIAA1576 protein	6.05	8.55
	436856	A1469355	Hs.127310	ESTs .	6.00	5.54
	433658	L03678	Hs.156110	immunoglobulin kappa constant	5.92	7.18
	424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	5.89 5.86	4.07 6.07
15	409417 431574	AA156247 AW572659	Hs.104879 Hs.261373	serine (or cysteine) proteinase inhibito hypothetical protein dJ434O14.3	5.74	6.03
13	458079	A1796870	Hs.54277	DNA segment on chromosome X (unique) 992	5.72	5.92
	440274	R24595	Hs.7122	scrapie responsive protein 1	5.69	3.22
	429412	NM_006235	Hs.2407	POU domain, class 2, associating factor	5.69	5.17
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	5.68	3.35
20	436315	BE390513	Hs.27935	hypothetical protein MGC4837	5.67	4.56
	452973	H88409	Hs.40527	ESTs	5.63	5.50
	426559	AB001914	Hs.170414	paired basic amino acid cleaving system	5.62	3.09 9.68
	406663	U24683	Un 4051	immunoglobulin heavy constant mu	5.54 5.52	6.42
25	416975 408380	NM_004131 AF123050	Hs.1051 Hs.44532	granzyme B (granzyme 2, cytotoxic T-tymp diubiquitin	5.51	4.49
23	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	5.43	4.50
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotactin)	5.42	3.54
	446341	AL040763	Hs.310735	ESTs, Moderately similar to ALU7_HUMAN A	5.41	5.29
	425234	AW152225	Hs.165909	ESTs, Weakly similar to 138022 hypotheti	5.40	4.35
30	434203	BE262677	Hs.283558	hypothetical protein PRO1855	5.38	4.16
	420338	AA825595	Hs.88269	Homo sapiens, clone MGC:17339, mRNA, com	5.37	5.77
	430580	AA805105	Hs.300697	immunoglobulin heavy constant gamma 3 (G	5.31	5.32
	428804	AK000713	Hs.193736	hypothetical protein FLJ20706	5.29 5.29	4.80 3.61
35	447735	AA775268	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L	5.29 5.27	5.35
22	410491 410361	AA465131 BE391804	Hs.64001 Hs.62661	Homo sapiens clone 25218 mRNA sequence guanylate binding protein 1, interferon-	5.26	6.00
	412561	NM_002286	Hs.74011	lymphocyte-activation gene 3	5.26	5.04
	450293	N36754	Hs.171118	hypothetical protein FLJ00026	5.23	3.60
	400750			Target Exon	5.18	3.62
40	417933	X02308	Hs.82962	thymidylate synthetase	5.14	3.33
-	413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	5.12	5.36
	445784	AI253155	Hs.146065	ESTs	5.12	4.06
	420602	AF060877	Hs.99236	regulator of G-protein signalling 20	5.06	7.68
45	421508	NM_004833	Hs.105115	absent in melanoma 2	5.03 4.96	5.59
43	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	4.95	6.25 5.13
	402474 400417	X72475		NM_004079:Horno sapiens cathepsin S (CTSS Target	4.90	3.93
	420137	AA306478	Hs.95327	CD3D antigen, delta polypeptide (TiT3 co	4.88	6.81
	409264	NM_014937	Hs.52463	KIAA0966 protein	4.88	3.18
50	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	4.87	4.20
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	4.85	5.86
	409142	AL136877	Hs.50758	SMC4 (structural maintenance of chromoso	4.83	5.94
	425088	AA663372	Hs.169395	hypothetical protein FLJ12015	4.82	5.19
55	405506		11- 000004	Target Exon	4.74 4.74	4.09 3.72
55	409512	AW979187	Hs.293591	melanoma differentiation associated prot	4.73	3.50
	430838 439963	N46564 AW247529	Hs.169395 Hs.6793	hypothetical protein FLJ12015 platelet-activating factor acetyfhydrola	4.72	3.66
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	4.71	5.16
	447217	BE465754	Hs.17778	neuropilin 2	4.70	4.52
60	422309	U79745	Hs.114924	solute carrier family 16 (monocarboxylic	4.69	3.51
	413670	AB000115	Hs.75470	hypothetical protein, expressed in osteo	4.68	3.69
	419956	AL137939	Hs.40096	cadherin 19, type 2	4.68	5.83
	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	4.68	5.29
65	449217	AA278536	Hs.23262	ribonuclease, RNase A family, k6	4.66	3.84
U.J	449722	BE280074	Hs.23960	cyclin B1 CD84 antigen (leukocyte antigen)	4.64 4.62	4.29 4.54
	424006 407846	AF054815 AA426202	Hs.137548 Hs.40403	Cbp/p300-interacting transactivator, wit	4.62	6.78
	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	4.59	5.81
	406673	M34996	Hs.198253	major histocompatibility complex, class	4.57	5.60
70	431620		Hs.264981	2-5-oligoadenylate synthetase 2 (69-71	4.56	4.44
	441224		Hs.7753	calumenin	4.56	3,75
	442739	NM_007274	Hs.8679	cytosofic acyl coenzyme A thioester hydr	4.56	3.22
	444371		Hs.239	forkhead box M1	4.53	5.28
76	448719		Hs.21858	trinucleotide repeat containing 3	4.48	9.08
75	420301		Hs.22030	paired box gene 5 (B-cell lineage specif	4.47 4.43	5.61
	430294 428513		Hs.32976 Hs.184697	guanine nucleotide binding protein 4 Homo sapiens clone 23785 mRNA sequence	4.43 4.41	4,11 4,43
	446006		Hs.13530	deafness, autosomal dominant 5	4.39	3.99
	432485		Hs.276770	CDW52 antigen (CAMPATH-1 antigen)	4.38	5.50
80	428242		Hs.2250	leukemia inhibitory factor (cholinergic	4.37	3.25
-	421633	AF121860	Hs.106260	sorting nexin 10	4.36	6.23
	414829		Hs.77436	pleckstrin	4.35	2.91
	417166	AA431323	Hs.42146	ESTs	4.35	4.08

	448410	AK000227	Hs.21126	hypothetical protein FLJ20220	4.34	5.35
	419381	AB023420	Hs.90093	heat shock 70kD protein 4	4,34	3.72
	411305	BE241596	Hs.69547	myelin basic protein	4.32	4.18
5	425289	AW139342	Hs.155530	interferon, gamma-inducible protein 16	4.28 4.27	2.44 4.48
,	451099 432642	RS2795 BE297635	Hs.25954 Hs.3069	interleukin 13 receptor, alpha 2 heat shock 70kD protein 98 (mortalin-2)	4.25	2.69
	422282	AF019225	Hs.114309	apolipoprotein L	4.25	3.75
	433867	AK000596	Hs.3618	hippocalcin-like 1	4.23	5.13
10	415817 438619	U88967 AB032773	Hs.78867	protein tyrosine phosphatase, receptor-t TU12B1-TY protein	4.20 4.19	2.15 3.32
10	426317	AA312350	Hs.169294	transcription factor 7 (T-cell specific,	4.16	5.14
	420208	8E276055	Hs.95972	silver (mouse homolog) like	4.16	5.08
	416602	NM_006159	Hs.79389	Protein kinase C-binding protein NELL2	4.16	2.38 3.67
15	430770 424541	AA765694 AW392551	Hs.123296 Hs.180559	ESTs ESTs, Wealdy similar to A56194 thromboxa	4.15 4.15	3.98
1.5	427337	Z46223	Hs.176663	Fc tragment of IgG, low affinity Illb, r	4,14	3.51
	456760	AW961251	Hs.127828	guanine nucleotide binding protein (G pr	4.14	4.42
	406868	AA505445	Hs.300697	immunoglobulin heavy constant gamma 3 (G	4.13 4.12	5.07 6.43
20	420931 410016	AF044197 AA297977	Hs.100431 Hs.57907	small inducible cytokine 8 subfamily (Cy small inducible cytokine subfamily A (Cy	4.11	8.73
	452698	NM_001295	Hs.301921	chemokine (C-C motif) receptor 1	4.11	4.48
	444863	AW384082	Hs.104879	serine (or cysteine) proteinase inhibito	4.10	4.78 2.76
	435080 442711	AI831760 AF151073	Hs.155111 Hs.8645	hypothetical protein FLJ14428 hypothetical protein	4.07 4.06	3.49
25	423605	AF047826	Hs.129887	cadherin 19, type 2	4.06	2.42
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	4.05	3.26
	421712	AK000140	Hs.107139	hypothetical protein	4.02 4.00	7.60 3.87
	422283 409415	AW411307 AA579258	Hs.114311 Hs.6083	CDC45 (cell division cycle 45, S.cerevis Homo sapiens cDNA: FLJ21028 fis, clone C	4.00	5.87
30	412719	AW016610	Hs.816	ESTs	3.99	5.46
	437179	AA393508		serologically defined colon cancer antig	3.96	4.51
	420319	AW406289	Hs.96593 Hs.6194	hypothetical protein chondroitin suffate proteoglycan BEHAB/b	3.95 3.91	5.47 4.58
	438380 418064	T06430 BE387287	Hs.83384	S100 calcium-binding protein, beta (neur	3.84	4.42
35	420286	AI796395	Hs.111377	ESTs	3.83	4.56
	410600	AW575742		ESTs, Moderately similar to S65657 alpha	3.80	5.70 4.86
	410326 424779	AI368909 AL046851	Hs.47650 Hs.153053	ESTs CD37 antigen	3.76 3.70	8.72
_	452194	AI694413	113.133000	Ubiquitin-like protein FAT 10??? - diubiq	3.69	6.38
40	411027	AF072099	Hs.67846	leukocyte immunoglobulin-like receptor,	3.65	5.40
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	3.65 3.64	4.48 5.82
	424153 421666	AA451737 AL035250	Hs.141496 Hs.1408	MAGE-like 2 endothelin 3	3.64	5.52
	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	3.60	5.56
45	422173	8E385828	Hs.250619	phorbolin-like protein MDS019 (CEM15)	3.59	4.35
	421563	NM_006433	Hs.105806	granutysin bacutoviral IAP repeat-containing 7 (liv	3.49 3.49	7.38 6.13
	453837 424326	AL138387 NM_014479	Hs.256126 Hs.145296	ADAM-like disintegrin protesse, decysin	3.48	4.23
	427247	AW504221	Hs.174103	integrin, alpha L (antigen CO11A (p180).	3.47	5.38
50	408838	A1669535	Hs.40369	ESTs	3.45 3.42	4.59 5.01
	402829 418918	X07871	Hs.89476	C1002500:gij6754254frefiNP_034610.1  hea CD2 antigen (p50), sheep red blood cell	3.42	8.14
	430594	AK000790	Hs.246885	hypothetical protein FLJ20783	3.40	4.35
<i>E E</i>	429714	BE561801	Hs.2484	T-cell leukemia/lymphoma 1A	3.36	4.84
55	414324	Y14768	Hs.890 Hs.109918	lymphotoxin beta (TNF superfamily, membe ras homolog gene family, member H	3.35 3.35	4.45 4.28
	421958 428291	AA357185 AA534009	Hs.183487	interferon stimulated gene (20kD)	3.34	5.18
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	3.31	8.00
60	451736	AW080356	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	3.29 3.28	4.50 5.42
UU	412790 404854	NM_014767	Hs.74583	KIAA0275 gene product Target Excen	3.28	4.28
	400860			Target Exon	3.26	4.41
	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	3.24 3.24	5.65 4.35
65	438209 422846	AL120659 BE513934	Hs.6111 Hs.1583	aryl-hydrocarbon receptor nuclear transl neutrophil cytosolic factor 1 (47kD, chr	3.24 3.24	4.90
05	440065	W03476	Hs.266331	hypothetical protein MGC4595	3.20	6.21
	440704	M69241	Hs.162	insulin-like growth factor binding prote	3.20	4.72
	411088	BE247593	Hs.145053	ESTs	3.18 3.18	4.20 4.68
70	447513 413190	AW955776 AA151802	Hs.313500 Hs.40368	ESTs, Moderately similar to ALU7_HUMAN A adaptor-related protein complex 1, sigma	3.15	4.27
. •	430017		Hs.35	protein tyrosine phosphatase, non-recept	3.15	4.28
	406837	R70292	Hs.156110	immunoglobulin kappa constant	3.12	4.09
	409103		Hs.112208	XAGE-1 protein hypothetical protein FLJ22570	3.04 3.04	4,04 4.28
75	425706 447656		Hs.122559 Hs.19126	src kinase-associated phosphoprotein of	3.03	4.30
	427792		Hs.180841	tumor necrosis factor receptor superfami	3.01	4.82
	402994		U. ASCAC	NM_002463*:Homo sapiens myxovirus (influ	2.99 2.97	5.74 5.07
	434276 449523		Hs.93605 Hs.54443	leucine zipper, putative tumor suppresso chemokine (C-C motif) receptor 5	2.96	4.15
80	439237		Hs.318893	ESTs, Wealdy similar to A47582 B-cell gr	2.96	5.81
	406621	X57809	Hs.8997	immunoglobulin lambda locus	2.93	7.88 13.22
	447131 426322		Hs.17466 Hs.2012	retinoic acid receptor responder (tazaro transcobalamin I (vitamin B12 binding pr	2.91 2.90	8.37
	420322	~~~~	113.4414			

					2.87	4.15
	448275	BE514434	Hs.20830	kinesin-like 2 chemokine (C-C motif) receptor 7	2.87 2.86	5.53
	423397 406782	NM_001838 AA430373	Hs.1652	gb:zw20f11.s1 Soares overy tumor NbHOT H	2.81	4.60
	400702 414915	NM_002462	Hs,76391	myxovirus (influenza) resistance 1, homo	2.80	5.89
5	412819	T25829	Hs.24048	FK506 binding protein precursor	2.78 2.76	4.90 4.21
	432886	BE159028	Hs.279704	chromatin accessibility complex 1	2.76	5.15
	428380 408209	NM_004271 NM_004454	Hs.184018 Hs.43697	MD-1, RP105-associated ets variant gene 5 (ets-related molecule	2.76	4.30
	416511	NM_006762	Hs.79356	Lysosomai-associated multispanning membr	2.75	4.13
10	422530	AW972300	Hs.118110	bone marrow stromal cell antigen 2	2.74 2.73	5.05 9.20
	428746	AW503820	Hs.192861	Spi-B transcription factor (Spi-1/PU.1 r	2.72	4.38
	453953 407241	AW408337 M34516	Hs.36972	CD7 antigen (p41) gb:Human ornega light chain protein 14.1	2.68	4.07
	437669	AI358105	Hs.123164	ESTs, Wealty similar to match to ESTs AA	2.66	4.71
15	453779	N35187	Hs.43388	28kD interferon responsive protein	2.65 2.64	4.31 4.15
	432874	W94322	Hs.279651	melanoma inhibitory activity	2.62	7.36
	410129	BE244074 AI879076	Hs.58831 Hs.75061	regulator of Fas-induced apoptosis macrophage myristoylated alanine-rich C	2.62	4.43
	412926 418739	AA310964	Hs.88012	SHP2 interacting transmembrane adaptor	2.61	5.42
20	424825	AF207069	Hs.153357	procollagen-lysine, 2-oxoglutarate 5-dio	2.60 2.60	9.69 5.17
	417370	T28651	Hs.82030	tryptophanyl-tRNA synthetase	2.59	4.01
	411358	R47479 8E271188	Hs.94761 Hs.155975	KIAA1691 protein protein tyrosine phosphatase, receptor t	2.58	13.24
	425367 426470	AA528794	Hs.128644	ESTs	2.54	4.52
25	425535	AB007937	Hs.158287	KIAA0468 gene product	2.52	11.31 7.80
	431629	AU077025	Hs.265827	interferon, alpha-inducible protein (clo	2.50 2.49	4.25
	425722	AI659076	Hs.97031	hypothetical protein MGC13047 Homo sapiens cDNA: FLJ22380 fis, clone H	2.49	4.04
	438291	BE514605 AA180256	Hs.289092 Hs.210473	Homo sapiens CDNA FLJ14872 fis, clone PL	2.48	4.08
30	416426 441859	AW194364	Hs.94814	ESTs. Weakly similar to FIG1 MOUSE FIG-1	2.48	5.25
30	416714	AF283770	Hs.79630	CD79A antigen (immunoglobulin-associated	2.48	4.88 6.04
	431186	NM_012249	Hs.250697	ras-like protein	2.46 2.45	5.34
	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor proteolipid protein 1 (Pelizaeus-Merzbac	2.43	6.57
35	424481	R19453 AV656017	Hs.1787 Hs.184325	CGI-76 protein	2.42	4.96
. 33	428437 427634	AI399745	Hs.18449	hypothetical protein MGC10820	2.39	8.46
	420842	AI083668	Hs.50601	hypothetical protein MGC10986	2.38 2.38	5.90 5.32
	428289	M26301	Hs.2253	complement component 2	2.37	6.99
40	417929	R27219	Hs.74647	Human T-cell receptor active alpha-chain interferon-stimulated protein, 15 kDa	2.34	9.69
40	413278 433671	BE563085 AW138797	Hs.833 Hs.132906	19A24 protein	2.34	4.81
	432403	AA550815	Hs.124840	ESTs	2.34	4.99
	427759	BE245578	Hs.2200	perforin 1 (pore forming protein)	2.32 2.30	4.56 4.22
4.5	419870	AW403911	Hs.266175	phosphoprotein associated with GEMs Homo sapiens, clone IMAGE:4054868, mRNA	2.30	6.18
45	421445	AA913059	Hs.104433	Target Exon	2.29	7.01
	401591 451708	Al306536	Hs.60975	ESTs	2.26	4.50
	452700	AI859390	Hs.288940	five-span transmembrane protein M83	2.24	4.90 5.40
	424618	L29472	Hs.1802	major histocompatibility complex, class	2.22 2.21	5.40 4.74
50	409208	Y00093	LI- 040122	integrin, alpha X (antigen CD11C (p150), G protein-coupled receptor 24	2.19	4.61
	436456	AW292677 NM_007019	Hs.248122 Hs.93002	ubiquitin carrier protein E2-C	2.17	7.43
	419741 416448		Hs.79339	lectin, galactoside-binding, soluble, 3	2.16	5.58
	438555		Hs.143878	Homo sapiens mRNA for FLJ00024 protein.	2.13 2.13	4.26 4.00
55	407260			gb:Homo sapiens mRNA fragment.	2.13	4.03
	448243			integrin, beta 8 gb:wq05c02.x1 NCI_CGAP_Kid12 Homo sapien	2.07	4.45
	437938 425262		Hs.155418	GS3955 protein	2.06	4.36
	414945		Hs.77667	lymphocyte antigen 6 complex, locus E	2.05	4.66 4.22
60	400261			Eos Control	2.04 2.02	4.23
	432468		Hs.3003	CD3E antigen, epsilon polypeptide (TiT3 interferon regulatory factor 1	1.99	4.45
	416967 420626		Hs.80645 Hs.99491	RAS guanyl releasing protein 2 (calcium	1.98	4.42
	440672		Hs.7345	MAD1 (mitotic arrest deficient, yeast, h	1.98	4.55
65	45292		Hs.288940	five-span transmembrane protein M83	1.96 1.95	4.54 4.23
	45224		Hs.176674	ESTs	1.94	4.93
	42723		Hs.167379	ubiquitin carrier protein cancer/testis antigen (NY-ESO-1)	1.94	5.28
	41867 43183		Hs.271411	beta-site APP-cleaving enzyme 2	1.93	4.17
70	44409		Hs.10306	natural killer cell group 7 sequence	1.93	5.06
	40406	7		Target Exon	1.92 1.91	6.16 4.23
	42689		Hs.41294	ESTs	1.91	4.10
	45359 40191		Hs.33713	myo-inositol 1-phosphate synthase A1 Target Exon	1.87	4.76
75	44849		Hs.77550	hypothetical protein MGC1780	1.87	5.17
, ,	43962		Hs.29076	hypothetical protein FLJ21841	1.85	6.59
	42592	3 NM_00502		phosphoinositide-3-kinase, catalytic, de	1.85 1.84	4.03 4.57
	41681		Hs.80205	pim-2 oncogene potassium voltage-gated channel, shaker-	1.84	6.40
80	42506 43037		Hs.298184 Hs.2556	tumor necrosis factor receptor superfami	1.78	4.02
50	43596			Integral membrane protein 3	1.76	5.26
	41042	23 AW402432	Hs.63489	protein tyrosine phosphatase, non-recept	1.75 1.74	4.30 4.91
	43422	24 AA380731	Hs.84	interleukin 2 receptor, gamma (severe co	1,79	7.31

	413566	AW604451	Hs.285814	sprouty (Drosophila) homolog 4	1,71	6.00	
	430148	BE387620	Hs.234489	tactate dehydrogenase B	1.70	4.34	
	410068	A1633888	Hs.58435	FYN-binding protein (FYB-120/130)	1.69	4.04	
_	437696	Z83844	Hs.5790	hypothetical protein dJ37E16.5	1.66	5.95	
5	423984	AF163825	Hs.136713	pre-B lymphocyte gene 3	1.64	6.26	
	426666	AW500131	Hs.171763	CD22 antigen	1.63	4.33	
	406908	Z25437		gb:H.sapiens protein-tyrosine kinase gen	1.62	7.19	
	440087	W28969	Hs.7718	hypothetical protein FLJ22678	1.61	4.33	
	421859	AA356620	Hs.108947	KIAA0050 gene product	1.59	4.30	
10	415198	AW009480	Hs.943	natural killer cell transcript 4	1.56	4.12	
	406827	AA971409		gb:op92c04.s1 NCI_CGAP_Lu5 Homo sapiens	1.55	4.29	
	413969	X14034	Hs.75648	phosphotipase C, gamma 2 (phosphatidylin	1.53	4.63	
	456086	AL161999	Hs.77324	eukaryotic translation termination facto	1.52	4.11	
	433320	D60647	Hs.250879	ESTs, Highly similar to CTXN RAT CORTEXI	1.52	4.36	
15	406906	Z25424		gb:H.sepiens protein-sertne/threonine ki	1.50	8.67	
	406885	D28423		gb:Human mRNA for pre-mRNA splicing fact	1.49	5.07	
	443759	BE390832	Hs.134729	FXYD domain-containing ion transport reg	1.48	4.50	
	452423	AA991724	Hs.180535	hypothetical protein MGC10966	1.48	4.91	
	448143	AF039704	Hs.20478	ceroid-lipofuscinosis, neuronal 2, late	1.43	4.26	
20	451524	AK001466	Hs.26516	hypothetical protein FLJ 10604	1,43	4.74	
	417287	AI831678	Hs.285714	KIAA1599 protein	1.41	4.01	
	432665	AW603880		ATPase, H transporting, lysosomal (vacuo	1,38	4.07	
	403043			Target Exon	1.36	4.89	
~~	407239	AA076350	Hs.67846	leukocyte immunoglobulin-like receptor,	1.32	4.57	
25	436553	AW407157	Hs.8997	immunoglobulin lambda locus	1.30	4.00	
	422934	BE244189	Hs.122492	hypothetical protein	1.30	4.37	
	442680	BE270707	Hs.8583	similar to APOBEC1	1.26	4.48	
20	TABLE 57					•	
30	Pkey:			t identifier number			
	CAT num!		duster number				
	Accession	: Gent	oank accession	numbers			
	Pkey	CAT Number	Accession				2222
35	438619	35124_1	NM_016575	AB032773 A1765521 BF593742 A1497757 A1761233 AW46	7938 BF000670 AI818496 NZ	4761 AL043306 BF476138 BF593836 AA	32/6/
			AJ147248 AJC	86795 AA151317 T95298 AW083548 AA058371 N27951 A	1769860 A1784548 AW20550	5 AIBUU5/9 AIU41/33 AIA599UZ BE3Z/64	1
				54736 Al302433 Al744176 Al241825 AA027842 AL52493			
				5901 AA682443 AA678249 AA719371 AA132582 T15981 I			MZU
40				318 H17331 H29327 R40829 R43395 R59573 A1749561 R			
40	437179	12239_1	AK055109 B	2019085 AA 187684 BG656226 BM023227 AI932311 AW2	54381 AA3983/1 BMU21483/	N432433 AI373777 AI129300 AW202702	2250
			AA134107 BI	M023515 AA977504 A1859222 A1348454 R69725 AA97526	8 BM021207 AL080074 AA12	3218 AW207842 N90581 AA771919 Alus	2233
				74114 BG656536 BE501677 AW193419 AA917040 W904		486 AWUZUU68 BI491U93 BF4/6U21 K41	220
			R69631 F041	25 C02343 AA115589 R56480 AI400988 R54266 R31422		DEC 10000 A1000004 A101400749 DE44404	22
	410600	497855_1	BF347859 A	N499616 AA191322 AW499617 AL601010 AW575742 AA	729043 BE463447 AA086179	BE549623 AI335824 AW408712 BM1491	12
45	452194	90339_1		994700 AI912946 N73548 AI082035 AW271652 W24189	W24182 AI719718 AA024658	AW810120 AW015394 179755 AA96804	3
			A1709339				
	406782	0_0	AA430373 A	A968771			14444272
	409208	10117_2	AK074047 A	144342 AW014280 BM145128 N28267 AW206231 AA989	041 H93197 AW594063 BGZ	36296 AWZ36606 AWU81U31 AA/65843 E	M1443/2
<b>~</b> ^			AA989341 A	824838 AI963970 AI637671 AW196330 BG427526 BM146	3789 BF893644 BF881946		•
50	448243	13061_2		A479726 BE622314 AL134913 BE006305 BE006312 BE0	06298 AA044582 AW994956 A	4A234175 AAU43906 BEUU6303 BF32760	9
			BE006317 B	F326759 BF541959			70
	437938	66997_1	U71456 AA4	82911 W78802 AW856538 BF737212 N36809 N35320 AA	282915 AW505512 Al653832	W8/891 AI961530 185904 H5939/ R9/2	/0 172467
			W01059 AIB	20532 T82391 AI820501 T63226 R66056 R67840 AW9611	01 AA337499 W37181 AA180	0000 AUT00000 AA400000 AUT00004 AU	172437
			BG751124 A	1741346 A1950344 A1689062 A1872193 AW102898 AW173	586 AI /632/3 AI89038/ AWI	5U329 AI/62000 AA400032 AI350339 AI3	13504Z
55			AA642789 A	1950087 BF589902 N70208 AA283144 AA488964 H60052	R97040 BF886630 AW96767	7 AW9/15/3 AW96/6/1 ALSUS119 AAZS1	1875
			AA908598 A	1819225 A1564269 AA908741 AA293273 AA969759 AW27	6905 AAU44209 H83488 1924	18/ 	40472
	400261	23110_1	BC006097 X	03066 NM_002120 M26040 AW469119 AW469127 AI2997	772 AW518149 AJ144456 AW	628U/U A1629U32 A135881U A166U433 A14	40472
			A1357070 A1	865365 AW014799 AI767973 AW518041 AA909398 AW76	8500	1202000 DC4200C2 DC04000C 41224001	
<b>C</b> O	427239	20459_2	AL532360 B	E794750 AA582906 AI015067 AW271034 BG271636 AW0	1/51// AWU/13/4 AI345565/	430/208 BE138333 BE049080 AI334001	1001000
60			AW075006 /	W075181 AA464019 AW302733 AW075100 AW073433 A	1802854 A1334909 A1802853	AJ345U36 Al348921 Al34U734 Al3U7470 P	MZ31203
			AW302327 /	W072520 Al312145 AW073656 AW072513 AW071289 Al	30/559 AA8/6186 12958/ AI	30/433 AIZ33000 AIZ3Z666 AIZ3Z633 AV	(U/40U3 64764
			A1252926 AI	252160 Al251662 Al251262 Al610913 Al270787 Al270156	AI2520/5 AW0/3469 AW0/2	19U1 AWU/2496 AWU/142U AI3U3/62 AI2	34/84 06/067
			AI802837 AI	251264 AW073049 AW071311 Al340643 BE138965 BE13	8502 AWU/3456 AI334/33 AI	U54333 BE 13920U AND943UZ AND9400U AN	U34U3/ DE0E7033
				289711 BE139228 AW470478 AW271039 AW302085 BE0	41872 A1254494 A1271496 AI	252427 BF / 18// J BF / 18045 AWU/4000	BE03/022
65	406827	0_0	AA971409				
	432665	27095_3	BG165971 E	BE143233 AL577712 AJ400326 AA769318 AA427866 AWO	88714 AL150755 Al924874 AL	186243 AA804195 AA768972 AW574769	-20
			AW341643	4W204520 AA235326 AI005076 BE826687 AW004816 AW	00/235 RE850039 RE85003	1 BF 222941 BE820031 BE820043 AA2920	233 1807E040
		•		A1690331 A1673409 AA627727 A1923685 AA931499 A1249	783 AIB10663 AA548622 AA7	UZUYS AABIZIYS BIZSYSUB AAZ6ZYYI AY	VU/304U
			AA810885				
70							
	TABLE 5						
	Pkey:	Uni	dne unwper cou	responding to an Eos probeset			
	Ref:			The 7 digit numbers in this column are Genbank Identifier		reters to the publication entitled "The UN	A
20				chromosome 22" Dunham, et al. (1999) Nature 402:489-4	<b>30</b> .		
75	Strand:			nd from which exons were predicted.			
	Nt_posit	ion: Ind	icates nucleotid	positions of predicted exons.			
			_	14			
	Pkey	Ref	Strand	NL position			
00	400750	8119067	Plus	198991-199168,199316-199548			
80	402474	7547175	Minus	53526-53628,55755-55920,57530-57757			
	405506	6466489	Plus	80014-80401,80593-81125			
	402829	8918414	Plus	101532-101852,102006-102263			
	404854	7143420	Ptus	14260-14537			

PCT/US02/29560 WO 03/025138

400860 9757499 Minus	151830-152104,152649-152744
402994 2996643 Minus	4727-4969
401591 9966977 Minus	55410-55835
404067 3282162 Plus	1615-2071
5 401914 9369520 Plus	62537-62945,63155-63308
403043 7768763 Minus	314423-316252

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TABLE 58A: ABOUT 183 GENES UPREGULATED IN MELANOMA METASTASES FROM PATIENTS WITH LIMITED DISEASE RELATIVE TO MELANOMA METASTASES FROM PATIENTS WITH PROGRESSIVE DISEASE
Table 58A lists about 183 genes upregulated in melanoma metastases from patients with limited disease relative to melanoma metastases from patients with progressive disease.
Genes were selected from 59680 probesets on the Eos/Affymetrix Hu/03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the retative level of mRNA expression.

Pkey: Unique Eos probeset identifier number
ExAcon: Exemplar Accession number, Genbank accession number
UnigenelD: Uniquene number
Uniquene Title: Uniquene gene title
R1: 90th percentite of Als for metastases from patients with limited disease divided by 90th percentite of Als for metastases from patients with progressive disease,
R2: 90th percentile of Als for metastases from patients with limited disease divided by 90th percentite of Als for metastases from patients with progressive disease,
where the 15th percentile of normal tissue Als was subtracted from both the numerator and denominator

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20		#11010	uic rom parochan	, or not the second sec		
	Pkey	ExAcon	UnigenelD	Unigene Title	R1	R2
	415668	AW957684	Hs.306814	hypothetical protein FLJ21889	12.74	12.92
	447414	D82343	Hs.74376	neuroblastoma (nerve tissue) protein	7.66	5.88
25	412659	AW753865	Hs.74376	olfactomedin related ER localized protei	7.23	5.76 14.26
	430154	AW583058	Hs.234726	serine (or cysteine) proteinase inhibito	6.91	7.10
	414430	Al346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	6.86	6.81
	436485	X59135	Hs.156110	immunoglobulin kappa constant	6.85 6.73	11.21
	426600	NM_003378	Hs.171014	VGF nerve growth factor inducible	5.53	4.63
30	430822	AJ005371	Hs.248017	glyceraldehyde-3-phosphate dehydrogenase	5.48	7.08
	416426	AA180256	Hs.210473	Homo sapiens cDNA FLJ14872 fis, clone PL	5.27	5.94
	423858	AL137326	Hs.133483	Homo sapiens mRNA; cDNA DKFZp434B0650 (f	5.27 4.78	3.07
	433658	L03678	Hs.156110	immunoglobulin kappa constant	4.68	3.27
	452436	BE077546	Hs.31447	ESTs, Moderately similar to A46010 X-lin	4.62	4.82
35	413916	N49813	Hs.75615	apolipoprotein C-II	4.55	3.12
	407825	NM_006152	Hs.40202	lymphoid-restricted membrane protein	4.31	4.15
	406648	AA563730	Hs.277477	major histocompatibility complex, class	4.23	3.44
	409060	AI815867	Hs.50130	necdin (mouse) homolog	3.89	3.19
	401941			Target Exon	3.88	2.43
40	447471	AF039843	Hs.18676	sprouty (Drosophila) homolog 2	3.66	4.16
	419628	H67546	Hs.49768	ESTs	3.63	2.81
	414863	AW131473	Hs.106185	ral guanine nucleotide dissociation stim	3.47	3.06
	423416	NM_004920	Hs.128316	apoptosis-associated tyrosine kinase	3.47	3.43
	400275			NM_006513":Homo sapiens seryl-tRNA synth	3.42	1.96
45	426283	NM_003937	Hs.169139	kynureninase (L-kynurenine hydrolase)	3.41	2.89
	442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447	3.37	6.31
	411763	AW862589		gb:QV0-CT0387-180300-167-a07 CT0387 Homo	3.34	3.74
	402007			C18000503*:gij8922165[ref]NP_060080.1] h	3.30	2.00
50	424775	AB014540	Hs.153026	SWAP-70 protein	3.30	3.16
50	424036	AA770688	22222	H2A histone family, member L	3.30	5.58
	453464	A1884911	Hs.32989	receptor (calcitonin) activity modifying NM_005622*:Horno sapiens SA (rat hyperten	3.30	3.23
	401739	004505	11. 7122	scrapie responsive protein 1	3.27	2.47
	440274	R24595	Hs.7122	nucleolar and coiled-body phosphprotein	3.26	2.61
55	413398	D21262	Hs.75337	Homo sapiens cDNA: FLJ21425 fis, clone C	3.26	2.58
55	417165	R80137	Hs.302738	cyclin-dependent kinase inhibitor 2A (me	3.14	4.04
	418478	U38945	Hs.1174 Hs.156110	gb:H.sapiens rearranged mRNA for immunog	3.13	2.38
	436965	Z11894	Hs.35861	DKFZP586E1621 protein	3.13	2.47
	453857	AL080235	15.55001	Target Exon	3.11	4.69
60	404405	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	3.11	2.10
UU	413719 443247	BE614387	Hs.333893	c-Myc target JPO1	3.10	2.26
	400417	X72475	113.330030	Target	3.08	2.32
	401512	AIZHIS		NM_014080:Homo sapiens dual oxidase-like	3.07	2.87
	423242	AL039402	Hs.125783	DEME-6 protein	3.06	2.78
65	417501	AL041219	Hs.82222	sema domain, immunoglobulin domain (lg),	3.06	2.81
03	451952	AL120173	Hs.301663	ESTs	3.05	2.65
	427419			histatin 3	3.05	4.24
	406663			immunoglobulin heavy constant mu	3.05	4.55
	442104		Hs.188	phosphodiesterase 4B, cAMP-specific (dun	3.03	1.90
70	451993		Hs.122983	ESTs	3.02	1.71
, ,	421097		Hs.125232	Homo sapiens cDNA FLJ13266 fis, clone OV	3.01	3.11
	430129		Hs.233955	hypothetical protein FLJ20401	3.00	3.47
	427700		Hs.180383	dual specificity phosphatase 6	3.00	2.22
	400237			NM_001087*:Homo sapiens angio-associated	2.98	3.43
75	414063		Hs.75736	apolipoprotein D	2.97	5.76 2.38
. •	426153		Hs.182771	vitelliform macular dystrophy (Best dise	2.94	2.36 2.88
	414781	D50917	Hs.77293	KIAA0127 gene product	2.94	1.98
	445823		Hs.145519	FKSG87 protein	2.92	2.57
	404439			ENSP00000067222*:Mitochondrial 28S ribos	2.92 2.90	2.47
80	421218	3 NM_00049		cytochrome P450, subfamily I (aromatic c	2.90 2.90	3.87
_	420350			Homo sapiens, clone MGC:17339, mRNA, com	2.89	2.61
	424855			ESTs	2.88	3.63
	435700	) A1593690	Hs.301406	hypothetical protein PP3501	2.00	J.00
				572		

				6m 14 6 4 8 1 1 1 1	207	2.92
	451131	AJ267586	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	2.87 2.87	2.11
	427157	U51166	Hs.173824	thymine-DNA glycosylase	2.87	2.48
	402273 414135	NM_004419	Hs.2128	Target Exon dual specificity phosphatase 5	2.83	3.09
5	430643	AW970065	Hs.287425	MEGF10 protein	2.83	3.04
,	451979	F06972	Hs.27372	endothelial tyrosine kinase (Etk) (BMX),	2.82	2.12
	406642	AJ245210	113.27072	gb:Homo sapiens mRNA for immunoglobulin	2.81	2.88
	407360	X13075		gb:Human 2a12 mRNA for kappa-immunoglobu	2.81	3.43
	405441			Target Exon	2.80	3.15
10	450816	BE271927	Hs.87385	ESTs	2.80	2.48
	435675	AA694099	Hs.266820	EST8	2.78	2.70
	426495	NM_001151	Hs.2043	solute carrier family 25 (mitochondrial	2.78	2.53
	441623	AA315805		desmoglein 2	2.78	2.27
16	413336	AI569936	Hs.296178	hypothetical protein FLJ22637	2.76	3.18 1.92
15	408527	AL135018	Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA,	2.76 2.76	1.88
	437740	AA810265	Hs.122915	ESTs transcobalamin I (vitamin B12 binding pr	2.75	8.06
	426322 411852	J05068 AA528140	Hs.2012 Hs.107515	ESTs, Weakly similar to T00329 hypotheti	2.74	3.30
	428422	AI557280	Hs.184270	capping protein (actin filament) muscle	2.73	2.31
20	426793	X89887	Hs.172350	HIR (histone cell cycle regulation defec	2.72	2.19
	401454			NM_014226":Homo sapiens renal tumor anti	2.72	1.99
	436825	AW341123	Hs.120275	ESTs	2.72	2.89
	407705	AB023139	Hs.37892	KIAA0922 protein	2.72	2.48
~ ~	416782	L35035	Hs.79886	ribose 5-phosphate isomerase A (ribose 5	2.72	263
25	449151	AI632331	Hs.196038	ESTs	2.72	2.99
	433464	N92481		gb:zb12g02.s1 Soares_fetal_lung_NbHL19W	2.69	3.17
	401009	. = . = . = .		Target Exon	2.69 2.68	3.28 2.02
	427227	AF103803	Hs.283690	hypothetical protein ENSP00000223174*:KIAA0783 PROTEIN.	2.67	2.18
30	405268 410295	AA741357		nidogen (enactin)	2.65	2.06
20	435905	AW997484	Hs.5003	KIAA0456 protein	2.65	2.12
	430378	Z29572	Hs.2556	tumor necrosis factor receptor superfami	2.65	2.52
	457423	AK000642	Hs.265018	hypothetical protein FLJ20635	2.64	2.51
	448752	AA593867	Hs.300842	KIAA1608 protein	2.63	2.20
35	414931	AK000342	Hs.77646	Homo sapiens mRNA; cDNA DKFZp761M0223 (f	2.63	1.83
	441283	AA927670	Hs.131704	ESTs	2.62	1.92
•	439352	BE614347	Hs.169615	hypothetical protein FLJ20989	2.60	2.21
	421391	AW304350	Hs.191958	immunoglobulin superfamily receptor tran	2.60	3.06
40	406678	U77534		gb:Human done 1A11 immunoglobutin varia	2.54	3.06
40	430278	A1673074	Hs.116567	ESTs, Weakly similar to T22914 hypotheti	2.49	3.44
	425970	AK001500	Hs.165186	hypothetical protein FLJ13852	2.47 2.45	3.46 3.45
	407363	AF035032	Hs.8997	gb:Homo sapiens clone MCA1L myosin-react	2.44	3.52
	408367	AK001178	Hs.44424	homolog of rat orphan transporter v7-3 aldehyde dehydrogenase 1 family, member	2.44	6.15
45	420103 418635	AA382259 L11329	Hs.95197 Hs.1183	dual specificity phosphatase 2	2.42	3.92
43	451558	NM_001089	Hs.26630	ATP-binding cassette, sub-family A (ABC1	2.41	3.08
	430354	AA954810	Hs.239784	human homolog of Orosophila Scribble	2.36	3.99
	405701	70.00.0.0	12.000	ENSP0000004954*:Adseverin (Scinderin).	2.33	4.25
	433427	AIB16449	Hs.171889	cholinephosphotransferase 1	2.30	3.30
50	401965			CGI-148 protein	2.29	3.45
	417866	AW067903	Hs.82772	collagen, type XI, alpha 1	2.23	4.07
	428142	NM_001308	Hs.2246	carboxypeptidase N, polypeptide 1, 50kD	2.19	3.17
	422103	AA984330	Hs.111676	protein kinase H11; small stress protein	2.18	4.18
E E	425746	NM_001701	Hs.159440	bite acid Coenzyme A: amino acid N-acyll	2.12	3.48
55	404835			NM_018943":Homo sapiens tubulin, alpha-l	2.09 2.09	5.72 4.38
	401127			Target Exon	2.08	3.22
	406161	414462267	U- 106460	Target Exon	2.08	3.03
	421654 406632	AW163267 AB006838	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like gb:Homo sapiens mRNA for HRV Fab N31-VH,	2.07	3.25
60	447940	D86982	Hs.20060	KIAA0229 protein	2.05	4.80
oo	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	2.05	5.33
	413211	AW967107	Hs.109274	hypothetical protein MGC4365	2.02	4.74
	425722	AI659076	Hs.97031	hypothetical protein MGC13047	2.01	3.76
	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an	1.96	5.27
65	436420	AA443966	Hs.31595	ESTs	1.94	3.68
	414809	A1434699	Hs.77356	transferrin receptor (p90, CD71)	1.92	3.88
	423420	AI571364	Hs.128382	Homo sapiens mRNA; cDNA DKFZp76111224 (f	1.90	3.63
	427923	AW274357	Hs.301406	hypothetical protein PP3501	1.90	3.04
70	406652	AW150304	Hs.277477	major histocompatibility complex, class	1.88	3.00
70	435624	AF218942	Hs.24889	formin 2	1.88 1.86	3.54 3.29
	436552	NM_014038		HSPC028 protein	1.86	3.78
	408204	AA454501	Hs.43666	protein tyrosine phosphatase type IVA, m C1002541*:gij4758590fref[NP_004249.1] im	1.86	3.14
	402728	AW374605	Hs.11607	ESTs, Weakly similar to T21697 hypotheti	1.84	4.72
75	420932 458559	AW028820	Hs.283614	ESTS	1.78	3.06
, ,	400278	711020020		ENSP00000243264: Oalichyl-diphasphaaligas	1.76	3.55
	425751	T19239	Hs.1940	crystallin, alpha B	1.76	5.31
	420737	L08095	Hs.99899	CD70; tumor necrosis factor (ligand) s	1.74	3.00
	410006	AW732308	Hs.57783	eukaryotic translation initiation factor	1.74	3.79
80	454429	BE273437	Hs.301406	hypothetical protein PP3501	1.73	3.57
	426321	8E046490	Hs.180677	zinc finger protein 162	1.72	3.27
	402897			NM_023068*:Homo sapiens sialoadhesin (SN	1.69	3.81
	423639	AB037826	Hs.130411	KIAA1405 protein	1.67	3.31

					4.00	4.27	
		AF131851	Hs.22241	hypothetical protein	1.65 1.60	3.02	
		AA043424	Hs.76095	immediate early response 3	1.56	3.28	
		AW297226	Hs.137840	ESTs, Moderately similar to SIX4_HUMAN H	1.55	3.73	
_	450635	AW403954	Hs.25237	mesenchymal stem cell protein DSCD75 NM_004651*:Homo sapiens ubiquitin specif	1,55	3.26	
5	400252	AV000224		hypothetical protein FLJ20327	1.55	3.18	
	411825	AK000334	Hs.300463	aconitase 2, mitochondrial	1.52	4.03	
	414328 400263	Z21666	15.300103	Eos Control	1.51	3.42	
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	1.50	3.19	
10	436673	AF201931	Hs.5268	hypothetical protein FLJ10479	1.49	3.33	
10	404739			Target Exon	1.49	3.10	
	438344	BE387726	Hs.343411	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	1.46	3.42	
	421696	AF035306	Hs.106890	Homo sapiens clone 23771 mRNA sequence	1.44	3.15	
	425240	AA306495	Hs.1869	phosphoglucomutase 1	1.44	3.04 3.71	
15	412099	U64198	Hs.73165	interleukin 12 receptor, beta 2	1.43 1.42	3.07	
	434642	W25739		chromobox hornolog 5 (Drosophita HP1 alph	1.42	3.87	
	404406			Target Exon	1.41	3.80	
	433320	D60647	Hs.250879	ESTs, Highly similar to CTXN RAT CORTEXI tubulin alpha 1	1.40	4.45	
20	447697	W52125	Hs.78846	heat shock 27kD protein 2	1.40	3.28	
20	415780	U75898 R75812	Hs.169248	p75NTR-associated cell death executor, o	1.39	3.77	
	447216 401772	K/3012	113.103240	NM 014520:Homo sapiens MYB binding prote	1.39	3.67	
	413031	BE515051	Hs.75160	phosphofructokinase, muscle	1.38	3.31	
	435604	AA625279	Hs.26892	uncharacterized bone marrow protein BM04	1.37	3.17	
25	428011	BE387514	Hs.181418	KIAA0152 gene product	1.37	3.05	
	445580	AF167572	Hs.12912	skb1 (S. pombe) homolog	1.35	3.11 3.05	
	436703	AW880614	Hs.146381	RNA binding motif protein, X chromosome	1.34	3.09	
	438277	AL022326	Hs.6139	synaptogyrin 1	1.34 1.32	3.23	
	451481	AA300228	Hs.295866	hypothetical protein DKFZp434N1923	1.31	3.01	
30	421818	AW992976	Hs.50098	NM_002489:Homo sapiens NADH dehydrogenas	1.28	3.58	
	412968	AW500508	Hs.75102	atanyl-tRNA synthetase KIAA1694 protein	1.25	3.08	
	452378	AA025855	Hs.19597	Homo sapiens mRNA for FLJ00058 protein,	1.24	3.45	
	447455	H38335	Hs.6750	KIAA0430 gene product	1.21	3.03	
25	402212	BE256238	Hs.193163	bridging integrator 1	1.20	3.20	
35	428773 430067	U79458	Hs.231840	WW domain binding protein 2	1.18	3.03	
	418289	AW403103	Hs.83951	Hermansky-Pudlak syndrome	1.17	3.32	
	405752	A11400100	110.0000	Target Exon	1.00	3.40	
	422836	AL037365	Hs.194093	AKAP-binding sperm protein ropportn	1.00	3.00	
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40	TABLE 5						
40	Pkey:	Uni	ique Eos probeset				
40	Pkey: CAT nurt	Uni ıber: Ge	ne cluster number				
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45	Pkey: CAT num Accessio Pkey	Uni nber: Ge n: Ge CAT Numbe	ne cluster number nbank accession i er Accession NM_006513 E BI256788 BE BG473378 BE AV749916 AA AL572871 AL	numbers 8C009390 X91257 BC000716 BMA50041 BI771139 AV7109 386217 AU143368 AU133780 AU139704 BG531086 BE268: 298813 BI772360 BE617354 AU140124 BE277005 BG746 374328 BM011248 AU098465 AW238888 BG940091 BG28 568117 AL571945 AL547790 AL581217 AL514659 AL5738	235 BE545230 AU 716 BE814960 AW 34599 AW410037 A 26 AL540816 AW4 34750 BC583509 A	161287 AV762084 BG898985 AW674875 AA313975 A378483 D49914 A1.573323 A1.549819 A1.572282 10038 B1262249 BG284713 A1659394 A1093582 AW96 W887824 A1818522 AA703770 BE562873 AA515504	
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45 50	Pkey: CAT num Accessio Pkey	Uni nber: Ge n: Ge CAT Numbe	ne cluster number nbank accession i er Accession NM_006513 6 B1256788 BE: BG473378 86 AV749916 A AL572871 AL AA652206 Al AU154982 A	numbers 3009390 X91257 BC000716 BM450041 BI771139 AV7109 386217 AU143368 AU133780 AU139704 BG531086 BE268: 298813 BI772350 BE617354 AU140124 BE277005 BG746 374328 BM011248 AU098465 AVV33888 BG940091 BG26 568117 AL571945 AL547790 AL581217 AL514659 AL5739: 685014 AA654357 AU146982 AW773447 AW157715 AW57 A831254 AA628521 AU088602 AA654654 AA190869 BF0627	215 BE545230 AU 716 BE814960 AW 84599 AW410037 A 26 AL540816 AW4* 4750 BG683509 A\ 816 AA464944 BG2 64742 BE764209 A	161287 AV762084 BG896985 AW674875 AA313975 A378483 D49914 AL573323 AL549819 AL572282 10038 BI262249 BG284713 AI659394 AI093582 AW96 W887824 AI818522 AA703770 BE542873 AA515504 961335 AI003584 BG40280 AA932098 W68695 AW11	82900 75
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20			AW189719 1 AW129549 A	156783 Al018819 Al476552 Bl492837 Al824440 BC996262 AA932887 Al380726 R79530 AA622108 Al262575 T56782 R27437 BE784153 N675567 Al866759 BC987935
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23			BG910597 A D52367 W2: W21941 AA	WY964988 BER36120 AL579715 H56512 D55956 BI044097 AL555239 BF220278 AA081991 AIB19544 AW001573 AW131600 AIB58764 2034 BGB18979 BG024561 BE702779 BI458863 BI910399 BG707755 BF348284 H10055 BI086315 BE620574 H41088 BG119517 W23267 328817
30	411825	7891_1	BE272330 A AK000334 B	IX000489 BC001688 BG235988 AW006329 A1887644 A1207230 A1148213 A1304333 A1634653 AW662636 A1281247 AA946921 AA424487 IL830588 AA159183 AA977141 BG231801 AA631793 AA975194 BF817537 AA477798 B1906631 AW083424 AA625199 NM_017767 IF984048 AW815634 AL573992 AA430612 AA928390 AA46447 AW340827 AA424290 A1927759 BG961502 AW881353 B1765535
	400263	18977_1	Z11692 X51 BM016525 /	466 NM_001961 M19997 BI224253 BG830478 AU122147 AU123437 BG113591 BG752624 BE886804 BI868669 BG337216 AW629935 AI560409 AL562866 AI909178 BF849556 AA371735 BF038841 BF727115 BC006547 BG757526 AL555664 BI261304 BG770095 BI033485 G876486 BI011828 AI313235 BG831724 BF869862 BG998348 BI011834 BF888337 BF898627 BF092380 AW803215 F01241 BF805719
35			BG876487 /	AW498536 BF988866 BG998849 AA248724 BG829202 BG756456 BG032392 BI859287 BM016990 BG332369 BE933685 BE166758
			BM452445 / BE772007 B BF761350 B	AI937808 AW026128 N23684 AW006041 AI337621 F33111 BF344301 BG105450 BG387343 BF569547 BF154671 BM007368 BF569385 31199487 BF761700 BI261519 BF944452 BF898506 AI038390 BM044934 AW381142 BG743618 BE769206 BE893973 BI015047 BF886479 3E769769 BG766117 BF847365 BE397834 AW371121 BF089125 BE082996 BF183193 BG180964 BF089940 BI000274 BG255503 3E774174 BI015084
40	434642	15461_1	AF 147443 E BF884215	3M471094 AA948055 AA973157 AA284289 W25739 BK021926 BF898367 W02720 BF798341 BF378312 AA427766 BG955568 BF899591
	447697	MH497_6	AI884599 A	AL528391 AA328484 W52125 AA321596 AA022458 AW971024 AI052029 AI761638 AA628498 BE619513 AA412069 AI027538 AW514954 1097362 A1499259 A1419408 AW469200 A1992152 A1142045 A1066572 A1275439 AA581877 A1347308 A1016726 A1127541 AW002064 W051842 A1355329 A1198198 A1347858 A1027870 A1039163 AA576695 A1183286 A1362001 A1361994 AA594668 AA459257 AA745778
45			A1139667 F AA385481 I	20651 AI201510 AA832171 BM464599 BM464574 AI972621 A1183887 AW131911 AW771584 BE619828 AA492218 AA025767 AA977354 N45137 W73596 AI864400 AI200026 AI270953 F18139 W46301 H55825 AI039867 AI457570 AI928639 AI824685 AI083898 AW024570 AW381097 AW582409 BE964181
	TABLE 5	BC:		
50	Pkey: Ref:	Se	quence source.	responding to an Eos probeset  The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA
	Strand:			n chromosome 22° Dunham, et al. (1999) <u>Nature</u> 402-489-495. Ind from which exons were predicted.
	Nt_positio			le positions of predicted exons.
55				
	Pkey	Ref	Strand	NLposition
	401941	4982556	Plus	112022-112204
	402007	7381786 2982169	Plus	143964-144081 132194-132404
60	401739 404405	7272262	Plus Plus	83251-83415
00	401512	7622346	Plus	136399-136557
	404439	7139680	Plus	55316-55585
	402273	2979528	Plus	28990-29203,32299-32402,32474-32668
15	405441	7408124	Plus	100952-101283
65	401454	9186923	Minus	114659-114832
	401009	8117391	Minus Minus	83179-83304 24404-24521
	405268 405701	4156151 4263751	Plus	93243-93364
	401965	3126781	Minus	18239-18389,19921-20076
70	404835	6970743	Plus	85462-85684,88139-88287,90338-91018,9482
	401127	8699701	Minus	88327-88458,96150-96266
	406161	7144954	Plus	16666-16836
	402728	9211639	Plus	3192-3569,4267-4728
75	402897	8570339	Plus	61939-62241,64304-64615,65140-65391 43742-43671
13	404739 404405	8217493 7329316	Plus Minus	42742-43671 47543-47928
	404406	9966243	Plus	183917-184042
	402212	7689783	Minus	69382-69936
	405752	9212305	Plus	91392-91528
80				

TABLE 59A: ABOUT 201 GENES UPREGULATED IN MELANOMA METASTASES FROM PATIENTS WITH PROGRESSIVE DISEASE RELATIVE TO MELANOMA METASTASES FROM PATIENTS WITH LIMITED DISEASE

PCT/US02/29560 WO 03/025138

Table 59A lists about 201 genes upregulated in melanoma metastases from patients with progressive disease relative to melanoma metastases from patients with limited disease. Genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Unique Eos probeset identifier number

ExAccn: Exemplar Accession number, Genbank accession number

UniquenelD: Uniquene umber

Uniquene Title: Unique gene title

R1: 90th percentifier of Alls for metastases from nationts with progression disease divided by the D0th percentifier of Alls for metastases from nationts with trivial

5

Unique of normalization from the control of the state of R1:

uscase 90th percentile of Als for metastases from patients with progressive disease divided by the 90th percentile of Als for metastases from patients with limited disease, where the 15th percentile of normal tissue Als was subtracted from both the numerator and denominator 10 R2:

		disease	e, where the 1501	beloailile of normal basise via was adoptioned norm outside in		-
	Pkey		UnigenelD	Unigene Title	R1	R2
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	8.58 7.43	13.77 5.91
15	448966		Hs.86149	phosphoinositol 3-phosphate-binding prot	7.43	4.56
	440099		Hs.6909	DKFZP564G202 protein gap junction protein, beta 2, 26kD (conn	6.91	3.51
	431211 420859	M86849 AW468397	Hs.323733 Hs.100000	S100 calcium-binding protein A8 (calgran	6.90	6.44
	418067	A1127958	Hs.83393	cystatin E/M	6.62	10.34
20	422156	W72424	Hs.112405	S100 catcium-binding protein A9 (calgran	6.47	13.26
	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	6.25	3.41
	401780			NM_005557°:Homo sapiens keratin 16 (foca	6.10 5.97	4.24 6.60
	437191	NM_006846	Hs.331555	serine protease inhibitor, Kazal type, 5	5.89	3.57
25	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1 desmoplakin (DPI, DPII)	5.82	3.51
25	412636 417124	NM_004415 BE122762	Hs.25338	ESTs	5.16	3.16
	430686	NM_001942	Hs.2633	desmoglein 1	5.03	3.57
•	421733	AL119671	Hs.1420	fibroblast growth factor receptor 3 (ach	4.84	4.15
	422192	AA305159	Hs.113019	fts485	4.79 4.33	4.59 · 2.37
30	407366	AF026942	Hs.17518	gb:Homo sapiens cig33 mRNA, partial sequ	4.33 4.28	4.79
	429493	AL134708	Hs.145998	ESTs S100 calcium-binding protein A8 (calgran	4.23	4.82
	456525	AW468397	Hs.100000	Horno sapiens, Similar to RIKEN cDNA 1700	4.23	3.69
	409010 410748	A1648675 BE383816	Hs.12532	chromosome 1 open reading frame 21	4.11	2.33
35	409760	AA302840	110.72002	gb:EST10534 Adipose tissue, white I Homo	4.06	3.65
55	424670	W61215	Hs.116651	epithelial V-like antigen 1	4.02	4.07
	417366	BE185289	Hs.1076	small proline-rich protein 18 (cornifin)	3.97	4.71 5.08
	418663	AK001100	Hs.41690	desmocollin 3	3.95 3.93	5.85
40	402075		U- DOCE	ENSP00000251056*:Plasma membrane calcium matrix metalloproteinase 7 (matrilysin,	3.90	3.19
40	428330	L22524	Hs.2256 Hs.180878	Reportein lipase	3.87	3.21
	427809 413859	M26380 AW992356	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	3.85	5.75
	431048	R50253	Hs.249129	cell death-inducing DFFA-like effector a	3.80	3.10
	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (	3.79	3.36
45	421485	AA243499	Hs.104800	hypothetical protein FLJ10134	3.67	3.35 4.14
	429852	AB010445	Hs.225948	small inducible cytokine subfamily A (Cy	3.65 3.65	3.62
	418686	Z36830	Hs.87268	annexin A8 calponin 1, basic, smooth muscle	3.64	3.18
	448429	D17408	Hs.21223 Hs.13234	ESTs	3.60	4.10
50	422963 428874	M79141 W32133	Hs.194366	transthyretin (prealbumin, amytoidosis t	3.58	3.97
50	401785	1132130	12.10.1555	NM_002275*:Homo sapiens keratin 15 (KRT1	3.58	5.05
	454117	BE410100	Hs.40368	adaptor-related protein complex 1, sigma	3.56	1.92
	419329	AY007220	Hs.288998	S100-type calcium binding protein A14	3.54 3.53	5.62 4.70
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	3.52	8.33
55	417515	L24203	Hs.82237	ataxia-tetangiectasia group D-associated chromosome 1 open reading frame 21	3.51	2.32
	430376 454229	AW292053 AW957744	Hs.12532 Hs.278469	lacrimal profine rich protein	3.50	3.12
	401781	A11331144	115.270405	Target Exon	3.45	3.57
	408000	L11690	Hs.198689	bullous pemphigoid antigen 1 (230/240kD)	3.45	5.07
60	431567	N51357	Hs.260855	Homo sapiens cDNA: FLJ21410 fis, clone C	3.44	5.03
	419648	T73661	Hs.91877	thyroid hormone responsive SPOT14 (rat)	3.42 3.41	7.72 2.65
	414798	AI286323	Hs.97411	hypothetical protein MGC12335 ESTs, Moderately similar to ZN91_HUMAN Z	3.41	5.03
	442315		Hs.7956 Hs.8364	Homo sapiens pyruvate dehydrogenase kina	3.32	2.86
65	442498 410883		Hs.66742	CCL17 chemokine (TARC) (SCYA17)	3.28	3.18
05	418026		Hs.83213	fatty acid binding protein 4, adipocyte	3.26	3.10
	453309		Hs.32949	defensin, beta 1	3.24	3.64
	420783		Hs.99923	lectin, galactoside-binding, soluble, 7	3.21	3.64 4.37
	409601		Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	3.19 3.16	5.48
70	413163		Hs.75216	protein tyrosine phosphatase, receptor t Homo sapiens cDNA FLJ14476 fis, clone MA	3.15	3.60
	452101		Hs.10844 Hs.74304	periplakin	3.15	3.98
	412633 407839		Hs.161566	ESTs	3.15	4,11
	427318		Hs.175783	zinc transporter	3.11	3.58
75	427899		Hs.332053	serum armytoid A1	3.10	3.53
	421948	L42583	Hs.334309	keratin 6A	3.08	2.75
	452744	AI267652	Hs.246107	Homo sapiens mRNA; cDNA OKFZp434E082 (fr	3.05 3.04	2.99 3.02
	410001		Hs.57771	kalifikrein 11 carboxypeptidase E	3.00	2.40
80	413435		Hs.75360 Hs.184641	fatty acid desaturase 2	2.98	5.22
οU	428500 410099			KIAA0036 gene product	2.97	2.05
	43767			inositol(myo)-1(or 4)-monophosphatase 2	2.93	3.45
	41383		Hs.249163	fatty acid hydroxylase	2.93	4.78
				627		

	446068	AL049801	Hs.13649	Novel human gene mapping to chomosome 13	2.89	2.93
	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	2.88	3.14
	428398	AI249368	Hs.98558	ESTs	2.88	2.05
_	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	2.86	2.12
5	427919	AA173942	Hs.326416	Homo sapiens mRNA; cDNA DKFZp564H1916 (f	2.84	2.98
	412676	NM_000165	Hs.74471	gap junction protein, alpha 1, 43kO (con	2.83	2.82
	428695	A1355647	Hs.189999	purinergic receptor (family A group 5)	2.83	2.37
	446989	AK001898	Hs.16740	hypothetical protein FLJ11036	2.62	2.73
10	428471 416305	X57348	Hs.184510	stratifin	2.79	3.31
10	433147	AU076628 AF091434	Hs.79187 Hs.43080	coxsackie virus and adenovirus receptor	2.79	3.72
	412326	R07566	Hs.73817	platelet derived growth factor C small inducible cytokine A3 (homologous	2.77 2.76	1.70 2.18
	425787	AA363867	Hs.155029	ESTs	2.75	2.42
	450172	NM_005864	Hs.24587	signal transduction protein (SH3 contain	2.75	2.36
15	421773	W69233	Hs.112457	ESTs	2.73	5.59
	408536	AW381532	Hs.135188	ESTs	2.73	5.17
	437143	AW204056	Hs.8917	EST8	2.72	1.84
	452862	AW378065	Hs.8687	ADAMTS2 (a disintegrin-like and metallo	2.70	1.82
20	418394	AF132818	Hs.84728	Kruppel-like factor 5 (intestinal)	2.69	4.62
20	410325	AB023154	Hs.62264	KIAA0937 protein	2.69	2.32
	447164 444984	AF026941 H15474	Hs.17518 Hs.132898	vipirin; similar to inflammatory respon	2.69	3.74
	434727	H43374	Hs.7890	fatty acid desaturase 1 Homo sapiens mRNA for KIAA1671 protein,	2.67 2.65	2.36 1.78
	420876	AA918425	Hs.177744	ESTs	2.64	7.26
25	426106	AI678765	Hs.21812	EST8	2.64	2.51
	419517	AF052107	Hs.90797	Homo sapiens clone 23620 mRNA sequence	2.64	2.66
	409509	AL036923	Hs.322710	ESTS	2.62	2.09
	426354	NM_004010	Hs.169470	dystrophin (muscular dystrophy, Duchenne	2.62	2.68
20	432503	AA551196	Hs. 188952	ESTs	2.62	4.64
30	409341	AI963376	Hs.12532	chromosome 1 open reading frame 21	2.62	1.74
	421116	T19132	Hs.101850	retinol-binding protein 1, cellular	2.62	2.90
	456247	R09746		gb:y127d10.r1 Soares fetal liver spleen	2.61	3.43
	414217	AJ309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	2.60	3.84
35	439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	2.58	3.49
33	440659 459710	AF134160 AI701596	Hs.7327 Hs.121592	claudin 1 ESTs	2.57 2.57	3.97 3.59
	430937	X53463	Hs.2704	glutathione peroxidase 2 (gastrointestin	2.56	3.35
	433882	U90441	Hs.3622	procollagen-proline, 2-oxoglutarate 4-di	2.51	3.75
	427666	AI791495	Hs.180142	calmodulin-like skin protein (CLSP)	2.51	3.02
40	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	2.47	3.53
	449550	AA353125	Hs.184721	ESTs	2.43	4.22
	424675	NM_005512	Hs. 151641	glycoprotein A repetitions predominant	2.40	6.22
	442000	H38671	Hs.8071	KIAA0735 gene product; synaptic vesicle	2.38	3.14
45	427122	AW057736	Hs.323910	HER2 receptor tyrosine kinase (c-erb-b2,	2.36	3.59
45	420039	NM_004605	Hs.94581	suffotransferase family, cytosolic, 2B,	2.36	2.91
	412477	AA150864		microsomal glutathione S-transferase 1	2.34	4.15
	450693	AW450461	Hs.203965	ESTs	2.32	3.93
	406433 423017	A14/1707C4	Hs.227948	Target Exon	2.29	3.20
50	423017	AW178761 L10343	Hs.112341	serine (or cysteine) proteinase inhibito	2.24 2.23	4.40 4.87
30	421314	BE440002	Hs.180324	protease Inhibitor 3, skin-derived (SKAL Horno sapiens, clone IMAGE:4183312, mRNA,	2.23	4.22
	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	2.22	5.71
	442503	AF147078	Hs.150853	p53-responsive gene 5	2.21	4.86
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	2.19	3.90
55	442572	AI001922	Hs.135121	hypothetical protein FLJ22415	2.16	2.87
	413278	8E563085	Hs.833	interferon-stimulated protein, 15 kDa	2.13	3.27
	414521	D28124	Hs.76307	neuroblastoma, suppression of tumorigeni	2.09	5.28
	428899	AA744610	Hs.194431	palladin	2.08	3.76
60	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	2.06	3.09
00	439496 450423	BE616501	Hs.32343	Homo sapiens, Similar to RIKEN cDNA 1110	2.05	2.88
	444105	AA486735 AW189097	Hs.31869	sialoadhesin ESTs	2.02 2.01	3.04 3.05
	430410	AF099144	Hs.347933	typtase beta 1	2.01	3.71
	409453	A1885516	Hs.95612	ESTs	2.01	4,34
65	429655	1148959	Hs.211582	myosin, light polypeptide kinase	2.00	5.28
	432374	W68815	Hs.301885	Homo sapiens cONA FLJ11346 fis, clone PL	1.99	3.59
	447990	BE048821	Hs.20144	small inducible cytokine subfamily A (Cy	1.92	4.16
	451541	BE279383	Hs.26557	plakophilin 3	1.89	3.90
~~	425206	NM_002153	Hs.155109	hydroxysteroid (17-beta) dehydrogenase 2	1.89	3.29
70	410197	NM_005518	Hs.59889	3-hydroxy-3-methylglutaryl-Coenzyme A sy	1.84	3.04
	401760	4490000	15-130000	Target Exon	1.84	3.32
	427579	AA366143	Hs.179669	hypothetical protein FLJ20637	1.83	4.69
	424263	M77640	Hs.1757	L1 cell adhesion molecule (hydrocephalus	1.83	2.96
75	452208 420074	AA024792 AA253425	Hs.31895 Hs.190074	hypothetical protein MGC4093 ESTs	1.82 1.81	3.70 2.90
7.5	420074	A1620463	Hs.347408	hypothetical protein MGC13102	1.79	2.90 3.65
	427540	R12014	Hs.20976	ESTs	1.77	2.92
	429259	AA420450	Hs.292911	Plakophilin	1.76	3.65
	422106	D84239	Hs.111732	Fc tragment of IgG binding protein	1.75	4.06
80	453556	AA425414	Hs.33287	nuclear factor I/B	1.74	3.07
	436895	AF037335	Hs.5338	carbonic enhydrase XII	1.73	3.22
	406851	AA609784		major histocompatibility complex, class	1.73	3.96
	444726	NM_006147		interferon regulatory factor 6	1.71	3.65

				and the state of t	1,71	4.13
	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	1.68	3.61
	446051	BE048061	Hs.37054 Hs.46320	ephrin-A3 Small proline-rich protein SPRK [human,	1.67	3.00
	408522 450835	AI541214 BE262773	Hs.25584	hypothetical protein FLJ10767	1.66	3.11
5	432004	BE018302	Hs.2894	placental growth factor, vascular endoth	1.66	3.23
,	431179	AI338644	Hs.195432	aldehyde dehydrogenase 2 family (mitocho	1.64	3.29
	415213	NM_002933	Hs.78224	ribonuclease, RNase A family, 1 (pancrea	1.57	3.94
	423184	NM_004428	Hs.1624	ephrin-A1	1.56	2.88 2.92
• •	414694	NM_015362	Hs.76907	HSPC002 protein	1.56 1.56	2.92
10	458746	AI380797	Hs.158992	ESTs	1.55	3.75
	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	1.54	4.56
	438367	N79688	Hs.204354	ras homolog gene family, member 8 C5001632*:gij10645308 gb AAG21430.1 AC00	1.53	3.99
	403903	wmnoco	Hs.21299	ESTs, Weakly similar to AF151840 1 CGI-8	1.52	3.16
15	445656 443604	W22050 C03577	Hs.9615	myosin regulatory light chain 2, smooth	1.50	4.25
13	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	1.50	3.35
	415274	AF001548	Hs.78344	myosin, heavy polypeptide 11, smooth mus	1.49	3.21
	418226	AA424202	Hs.83834	cytochrome b-5	1.49	3.90
	454194	BE141599		gb:QV2-HT0083-071299-018-h01 HT0083 Homo	1.48	2.98
20	434879	M34572	Hs.159263	collagen, type VI, alpha 2	1.46	3.26 4.00
	418400	BE243026	Hs.301989	KIAA0246 protein	1.46 1.45	2.94
	409178	BE393948	Hs.50915	kallikrein 5	1.44	3.18
	433662	W07162	Hs.150826	RAB25 RAB25, member RAS oncogene family	1.43	3.07
25	429002	AW248439	Hs.2340	junction plakoglobin matrix metalloproteinase 2 (gelatinase A	1.40	4.61
25	422087	X58968	Hs.111301 Hs.4213	hypothetical protein MGC16207	1.38	3.11
	452934 417483	AA581322 BE549343	Hs.82208	acyl-Coenzyme A dehydrogenase, very long	1.37	4.32
	417403	BE613835	Hs.181159	Homo sapiens mRNA; cDNA DKFZp434F0217 (f	1.37	2.99
	425184	BE278288	Hs.155048	Lutheran blood group (Auberger b antigen	1.36	<b>3.17</b> .
30	407143	C14076	Hs.332329	EST	1.36	2.99
-	416950	AL049798	Hs.80552	dermatopontin	1.35	3.39
	406799	AA908548		gb:og83g12.s1 NCI_CGAP_Ov8 Horno sapiens	1.34	3.17 3.30
	442599	AF078037	Hs.324051	RetA-associated inhibitor	1.33 1.32	2.89
2.5	413659	BE155647		gb:PM2-HT0353-130100-002-e09 HT0353 Homo	1.32	3.50
35	454478	AW805749		superoxide dismutase 2, mitochondrial	1.29	3.57
	404467	4.4050030	Hs.29759	Target Exon RNA POLYMERASE I AND TRANSCRIPT RELEASE	1.28	3.00
	452516	AA058630 AA417813	Hs.44208	hypothetical protein FLJ23153	1.27	3.05
	412524	U20982	Hs.1516	insulin-like growth factor-binding prote	1.24	2.86
40	422354 406711	N25514	Hs.77385	myosin, light polypeptide 6, alkati, smo	1.24	3.29
70	450796	NM_001988		envoplakin	1.23	3.21
	431526	Y10129	Hs.258742	myosin-binding protein C, cardiac	1.23	3.65
	452791	AA227581	Hs.30634	hypothetical protein FLJ20509	1.22	2.90
	406742	AI468091	Hs.279860	tumor protein, translationally-controlle	1.19	3.47
45	406712	M31212	Hs.77385	myosin, light polypeptide 6, alkali, smo	1.18	2.91
	443672	AA323362	Hs.9667	butyrobetaine (gamma), 2-oxoglutarate di	1.10	3.50 2.99
	413048	M93221	Hs.75182	mannose receptor, C type 1	1.00 1.00	2.91
	453165	S74727	Hs.32042	aspartoacylase (aminoacylase 2, Canavan	1.00	2.31
50						
50	TABLE	598:	Con ambanatia	inalifies number		
	Pkey:		ique Eos probeset id ne cluster number	enute noncei		
	CAT nui Accessi		nbank accession nu	mhers		
	WCC622I	JR1. GC	IIUQIN QUUSSION IIU	mboro -		
55	Pkey	CAT Numb	er Accession			
	412636		1477020 MM O	4415 AF139065 BG681115 BG740377 BI712964 BG00065	S AA128470 B143	8324 H27408 BE931630 BE16/165 AW3/082/ AW3/0813
	***************************************		INCOME DOCUME	ner negaeta eeconcaa prittatta Bitteskii HMASSAIII	HALISIZAN AVVII	I I ME AVV ZUDI DE CATADI DI DI CATADI DE LOS LOS LOS
			BF149266 BE9	40187 BI060445 BI060444 BF350983 BE720095 BE720069	BE715154 BE08	2084 BE0825/6 BE004047 AAGS1316 GIGGS174 BE115010
			BE713548 AW	170253 BE160433 BI039775 AW886475 BM462504 BE9317 23489 BE819009 BF381184 BE715956 R58704 AA852212	34 BF149264 AA	340/// BF381103 BG021/3/ AD12/200 AV1304033
60			BF993352 BG2	23489 BE819009 BF381184 BE715955 K58704 AA652212	AVV300300 BRUSU : A1061766 A1474	5518 AW804674 BF752969 BE837009 BE925826 BF149265
			***** ***** PE	140000 414477013 DEB73E70 AW178000 RENRYSSE REATE	rrr rforroga ri	1-547776 REUKZSO7 BEUGZS14 BEUGZSOS BEG73033
					5153 RF 182041 F	4F/A4471 KF1X49/U BF03330Z BE104333 DF044434
65			DC44444 DC4	124 5 40 DECCCOOR DECCCOOR DE 194024 DE 150646 RE7146	77 RE184948 RG	986845 AA131128 AA099891 W39488 CU47 19 DF 070124
05			00000044 4144	700204 41 602446 BE140760 BE706067 BE706066 RF7069	KR AWRAR723 AV	W376699 AW3/681/ AW3/669/ BG00509/ BF/71113
			DECCESS 4 444	0.40074 AMPRETOR AMPROTOD AMPRIONZA AMPELIAL REQ	17775 RED94211.	AW947139 RE865474 RE183187 BE130021 DC113003
			00343003.003	143000 DE 130015 AMIZOO 300 DE 273345 DE 088676 RE 7059	139 AW752599 RI	C/N15197 HF350086 BE/15196 BE/15133 BF/32399
			00000047 000	134400 PE753400 PE006561 PC959922 RE094833 RE0947	AR REOGASR3 AW	/3/7699 AW60/238 BE082519 AW3///00 DF34340/
70			Al190590 Al55	4403 Al392926 AU158477 BI467252 AU159919 Al760816 E	3F082516 AI4391	01 AA451923 AI340326 AI330973 BI791333 AI700903
			AI142882 AA0	39975 AA946936 AA644381 BM314884 AA702424 Al41761	2 AW190555 AIZ	205/3 AI304/72 AI270343 AI027303 AA332300 AI311702
			AW166807 AI	346078 W95070 AA149191 AA026864 AI830049 AW780435	A1078449 A1819	984 AIB38282 BI400308 AIB00304 AID23332 AAD2004
			AA703232 AA	558154 AA515500 AW192085 AA918281 T77861 AI927207 782109 W19287 W02156 AW150038 AA022701 T87181 H4	A1200203 BF082	Engos 12 AMMANGO A1270027 A1635878 AA128330
76			AA056527 AA	782109 W19287 W02156 AW150038 AA022701 107101 FF 706078 R20904 BG680059 BG676647 BF764409 AA02665	4403 A310434 B	2796 RG287391 AW798780 BE706045 BE926470
75			BG681425 BE	706078 R20904 BG680059 BG676647 BF764405 A402665 087996 BE002273 AW879451 AI571075 BE067786 AV721:	320 AIN22862 N2	9754 C03378 N84767 AA131077 H30146 BE714290
			AICOCOCO AIC	-none ainacene alaianceaa alborraco alerbert DEORATA	なたいらファマア なにろりり	94RR &&747685 AW/98883 AW1U3521 BF9691/3
			A14/0000070 Of	·^^^*** nc+0e7en 0C7+40C4 0C7+30N3 RE713R6R RF713	763 RG950164 R	F713810 AW365151 BG955489 BE005272 BF915937
			414/2CE440 A1	nacaar penaaran wwasaria pens <i>akka</i> Ri770853 RG679/	IOG RG740X32 RI	(#XX10X/ KC4698430 AA433100 16/26/ BE696209 BE696410
80			01/00/493 DE/	neara nearasas AW301012 RE025515 RG677012 RG741	970 AAD2648D RI	F705999 BG67/157 BE009090 BG681378 BE712291
ÇÜ			DC0C1400 DC	*e>ooo4 DIAAOA1 AA337270 AW384371 AW847442 RI058I	659 RF813665 W	95048 W25458 AW1///86 AA025851 BE931/33 BF15463/
			BG949393 BE	714441 AW996245 BE711801 AJ284090 BE064323 BE719	390 BE940148 BC	G991212 BF375714 BF349522 BG996267 T48793 BI013292
			BE001925 AV	v365156 AW365154 AW606653 BF763109 BE931637 BE16	7181 BE/138/9	BF354008 BF678726 H90899 AW365145 W38382 AI498487
				579		

	409010	10331_1	AA059411 A175	51714 BM014781 BG542863 BC 6263 A494075 A1572127 AAA2 9169 A1758175 AA976350 BG7 56883 BF435859 AA196423 A1	0992 BF436083 Al648675 AA 01414 BF057794 AW13S598.	.878813 BI488614 E AA062583 BI54963	3G700886 AA12860 1 AI185077 AA9338	9 AV 102879 AA 731146 AI 360336 179 AW 024454 AA 193289 AA 045194		
5	409760 410099	865166_1 16732_1	AKOSSETA AVA	016 T92950 AU184997 AA0775 B65247 AV751598 AA290926 R	53043 AA331387 AK056148 P	BI917678 BG819395	5 BG911971 BG820 0 At 563737 RG029	167 Al174254 AA348720 AA364503 709 W52882 Al439658 BE551237		
10			AA283724 BF1 BE327043 AA7 AA211402 AW	714279 AW893230 AA081774 H24222 AV727176 BF875715 AA081630 BE000834 AA334880 AL563737 BG029709 W52882 A4439658 BE551237 283724 BF109530 A457096 AI805992 BE467736 AA693467 AI697593 AI887883 AI167419 AW901980 AW901768 BE702179 AA484549 T23811 327043 AA716027 AA917004 AA167714 BF339675 AA084618 A418634 T31586 AA436630 AI69472 AA706191 AI422304 AI204899 AI041169 211402 AW827081 AA788593 T32736 AI767935 AA747914 T03534 AW959843 AL119527 B6327037 AW901982 AW993370 AW901977 AW902071 0090 N79906 D52685 T07735 BE702069 BE702172 T08671 BE767121 BE767117 BE767113						
15	456247 412477	2142387_1 8669_2	R10170 R0974 AI220117 AI85 BF594181 BF1 AI281153 N511							
20		G10700 4	AI247247 T956 AA804572 AI0 AI382839 AA1	564 BF593863 A1749637 AWO8 B5786 AA994396 AA991209 AA 94837 AA406284 A1250750 R3	3541 AA991294 AA887452 AK 1948663 AA929054 AA927952	073726 AA633132 A	VA629674 AA62964	9 AA629656 AA578595 AI168758 267 AW384129 BF744400 AA194110		
25	444105 406851 444726	649788_1 0_0 3503_2	AA609784 R93 BG285809 BE AW188320 All AW664668 AV AW849405 AV	189097 A1123917 A1123926 609784 R97304 285809 BE940673 BG432524 BE157554 BG676980 AU144284 A1745383 AU159045 A1693500 AW293668 AW371408 BE856107 A1338042 285809 BE940673 BG432524 BE157554 BG676980 AU144284 A1745383 AU159045 A1693500 AW293668 AW371408 BE856107 A1338042 7188320 A1698246 BE673290 AW297653 AA156532 A1017342 A1916754 A1190644 A1184302 AA857671 BE857018 A1307420 A1318157 AW204327 664668 AW2774339 AA582788 A1345741 AW301433 A1873468 AW137388 BF718731 BF718413 AA877495 BF001575 A1824693 AW849604 718495 A1889874 A1744241 BE71713 BE717108 BE715584 A1872527 AA029457 C00338 A1469558 BE715577 AA045413 BF843813						
30	454194 406799 413659 454478	171445_1 0_0 1526081_1 4273_16	BE141599 AV AA908548 BE155647 BE	7845895 AW178095 BE140914	BE140909 AW178107 AW178	3094 AW845883 BF	349267 AW845898 .	AW845811 AW845814 BF767720		
35	TABLE 59 Pkey: Ref:	Unix Seq seq	uence source. Tuence of human	sponding to an Eos probeset he 7 digit numbers in this colum thromosome 22" Dunham, et al.	(1999) Nature 402:489-495.	numbers. "Dunham,	et al." refers to the	publication entitled "The DNA		
40	Strand: Indicates DNA strand from which exons were predicted.  NL position: Indicates nucleotide positions of predicted exons.									
45	Pkey 401780 402075 401785 401781	Ref 7249190 8117407 7249190 7249190	Strand Minus Plus Minus Minus	Nt_position 28397-28617,28920-29045,291 121907-122035,122804-12292 165776-165996,166189-16631 83215-83435,83531-83656,837	1,124019-12416 4,166408-16656		·			
73	406433 401760 403903 404467	.9256507 9929699 7710671 8077630	Plus Plus Minus Minus	58094-58565 83126-83250,85320-85540,94 101165-102597 24951-25853						
50	404401	00//030	(em in 2	24331-23000						
	Toble 60	A liete about 53	tchingson sonos	ULATED IN BENIGN NEVI REI	nal fissues. These genes wen	e selected from 596	80 probesets on the	Eos/Affymetrix Hu03 Genechip array.		
55	Gene exp Pkey:	ression data fo	x each probesel ( inue Ens norbese	obtained from this analysis was It identifier number	expressed as average intensity	y (AI), a normalized	value renecting the	relative level of mRNA expression.		
33	ExAcon:	Ex	emplar Accession	number, Genbank accession n	umber					
	Unigenel		igene number							
	Unigene R1;	200	igene gene title erage of benign n	evi Als divided by the 90th perc	entile of normal tissue Als					
60	R2:	av	erage of benign n merator and deno	evi Als divided by 90th percenti	e of normal tissue Als, where	the 15th percentile o	of normal tissue Als	was subtracted from both the		
	Pkey	ExAcon	UnigenelD	Unigene Title		R1	R2 5.62			
65	430377	NM_00192 AF237621	2 Hs.301865 Hs.80828	dopachrome tautomera keratin 1 (epidermolytic	• •	8.69 8.37	5.62 13.47			
05	409601 430686	NM_00194		desmoglein 1	Hyperica alasasy	7.26	4.78			
	406964	M21305		FGENES predicted nov		6.50	3.73			
	426555	NM_00037		tyrosinase (oculocutani small inducible cytokini		6.40 6.23	7.35 8.85			
70	429852 430822	AB010445 AJ005371	Hs.225948 Hs.248017	glyceraldehyde-3-phos		5.49	4.32			
, ,	420208	BE276055	Hs.95972	silver (mouse homolog		5.45	9.84			
	431360	NM_00042		loricrin		3.88 3.80	3.00 9.04			
	421773 438380	W69233 T06430	Hs.112457 Hs.6194	ESTs chondroitin sulfate prof	eoglycan BEHAB/b	3.60 3.74	4.23			
75	438380	BE041395		ESTs, Weakly similar t		3.21	2.34			
	420798	W93774	Hs.99936	keratin 10 (epidermoly	ic hyperkeratosis	3.08	3.20			
	442503	AF147078	Hs.150853	p53-responsive gene : dihydropyrimidinase-li)		2.88 2.88	5.01 2.85			
	405451 452240	AI591147	Hs.61232	ESTs		2.86	1.90			
80	402525			NM_002699*:Homo sa	piens POU domain, clas	2.78	2.72			
	413171			tyrosinase-related prof	ein 1 to RIKEN cONA 1110	2.65 2.55	5.58 3.18			
	439496 422656			LIM homeobox protein		2.45	2.38			
	422000	,		_ ,						

	453317	NM_002277	Hs.41696	keratin, hair, acidic,1	2.34	3.76	
	4207B3	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7	2.33 2.28	2.43 2.00	
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	2.28	2.50	
5	427666	AI791495	Hs.180142	calmodulin-like skin protein (CLSP) gb:an03c03.x1 Stratagene schizo brain S1	2.25	1.85	
3	459702 451668	A1204995 Z43948	Hs.326444	cartilage acidic protein 1	2.23	2.42	
	431703	AA514264	Hs.4437	triosephosphate isomerase 1	2.15	2.20	
	453511	AL031224	Hs.33102	AP-2 beta transcription factor	2.13	2.20	
	401780			NM_005557*:Homo sapiens keratin 16 (foca	2.13 2.11	2.02 2.02	
10	416640	BE262478	Hs.79404	neuron-specific protein	211	1.46	
	444105	AW189097	41- 0070E	ESTs Ksp37 protein	2.09	1.52	
	428748 418067	AW593206 AI127958	Hs.98785 Hs.83393	cystatin E/M	2.09	2.32	
	417017	AA976064	Hs.180842	ribosomal protein L13	2.08	2.52	
15	401781	74.000		Target Exon	2.02	2.03	
	407178	AA195651		AP-2 beta transcription factor	1.88 1.84	2.17 2.38	
	452308	AI167560	Hs.61297	ESTs	1.83	3.26	
	429348	AJ242859	Hs.199731	Langerhans cell specific c-type lectin Target Exon	1.69	2.10	
20	402880 434276	AF123659	Hs.93605	leucine zipper, putative tumor suppresso	1.69	2.20	
20	401963	AI 125003	1.0.0000	NM_006311:Homo sapiens nuclear receptor	1.66	2.02	
	424010	AL080188	Hs.137556	Homo sapiens mRNA; cDNA DKFZp434A132 (fr	1.65	2.05 2.83	
	432800	BE391046	Hs.278962	AIM-1 protein	1.61 1.57	2.03	
0.5	400328	X87344	47704	transporter 2, ATP-binding cassette, sub Homo sapiens, clone IMAGE:3937015, mRNA,	1.55	2.42	
25	412580	AA113262	Hs.17901 Hs.172965	ESTs	1.53	2.21	
	435292 408561	N20514 AI308037	Hs.84120	hypothetical protein MGC13016	1.52	2.01	
	427923	AW274357	Hs.301406	hypothetical protein PP3501	1.47	2.71	
	447763	BE619911	Hs.115803	hypothetical protein	1.40	2.10 2.36	
30	454478	AW805749		superoxide dismutase 2, mitochondrial	1.30 1.24	2.02	
	427289	AJ097346	044500	phosphoserine aminotransferase G6C protein	1.20	2.18	
	430513	AJ012008 X72925	Hs.241586 Hs.69752	desmocollin 1	1.00	2.43	3
	411388	Al 2923	115.03132	555:110-5-117			
35	TABLE 6	0B:					
	Pkey:		ique Eos probeset i	dentifier number			
	CAT nun		ne cluster number				
	Accessio	n: Ge	nbank accession n	impers			
40	Pkey	CAT Numbe	er Accession				
70	431089	125941_2	DC0/0189 AW	063489 AA715980 BF001091 BF880066 AA666102 AA6	21946 AA491826		
	459702	539529_1	BG207209 BE	166299 A1204995 BG199355 AW969908 AA528756 AW4	4D776 B1044354		
	444105	649788_1		23917 AI123926			
45	407178	683007_1	AW235123 AA	THE PARTY OF THE P	380449 AW79446	6 AW794	538
45	454478	4273_16			1/10510 AVV.1/1038	L AAST DJ	27 VII 35 1 2 1 2 VII 405 452 VII 00 2000 1 4 90000 1
	427289	1820_2					
			AV703420 H6	505495 AA515380 BG760793 AW370651 BG760223 AW 5047 AA485582 R56186 H90385 R55913 BI261497 BI011 953 BF933343 BF932871 H08334 R14012 BF897622 T5	5403 BF3/6945 I / 0916 BC698803 R	2340083	720199
50			BI018121 N41	953 BF933343 BF9328/1 H08334 K14012 BF63/022 13	0010 000000000	, 0 10000	
	TABLE	enc-					
	Pkey:		nique number corre	sponding to an Eos probeset			and the state of the control of the
	Ref:	e.	Time entire	he 7 digit numbers in this column are Genbank Identifier (	Gi) numbers. "Our	mam, et a	al. refers to the populacement entitued. The one
55		SE	equence of human (	thromosome 22" Dunham, et al. (1999) Nature 402:469-4:	93.		
	Strand:			from which exons were predicted. positions of predicted exons.			
	Nt_pos	mon: In	igicates mucieoude	positions or predicted exerts.			
	Pkey	Ref	Strand	Nt_position			
60	405451		Minus	145949-146227			
	402525		Minus	19748-20683			
	401780		Minus	28397-28617,28920-29045,29135-29296,2941 83215-83435,83531-83656,83740-83901,8423			
	40178		Minus Minus	41555-41865			
65	40288 40196		Plus	51382-51521			
03	40130	0120700					
				TO DOMARY ME	ZAMONA I		
				BULATED IN BENIGN NEVI RELATIVE TO PRIMARY ME and in benign nevi relative to primary metanomas. Genes to		59680 or	robesets on the Eos/Affyrnetrix Hu03 Genechip array.
70	Table	61A lists about	/2 genes upregulat	ed in benigh nevi relative to primary metallicinas. Genes obtained from this analysis was expressed as average into	ensity (Al), a norma	alized val	ue reflecting the relative level of mRNA expression.
70	Gene Pkey:	expression data	Unique Eos probes	et identifier number			
	ExAcc		Exemplar Accession	number, Genbank accession number			
	Unige		Unigene number				
		oo Titlo:	Unigene gene title		na Ala		•
75	R1	4	average of benign r	evi Als divided by the 90th percentile of primary melanomeri Als divided by the 90th percentile of primary melanom	121 AlS 12 Als where the 1	5th neme	ntile of normal tissue Als was subtracted from both the
	R2		average of benigh f numerator and den		Drug whole to		
		'	INTEGRAL GIAL GET				
_	Pkey	ExAcon	UnigenelD	Unigene Title	R1		R2
80	43110		Hs.44	pleiotrophin (heparin binding growth fac	3.8 3.4		2.50 2.69
	42489		Hs.153684	trizzled-related protein small inducible cytokine subfamily A (Cy	2.9		3.25
	42985 4310			ESTs, Weakly similar to unknown protein	2.6		1.56
	4310	,, 50,0413		501			

	456034	AW450979	)	gb:UI-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su	2.73	3.00		
	417017	AA976064	Hs.180842	ribosomal protein L13	2.71	3.73		
	402880			Target Exon	2.56	3.55		
5	422656	AI870435	Hs.1569	LIM homeobox protein 2	2.45	3.38		
)	426451 423467	AI908165 AK000214	Hs.169946	GATA-binding protein 3 (T-cell receptor hypothetical protein FLJ20207	2.41 2.32	1.91 2.24		
	424797	AA622394		ribosomal protein S28	2.29	2.53		
	459702	Al204995	15.155177	gb:an03c03.x1 Stratagene schizo brain S1	2.25	2.19		
	406964	M21305		FGENES predicted novel secreted protein	2.24	1.65		
10	428748	AW593200	6 Hs.98785	Ksp37 protein	2.09	1.43		
	402525			NM_002699*:Homo sapiens POU domain, clas	2.06	2.03		
	415823	R81864	Hs.205103	ESTs	2.05	1.87		
	412432	AA126311		ESTs	2.05	2.48		
16	421733	AL119671		fibroblast growth factor receptor 3 (ach	2.03	2.20		
15	414876	AW95092		crystallin, mu	2.02	2.30		
	432306	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib	2.02 1.95	2.39 2.72		
	424010 453317	AL080188		Homo sepiens mRNA; cDNA DKFZp434A132 (Ir	1.95	2.66		
	453317 452887	NM_00223 AJ702223	77 Hs.41696 Hs.107253	keratin, hair, acidic,1 hypothetical protein DKFZp761F241	1.88	2.85		
20	410545	U32324	Hs.64310	interleukin 11 receptor, alpha	1.85	3.07		
20	400496	OJEJET	113.04010	ENSP00000224716*:GTP-binding protein SAR	1.84	2.09		
	406972	M32053		gb:Human H19 RNA gene, complete cds.	1.83	4.14		
	406266			Target Exon	1.75	2.38		
	414309	AK000639	Hs.75884	DKFZP586A011 protein	1.73	2.80		
25	416250	AA581386		hypothetical protein MGC10791	1,72	2.27		
	451849	Al199261	Hs.27191	hypothetical protein from clone 24796	1.70	2.09		
	441134	W29092	Hs.346950	cellular retinoic acid-binding protein 1	1.68	2.37		
	401963			NM_006311:Homo sapiens nuclear receptor	1.66	2.38		
••	430947	U01212	Hs.248153	olfactory marker protein	1.65	2.00		
30	413391	A1223328	Hs.75335	glycine amidinotransferase (L-arginine:g	1.63	2.18		
	406387			Target Exon	1.57	2.14		
	405776			cytochrome c-1	1.55	2.23		
	410677	NM_0032		tetranectin (plasminogen-binding protein	1.53	3.26		
26	406807	AA05760		ribosomal protein S9	1.53	2.67		
35	420438	AW40362		CD1C antigen, c polypeptide	1.52	2.09		
	422089	AA52317		ESTs, Weakly similar to SFR4_HUMAN SPLIC	1.52	2.66		
	456898	NM_0019	28 Hs.155597	D component of complement (adipsin)	1.48	2.57		
	402412	000000		Target Exon	1.48	2.42 3.48		
40	427795	BE26826		ribosomal protein L13	1.48 1.47	3.89		
40	452547	AA33529		adipose specific 2	1.46	3.14		
	414323	NM_0147		KIAA0273 gene product aldehyde dehydrogenase 3 family, member	1.45	2.09		
	425831	U46689 AL08024	Hs.159608 3 Hs.180920	ribosomal protein S9	1.40	2.86		
	457090	AF13738		plasmolipin	1.39	2.00		
45	445431 445636	AV 13736		ribosomal protein L29	1.38	2.08		
73	414682	AL02115		inhibitor of DNA binding 3, dominant neg	1.37	3.32		
	406845	AI567284		ribosomal protein L3	1.37	· 2.04		
	406808	AI690307		ribosomal protein S9	1.36	3.32		
	403986	7400000		Target Exon	1.34	2.09		
50	402218		•	NM_022165*:Homo sapiens Lin-7b protein (	1.31	2.16		
	400649			Target Exon	1.29	2.07		
	432647	AI80748	Hs.278581	fibroblast growth factor receptor 2 (bac	1.28	2.40		
	403211			NM_005400":Homo sapiens protein kinase C	1.26	2.13		
	452678	AI24313	Hs.164661	ESTs, Weakly similar to TGLX_HUMAN PROTE	1.26	2.14		
55	406889	D50310	Hs.79933	cyclin I	1.26	2.37		
	447299	AF04389	7 Hs.18075	chromosome 9 open reading frame 3	1.25	2.39		
	404406			Target Exon	1.24	2.09		
	432894	AW1676		brain specific protein	1.23	2.28		
۲۸	406757	T65957	Hs.77039	ATP synthase, H transporting, mitochondr	1.21	2.01 2.07		
60	425883	AL13770		Homo sapiens mRNA; cDNA DKFZp434K0322 (I	1.20 1.17	2.62		
	409726	AI47934		thyroid hormone receptor, alpha (avian e ribosomal protein S17	1.17 1.17	2.42		
	435398 444674	H87136 BE56220	Hs.5174 00 Hs.244	emino-terminal enhancer of split	1.16	2.02		
	402450	BEJOZZ	U NS.244	Target Exon	1.16	2.08		
65	406758	AA5523	26 Hs.77039	ATP synthase, H transporting, mitochondr	1.16	2.03		
03	431243	U46455	Hs.252189	syndecan 4 (amphiglycan, ryudocan)	1.13	2.23		
	407032	U73799	15.252105	ob:Human dynactin mRNA, partial cds.	1.10	2.01		
	402921	0,0,00		ENSP00000244047":Cadherin-like protein V	1.00	2.00		
	40252.							
70	TABLE 6	18:						
	Pkey:		Unique Eos probeset	identifier number				
	CAT nur	nber.	Gene cluster number					
	Accessio		Genbank accession r	numbers				
		•						
75	Pkey	CAT No	mber Accession					
	431089	125941	2 BG940189 AV	V063489 AA7.15980 BF001091 BF880066 AA666102 AA6	21946 AA491826			
	456034	685586	1 AA136653 AA	136656 AW450979 AA984358 AA809054 AW238038 AA4				
	459702	539529	1 BG207209 BE	166299 Al204995 BG199355 AW969908 AA528756 AW4				
	445636	8561_5	BF339388 AL	345516 BG391657 BE708967 BG026034 BE261703 H567	16 H65572 H93801	T48830 R96953 R9	:96989 R39707 BE867593 AA0	/90310
80			AA090672					
	TABLE	61 <b>C</b> :		according to the East number of				
	Pkey:		Unique number corre	sponding to an Eos probeset				
				592				

PCT/US02/29560 WO 03/025138

Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495. Indicates DNA strand from which exons were predicted.

Strand: Nt_position: Indicates nucleotide positions of predicted exons.

5	_			
-	Pkey	Ref	Strand	Nt_position
	402880	9926561	Minus	41555-41865
	402525	9800048	Minus	19748-20683
	400496	9743564	Plus	41515-41695
10	406266	7528342	Minus	2365-2518
	401963	3126783	Plus	51382-51521
	406387	9256180	Plus	116229-116371,117512-117651
	405776	7159748	Minus	105911-107251
	402412	7408036	Plus	75075-75679
15	403986	8576059	Plus	90692-91238
	402218	7689783	Ptus	127677-127886
	400649	8117705	Plus	93097-93792
	403211	7630841	Minus	159211-159369
	404406	7329316	Minus	47543-47928
20	402450	9796674	Plus	137536-137682,137920-138045
	402921	7981303	Minus	52242-52384,55599-55858,57124-57309,5963

TABLE 62A: ABOUT 121 GENES UPREGULATED IN BENIGN NEVI RELATIVE TO NORMAL SKIN
Table 62A lists about 121 genes upregulated in benign nevi relative to normal skin. These genes were selected from 59680 probesets on the Eos/Aflymetrix Hu03 Genechip array.
Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.
Pkey:
Unique Eos probeset identifier number
ExACCn:
Exemptar Accession number, Genbank accession number
Uniquene IIIe:
Uniquene gene title:
Uniquene gene title
R1
average of benign nevi Als divided by the 90th percentile of normal skin AIs
average of benign nevi Als divided by the 90th percentile of normal skin AIs, where the 15th percentile of normal tissue AIs was subtracted from both the
numerator and denominator 25

30

Ref:

numerator and denominator

35	Ot-m.	EuAann	UnicenelD	Unigene Title	R1	R2
33	Pkey 430377	ExAcon NM_001922	Hs.301865	dopachrome tautomerase (dopachrome delta	8.69	7.66
	430377	T06430	Hs.6194	chondroitin sulfate proteoglycan BEHAB/b	6.71	8.11
	406964	M21305	115.0134	FGENES predicted novel secreted protein	6.50	3.35
	426555	NM 000372	Hs.2053	tyrosinase (oculocutaneous albinism IA)	6.40	4.32
40	430822	AJ005371	Hs.248017	glyceraldehyde-3-phosphate dehydrogenase	5.16	4.12
40	430022	BE314524	Hs.78776	putative transmembrane protein	4.77	3.59
	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	4.63	4.99
	451668	Z43948	Hs.326444	cartilage acidic protein 1	4.62	6.04
	449644	AW960707	Hs.148324	ESTs	3.97	3.41
45	435056	AW023337	Hs.5422	alycoprotein M6B	3.42	2.29
7.7	433030	BE041395	113.5722	ESTs, Weakly similar to unknown protein	3.21	2.57
	452973	H88409	Hs.40527	ESTs	3.16	3.12
	408393	AW015318	Hs.23165	ESTs	3.12	2.00
	417355	D13168	Hs.82002	endothelin receptor type B	3.11	2.45
50	415314	N88802	Hs.5422	glycoprotein M6B	2.86	2.39
50	417632	R20855	Hs.5422	glycoprotein M6B	2.78	2.16
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	2.75	3.71
	456034	AW450979	16.5255	qb:UI-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su	2.73	3.00
	404356	A11430373		Target Exon	2.63	2.69
55	414876	AW950925	Hs.924	crystallin, mu	2.57	3.15
55	420208	BE276055	Hs.95972	silver (mouse homolog) like	2.46	2.89
	422656	AI870435	Hs.1569	LIM homeobox protein 2	2.45	2.20
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	2.43	2.11
	432222	AI204995	110.0.00	gb:an03c03.x1 Stratagene schizo brain S1	2.31	1.96
60	401116	MEUTOS		Target Exon	2.29	2.24
O	410326	AI368909	Hs.47650	ESTs	2.27	277
	459702	AI204995	114.47000	gb:an03c03.x1 Stratagene schizo brain S1	2.25	3.49
	435730	AB020635	Hs.4984	KIAA0828 protein	2.24	2.24
	404977	ADUZUUU	120.720	Insufin-like growth factor 2 (somatomedi	2.24	1.99
65	414221	AW450979		gb:UI-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su	2.16	2.36
03	437862	AW978107	Hs.5884	Homo sapiens mRNA; cDNA DKFZp586C0224 (f	2.13	2.09
	402181	7111310101		Target Exon	2.12	2.74
	447907	A1439110	Hs.170796	ESTs	2.05	2.02
	434276	AF123659	Hs.93605	leucine zipper, putative tumor suppresso	2.04	3.14
70	459246	NM_006834		RAB32, member RAS oncogene family	2.02	1.83
, 0	405451			dihydropyrimidinase-like 3	2.01	2.00
	446727	AB011095	Hs.16032	KIAA0523 protein	2.01	2.36
	417017	AA976064	Hs.180842	ribosomal protein L13	2.00	2.37
	413171	AA318325	Hs.75219	tyrosinase-related protein 1	1.94	2.77
75	408209	NM_004454	Hs.43697	ets variant gene 5 (ets-related molecule	1.94	2.76
, ,	455657	BE065209		gb:RC1-8T0314-310300-015-b12 BT0314 Homo	1.92	2.91
	419200	AW966405		EST	1.85	2.91
	419687	AI638859	Hs.227699	ESTs, Weakly similar to T2D3_HUMAN TRANS	1.84	2.27
	402217	,		C19001662*:gi[6753872 ref]NP_034345.1  i	1.83	2.33
80	406040			Target Exon	1.81	2.04
	435292		Hs.172965	ESTs	1.81	3.41
	430947		Hs.248153	olfactory marker protein	1.79	2.00
	434574		Hs.33470	ESTs	1.78	4.00
				603		

	403532			NM_024638:Homo sapiens hypothetical prot	1.75	2.06
	402829			C1002500:gij6754254 refjNP_034610.1  hea	1.72 1.72	2.20 2.04
	403828 453837	AL138387	Hs.256126	C4000447*:gij7705570jref NP_038851.1  KI bacutoviral IAP repeal-containing 7 (liv	1.68	2.40
5	407826	AA128423	Hs.40300	calpain 3, (p94)	1,67	2.13
•	441253	AJ632744	Hs.129501	ESTs	1.67	2.13
	405776			cytochrome c-1	1.66	2.36
	430540	AW245422		Homo sapiens cDNA: FLJ22105 fis, clone H	1.66	2.08
10	445745	AB007924	Hs.13245	KIAA0455 gene product	1.66	2.34
10	401963			NM_006311:Homo sapiens nuclear receptor	1.66	2.97 2.56
	402994			NM_002463*:Homo sapiens myxovirus (influ	1.66 1.65	2.23
	406016 429186	BE503443	Hs.112095	Target Exon hypothetical protein DKFZp434F1819	1.65	2.30
	402911	00303443	ns.112099	NM_021158*:Homo sapiens protein kinase d	1.63	2.46
15	412926	AI879076	Hs.75061	macrophage myristoylated alanine-rich C	1.61	2.28
	440437	AJ923201	Hs.192352	ESTs	1.59	2.07
	403960			ENSP00000174317*:KIAA0303 (FRAGMENT).	1.59	2.41
	406266			Target Exon	1.56	2.16
~~	424481	R19453	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	1.55	3.14
20	403803			C4001432*:pij6009515ktbijBAA84941.1  (A8	1.54	2.04
	407038	X00237		gb:Human F variable segment 5 to antith	1.53	2.09
	424412	H15512	Hs.10043	hypothetical protein FLJ13074	1.53 1.52	2.46 2.76
	431836 427923	AF178532 AW274357	Hs.271411 Hs.301406	beta-site APP-cleaving enzyme 2 hypothetical protein PP3501	1.52	3.04
25	419849	BE041436	Hs.93379	eukaryotic translation initiation factor	1.51	3.42
23	404790	DE011430	113.30013	C12001707*:gi[7305215[ref]NP_038599.1] k	1.50	2.16
	434596	T59538		gb:yb65g12.s1 Stratagene ovary (937217)	1.48	2.02
	425069	AA687465	Hs.298184	potassium voltage-gated channel, shaker-	1.47	4.05
	438549	BE386801	Hs.21858	trinucleotide repeat containing 3	1.46	2.48
30	427289	AI097346		phosphoserine aminotransferase	1.44	4.46
	425818	AB021225	Hs.159581	matrix metalloproteinase 17 (membrane-in	1.43	2.32
	432800	BE391046	Hs.278962	AIM-1 protein	1.43	2.08
	447763	BE619911	Hs.115803	hypothetical protein	1.42	2.21 2.31
35	443219	AJ354669	Hs.187461	ESTs, Weatdy similar to C29149 profine-r	1.41 1.41	2.35
33	451489	NM_005503 AW064121	3 Hs.26468 Hs.279175	amyloid beta (A4) precursor protein-bind ESTs	1.41	2.01
	459641 405318	AW004121	115.275175	C7002129°:gij3638957jgbjAAC36301.1j (AC0	1.40	2.31
	402343			Target Exon	1.40	2.35
	447108	AW449602	Hs.241493	natural killer-tumor recognition sequenc	1.40	2.11
40	431222	X56777	Hs.273790	zona pettucida glycoprotein 3A (sperm re	1.39	2.06
	400263			Eos Control	1.39	2.60
	403986			Target Exon	1.38	2.09
	437912	8E27B594	Hs.5912	F-box only protein 7	1.36	2.27
45	426020	AL110195	Hs.166017	microphthalmia-associated transcription	1.36	2.77
45	401914	nro.101.11	464757	Target Exon	1.33 1.29	2.43 2.01
	450395	BE048545	Hs.161757	ESTs	1.29	2.94
	425535	AB007937 AB010098	Hs.158287 Hs.24907	KIAA0468 gene product coronin, actin-binding protein, 2B	1.28	2.84
	450358 427560	AA405394	Hs.161851	ESTs	1,27	2.14
50	402450	7440004	113.101001	Target Exon	1.27	2.89
•	406885	D28423		gb:Human mRNA for pre-mRNA splicing fact	1.26	3.19
	404067			Target Exon	1.26	2.45
	406368			NM_022355:Homo sapiens putative dipeptid	1.25	2.06
	454429	BE273437	Hs.301406	hypothetical protein PP3501	1,23	2.07
55	414580	BE386918		gb:601275386F1 NIH_MGC_20 Homo sapiens c	1.22	2.21
	414060	BE246327	Hs.123164	gb:TCBAP1E1967 Pediatric pre-B cell acut	1.22 1.21	2.01 2.19
	400867	*********		cofilin 1 (non-muscle)	1.21	2.19
	437026	AW976573	•	ESTs Target Exon	1.20	2.09
60	402605 431008	H84058	Hs.25734	ESTs, Wealdy similar to BING1 (H.sapiens	1.17	2.22
00	448143	AF039704	Hs.20478	ceroid-tipofuscinosis, neuronal 2, late	1.17	2.25
	416630	H69392	Hs.174051	small nuclear ribonucleoprotein 70kD pol	1.16	2.34
	407239	AA076350		leukocyte immunoglobulin-like receptor,	1,14	2.58
	419045	T85693		gb:yd60d06.r1 Soares fetal liver spleen	1.13	2.08
65	443923	X60702	Hs.210	leukocyte tyrosine kinase	1,11	2.24
	457585	AB040799		G protein-coupled receptor 27	1.08	2.04
	452958	AA883929	Hs.40527	ESTs	1.03	2.28 2.04
	403969	DE 100001	43440	ENSP0000034663:Zinc finger protein 131	1.00 1.00	2.12
70	436878	BE465204		ESTs hypothetical protein FLJ11006	1.00	2.18
70	415929 404632	AA724373	115.43344	NM_022490:Homo sapiens hypothetical prot	1.00	2.19
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	1.00	2.35
	447937	AL109716		Homo sapiens mRNA full tength insert cDN	1.00	2.41
75	TABLE (	: <b>7</b> 0-				
, ,	Pkey:		nique Eos probese	identifier number		
	CAT nur	_	ene cluster numbe			
	Accessi		enbank accession			
80	Pkey	CAT Num	ber Accession	MC2400 A 474 F000 DE004004 DE000000 A 4 C00400 A 4 C004	246 AA401036	
	431089	125941_2 685586_1		M063489 AA715980 BF001091 BF880066 AA666102 AA6219 N136656 AW450979 AA984358 AA809054 AW238038 AA492		
	456034	539529_1		X136636 AW450979 AAS64338 AAB09034 AW236036 AAA92 E166299 A1204995 BG199355 AW969908 AA528756 AW4407		
	432222	ا_تعددين	0.05015030			

				100 A
		539529_1	BG207209 BE	166299 AIZ04995 BG1993S5 AW969908 AA528756 AW440776 BI044354 136656 AW450979 AA9843S8 AA8090S4 AW238038 AA492073 BE168945
		685586_1		
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				30627 AAA4362 40793232 40793232 407932 407932 407932 407932 407932 407932 407932 407932 407932 407932 407932 407932 407932 407932 407932 407932 407932 407932 407932 407932 407932 407932 407932 407932 407932 407932 407932 407932 407932 407932 407932 407933
			BE093545 AV	901107 AA383529 BI021552 R56420 N39976 AA37261 H82395 AA3543 BF08341 AV745131 D53074 AW954476 AW954472 AA376836 035969 Al267384 Al267232 BE348320 AA621574 AA861212 BF083343 BF08341 AV745131 D53074 AW954476 AW954472 AA376836
10				2000 044000 14002007 140C2C20 DC4D2EED DEDANDEN DA76550A 1707 / BESSO / D BESSOON DEDAUG/
			014400200 A	1402444 AMIAAA700 AMDESAGE ABRITGIT REARIOAR RIAGRITG AISHASS HMI 28483 AIDZ4037 AIDOSSU I AISUSHUI AADU 1003 AACU 1003
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15	430540	713_2		
	.5			
			A1770171 BF	0172337 BG7/023 BG80674 BG9057325 AG58810 AA948193 AA499916 AI459893 AI458188 AI240408 AI191843 AI191029 AW768399 196861 BE556897 AA453976 AI375927 AA648810 AA948193 AA499916 AI459893 AI45888 AI240408 AI191843 AI191029 AW768399 17337984 AW026150 BE466691 BE674599 AI818438 AA772197 AI651927 AW151143 BI198825 BG819083 BM45876 BE90367 17337984 AW026150 BE466691 BE674599 AI818438 AA772197 AI651927 AW151143 BI198825 BG819083 BM45876 BE90367
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			A1243844 AA	1809493 AAA81029 AA825/18 AL34/866 Al4316/0 AA614436 Al231103 AU7 (0-4-4-4-4-4-4-4-4-4-4-4-4-4-4-4-4-4-4-4
			AW008188 F	G746251 BE962912 BM454584 AL134894 BF104082 H80591
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25				400 NIA 004004 A40007 DISSASES DISSASES ANTISSAS
35	400263	18977_1		cop.ecc. 41000cc 41000470 0/C040EEE 4.4771735 QED38841 RE77/115 K(3Kb54/ K(5/5/5/0 AL553009 DIZ01304 DO770033 DIOGATO
•				~~~~ 4~~ 64644666 41949996 6/C094794 DE0E09E9 DEC0937/19 RIDI 1844 REXBR.S/ REXBRID// BEU9/2300/AVIOU3/13/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/71/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI/TI/EVI
40			BE772007 E	AIS37808 AW026128 N25984 AW006041 AIS078217531 BIS SMD44934 AW381142 BC743618 BE769206 BE893973 BI015047 BF886479 316789769 BC766117 BF847365 BE397834 AW371121 BF089125 BE082996 BF183193 BG180964 BF089940 BI000274 BG255503
	44.4500	caanaa 4	BG6/44991	BG774174 BI015084 BE385437 BE408833 BE387650
	414580 437026	623093_1 1240260_1		AA742335 AA830000
45	419045	348516_2		BG723297 T85693 T81681 T81909
		• • • • • • • • • • • • • • • • • • • •		
	TABLE 6			To the second se
	Pkey:	U	nique number co	rresponding to an Eos probeset  The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA"
50	Ref:	9	equence of hims	on chromosome 22" Dunham, et al. (1999) <u>Nature</u> 402:489-495.
50	Strand:	In	dicates DNA stra	and from which exons were predicted.
	Nt_positi	on; tr	dicates nucleotic	de positions of predicted exons.
				No. of the second secon
55	Pkey	Ref 7530858	Strand Minus	NL_position 126433-126623
در	404356 401116	7630858 9966559	Minus Plus	123579-12447
	404977	3738341	Minus	43081-43229
	402181	8575912	Plus	449746-450040
	405451	7622517	Minus	145949-146227
60	402217	9795981	Minus	21521-21757
	406040	6758938 8076842	Minus Minus	23063-23599 81750-81901
	403532 402829	8076842 8918414	Plus	101532-101852,102006-102263
	403828	9838214	Plus	31755-32148
65	405776		Minus	105911-107251
	401963	3126783	Plus	51382-51521
	402994		Minus	4727-4969
	406016		Plus	41341-41940 142689-142979
70				
70	402911		Plus Minus	
	402911 403960	8224409	Minus	90999-94843
	402911 403960 406266	8224409 7528342	Minus Minus	
	402911 403960 406266 403803 404790	8224409 7528342 8112965 7230958	Minus Minus Plus Plus	90999-94843 2385-2518 55513-55778 38611-38761
<b>2</b> 5	402911 403960 406266 403803 404790 405318	8224409 7528342 8112965 7230958 3638954	Minus Minus Plus Plus Plus	90999-94843 2365-2518 55513-55778 33611-38761 79689-79967
75	402911 403960 406266 403803 404790 405318 402343	8224409 7528342 8112965 7230958 3638954 8099256	Minus Minus Plus Plus Plus Plus	90999-94843 2365-2518 55513-55778 38611-38761 79689-79967 4677-6084
75	402911 403960 406266 403803 404790 405318 402343 403986	8224409 7528342 8112965 7230958 3638954 8099256 8576059	Minus Minus Plus Plus Plus Plus Plus	90999-94843 2365-2518 55513-55778 38611-38761 79689-79967 4577-6084 90682-91238
75	402911 403960 406266 403803 404790 405318 402343 403986 401914	8224409 7528342 8112965 7230958 3638954 8099256 8576059 9369520	Minus Minus Plus Plus Plus Plus Plus Plus	90999-94843 2365-2518 55513-55778 38611-38761 79689-79967 4677-6084
	402911 403960 406266 403803 404790 405318 402343 403986 401914 402456	8224409 7528342 8112965 7230958 3638954 8099256 8576059 9369520 9796674	Minus Minus Plus Plus Plus Plus Plus Plus Plus Pl	90999-94843 2365-2518 55513-55778 38611-38761 79689-79967 4677-6084 90692-91238 62537-62945,63155-63308 137536-137682,137920-138045 1415-2071
75 80	402911 403960 406256 403803 404790 405318 402343 403986 401914 402450 404067	8224409 7528342 8112965 7230958 83638554 8099256 8099256 9369520 9796674 7 3282162 9256126	Minus Minus Plus Plus Plus Plus Plus Plus Plus Pl	90999-94843 2365-2518 55513-55778 33611-38761 79689-79967 4677-6084 90692-91238 62537-62945,63155-63308 137536-137682,137920-138045 1415-2071 72447-72588,72673-72802,73119-73245
	402911 403960 406266 403803 404790 405318 402343 403986 401914 402456 404667 406368	8224409 7528342 8112965 7230958 83638954 8099256 9369520 9369520 9369520 9389520 9389520 9389520 9389520	Minus Minus Plus Plus Plus Plus Plus Plus Plus Minus Plus Minus	90999-94843 2365-2518 55513-55778 33611-38761 79689-79967 4577-6084 90692-91238 62537-62945,63155-63308 137536-137682,137920-138045 1415-2071 72447-72588,72673-72802,73119-73245 34136-34846
	402911 403960 406256 403803 404790 405318 402343 403986 401914 402450 404067	8224409 7528342 8112965 7230958 83638954 8699256 8576059 9369520 9796674 3282162 93838275 9909420	Minus Minus Plus Plus Plus Plus Plus Plus Plus Pl	90999-94843 2365-2518 55513-55778 33611-38761 79689-79967 4677-6084 90692-91238 62537-62945,63155-63308 137536-137682,137920-138045 1415-2071 72447-72588,72673-72802,73119-73245

404632 9796668 Plus 45096-45229

TABLE 63A: ABOUT 181 GENES UPREGULATED IN BENIGN NEVI RELATIVE TO MELANOMA METASTASES
Table 63A fists about 181 genes upregulated in benign nevi relative to melanoma metastases. Genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA 5 expression.

Unique Eos probeset identifier number Exemplar Accession number, Genbank accession number Unigene number

Pkey: ExAccn: UnigenalD: Unigene Title: R1 R2 10 Unigene gene title

uragers generated average of benigh nevi Als divided by the 90th percentile of metanoma metastasis Als average of benigh nevi Als divided by the 90th percentile of metanoma metastasis Als, where the 15th percentile of normal tissue Als was subtracted from both average of benigh nevi Als divided by the 90th percentile of metanoma metastasis Als, where the 15th percentile of normal tissue Als was subtracted from both

	R2			Als divided by the 90th percentile of melanoma metastasis	Als, where th	e 15th percenti
		the nu	merator and deno	minator		
15	_	<b>5</b> A	44-110	Mainena Tilla	R1	R2
	Pkey	ExAcon	UnigenelD	Unigene Title	19.33	19.21
	401781	AU076442	Hs.117938	Target Exon collagen, type XVII, alpha 1	13.54	14.18
	422511 401780	AUU/0442	ns.117530	NM_005557*:Homo sapiens keratin 16 (foca	12.97	13.63
20	409601	AF237621	Hs.80828	keratin 1 (epidermotytic hyperkeratosis)	12.61	31.19
20	412636	NM_004415	113.00020	desmoplakin (DPI, DPII)	11.73	6.91
	420783	AI659838	Hs.99923	tectin, galactoside-binding, soluble, 7	10.18	14.08
	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	8.48	6.79
	421733	AL119671	Hs.1420	fibroblast growth factor receptor 3 (ach	8.28	9.62
25	430686	NM_001942	Hs.2633	desmoglein 1	7.26	5.64
	429852	AB010445	Hs.225948	small inducible cytokine subfamily A (Cy	7.12	10.88
	442577	AA292998	Hs.163900	ESTs	7.01	6.59
	406964	M21305		FGENES predicted novel secreted protein	6.50	8.82
	401785			NM_002275":Homo sapiens keratin 15 (KRT1	6.40	9.77
30	410001	AB041035	Hs.57771	kallikrein 11	6.18	6.16
	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	5.73	16.57
	418686	Z36830	Hs.87268	annexin A8	5.32	5.27 9.81
	439496	BE616501	Hs.32343	Homo sapiens, Similar to RIKEN cONA 1110	4.89	6.67
25	452240	Al591147	Hs.61232	ESTS	4.89 4.74	4.80
35	402525	**** ****	11- 054000	NM_002699*:Horno sapiens POU domain, clas	4.66	3.98
	431360	NM_000427	Hs.251680	loricrin	4.63	5.69
	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	4.56	6.78
	418067	Al127958	Hs.83393	cystatin E/M tumor protein 63 kDa with strong homolog	4.56	5.73
40	424012	AW368377	Hs.137569 Hs.41690	desmocollin 3	4.44	5.23
40	418663 419329	AK001100 AY007220	Hs.288998	S100-type calcium binding protein A14	4.24	6.49
	439706	AW872527	Hs.59761	ESTs, Weathy similar to DAP1_HUMAN DEATH	3.95	3.37
	421773	W69233	Hs.112457	ESTs	3.88	9.60
	408536	-AW381532	Hs.135188	ESTs	3.82	10.18
45	418394	AF132818	Hs.84728	Kruppel-like factor 5 (intestinal)	3.78	6.33
	408000	L11690	Hs.198689	bullous pemphigoid antigen 1 (230/240kD)	3.77	4.92
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	3.70	5.30
	424049	AB014524	Hs.138380	KIAA0624 protein	3.68	4.41
	421948	L42583	Hs.334309	keratin 6A	3.62	3.13
50	427666	A1791495	Hs.180142	catmodutin-like skin protein (CLSP)	3.59	4.40
	422168	AA586894	Hs.112408	\$100 calcium-binding protein A7 (psorias	3.48	6.09
	436895	AF037335	Hs.5338	carbonic anhydrase XII	3.42	3.28
	437191	им_006846	Hs.331555	serine protease inhibitor, Kazal type, 5	3.28	3.89 7.11
66	401760			Target Exon	3.21 3.21	5.78
55	431089	BE041395	11- 270C	ESTs, Wealdy similar to unknown protein	3.14	3.11
	434293	NM_004445		EphB6	3.14	4.85
	412432	AA126311	Hs.9879 Hs.150853	ESTs p53-responsive gene 5	3.11	5.92
	442503	AF147078 AA524394	Hs.294022	hypothetical protein FLJ14950	3.07	4.89
60	41,4987 420798	W93774	Hs.99936	keratin 10 (epidermolytic hyperkeratosis	2.99	3.09
00	433339	AF019226	Hs.8036	glioblastoma overexpressed	2.96	2.75
	414876	AW950925	Hs.924	crystallin, mu	2.94	3.82
	437233	D81448	Hs.339352	Horno sapiens brother of CDO (BOC) mRNA,	2.87	3.42
	424897	D63216	Hs.153684	frizzted-related protein	2.87	1.96
65	456034	AW450979		gb:UI-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su	2.73	2.54
	424364	AW383226	Hs.163834	ESTs, Weakly similar to G01763 atrophin-	2.72	2.92
	427318	AF186081	Hs.175783	zinc transporter	2.71	2.21
	452887	AI702223	Hs.107253	hypothetical protein DKFZp761F241	2.67	5.47
	452308	AI167560	Hs.61297	ESTs	2.67	4.61
70	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	2.64	2.68
	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (	2.57	3.91 5.47
	451541	BE279383	Hs.26557	plakophilin 3	2.49 2.45	4,17
	453317	NM_002277		keratin, hair, acidic, 1	2.43	4.90
75	412633	AF001691	Hs.74304	periplakin small inducible cytokine subfamily B (Cy	2.41	2.68
75	417233	W25005 AA622394	Hs.24395 Hs.153177	ribosomal protein S28	2.39	2.67
	424797	AL080188	Hs.137556	Homo sapiens mRNA; cDNA DKFZp434A132 (fr	2.39	4.07
	424010	H58995	Hs.37648	ESTs	2.39	2.34
	453241 426451	AJ908165	Hs.169946	GATA-binding protein 3 (T-cell receptor	2.36	1.88
80	423467	AK000214	Hs.129014	hypothetical protein FLJ20207	2.32	2.24
00	432222	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	2.31	1.99
	430168	AW968343	Hs.145582	DKFZP434I1735 protein	2.30	2.60
	457121	AI743770	Hs.180513	ESTs, Weakly similar to KIAA0822 protein	2.28	1.91
				586		
				-200		

					2.27	8.50
			Hs.3185	lymphocyte antigen 6 comptex, locus D hypothetical protein FLJ11036	2.27	2.21
			Hs.16740 Hs.99249	ESTs	2.25	2.54
		AA451798 A1204995	rt5.33243	gb:an03c03.x1 Stratagene schizo brain S1	2.25	2.35
5			Hs.98485	gap junction protein, beta 3, 31kD (conn	2.23	2.17
,		AW139205	Hs.156457	hypothetical protein FLJ22408	2.23	3.23
	417017	AA976064	Hs.180842	ribosomal protein L13	2.21	2.74
	433124	U51712	Hs.13775	hypothetical protein SMAP31	2.21 2.20	1.68 3.32
	430152	AB001325	Hs.234642	aquaporin 3	2.15	5.20
10	444726	NM_006147		interferon regulatory factor 6	2.15	2.82
	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member FAT tumor suppressor (Drosophila) homolo	.2.14	2.96
	425483	AF231022	Hs.158159 Hs.6066	Rho guanine nucleotide exchange factor (	2.14	2.25
	419912	AF249745 U81961	Hs.2794	sodium channel, nonvoltage-gated 1 alpha	2.12	2.99
15	431441 444105	AW189097	113.27 34	ESTs	2.11	2.98
13	428748	AW593206	Hs.98785	Ksp37 protein	2.09	1.51
	456826	AI871742	Hs.302428	wingless-type MMTV integration site fami	2.09	3.25
	413163	Y00815	Hs.75216	protein tyrosine phosphatase, receptor t	2.09	4.97 5.68
	410677	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein	2.06 2.06	2.04
20	430285	AI917602	Hs.106440	ESTs	2.05	5.92
	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	2.04	2.19
	451668	Z43948	Hs.326444	cartilage acidic protein 1 callular retinoic acid-binding protein 1	2.04	3.08
	441134	W29092	Hs.346950 Hs.33104	Huntingtin interacting protein C	2.04	1.63
25	433428	T29975 U46689	Hs.159608	aldehyde dehydrogenase 3 family, member	2.03	3.92
23	425831 446727	AB011095	Hs.16032	KIAA0523 protein	2.01	2.60
	431703	AA514264	Hs.4437	triosephosphate isomerase 1	2.01	2.05
	452554	AW452434	Hs.58006	ESTs, Wealty similar to ALU5_HUMAN ALU S	1.99	4.04
	439625	AF086453	Hs.58611	ESTs	1.99	2.31
30	402880			Target Exon	1.99	2.75 2.10
	428471	X57348	Hs.184510	stratifin	1.98 1.97	3.16
	413859	AW992356	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	1.97	3.89
	452547	AA335295	Hs.74120	adipose specific 2	1.94	2.06
26	437679	NM_014214	Hs.5753	inositol(myo)-1(or 4)-monophosphatase 2	1.93	2.96
35	429259	AA420450	Hs.292911	Plakophilin Targel Exon	1.92	2.97
	406387	BE091833		gb:IL2-BT0731-260400-076-F04 BT0731 Homo	1.91	3.46
	455797	AA326110		nuclear transcription factor Y, gamma	1.89	2.00
	437202 426150	NM_003658	Hs.167218	Barti-like homeobox 2	1.86	2.60
40	434574	AI424458	Hs.33470	ESTs	1.85	4.61
40	446051	BE048061	Hs.37054	ephrin-A3	1.85	3.48
	424471	AA341329	Hs.311524	ESTs	1.84	2.62
	422106	D84239	Hs.111732	Fc fragment of IgG binding protein	1.83 1.82	4.69 2.00
	451721	NM_006946	Hs.26915	spectrin, beta, non-erythrocytic 2	1.81	2.31
45	451849	AI199261	Hs.27191	hypothetical protein from clone 24796	1.79	3.07
	429348	AJ242859	Hs.199731	Langerhans cell specific c-type lectin	1.77	3.37
	423523	AW299828	Hs.193580	ESTs Homo sapiens cDNA: FLJ21274 fis, clone C	1.76	2.46
	432543	AA552690	Hs.152423	C4000447*:gi[7705570]ref[NP_038851.1] KI	1.73	2.06
50	403828	A1768015		ESTs	1.68	3.16
20	412446 420039	NM_004605	Hs.94581	sulfotransferase family, cytosolic, 28,	1.67	2.22
	411274	NM_002776		kallikrein 10	1.66	2.26
	401963			NM_006311:Homo sapiens nuclear receptor	1.66	2.52
	435016	AI284219	Hs.130749	ESTs, Weakly similar to 138022 hypotheti	1.65	2.20
55	437897	AA770561	Hs.146170	hypothetical protein FLJ22969	1.64	3.21 2.94
	419648	T73661	Hs.91877	thyroid hormone responsive SPOT14 (rat)	1.63 1.62	2.58
	410545	U32324	Hs.64310	interleukin 11 receptor, alpha	1.62	3.92
	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3 D component of complement (adipsin)	1.60	3.43
60	456898	NM_001928	3 Hs.155597 Hs.129739	KIAA0514 gene product	1.60	2.18
VV	423526	AB011086 AU076628	Hs.79187	coxsackie virus and adenovirus receptor	1.60	2.47
	416305 413966	AA133935	Hs.173704	ESTs, Moderately similar to A53959 throm	1.59	2.99
	414217	A1309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	1.59	2.82
	429299	AI620463	Hs.347408	hypothetical protein MGC13102	1.57	2.64
65	432647	AJ807481	Hs.278581	fibroblast growth factor receptor 2 (bac	1.56	2.74
	429002		Hs.2340	junction plakoglobin	1.56	2.97
	430171		Hs.234766	skin-specific protein	1.54	2.18 2.19
	422717		Hs.119475	cold inducible RNA-binding protein	1.51 1.51	3.73
70	414323			KIAA0273 gene product	1.50	2.18
70	423184			ephrin-A1 Homo sapiens mRNA; cDNA DKFZp566L203 (fr	1.50	2.00
	433101			Homo sapiens mRNA; cDNA DKFZp586F0824 (f	1.48	2.04
	424362		Hs.150826	RAB25 RAB25, member RAS oncogene family	1.46	2.83
	433662			plasmolipin	1.46	2.00
75	445431 456906			Cas-Br-M (murine) ectropic retroviral tr	1.44	2.04
13	442599			RetA-associated inhibitor	1.42	3.50
	44565		Hs.21299	ESTs, Weakly similar to AF151840 1 CGI-8	1.42	2.53
	44467		Hs.11669	taminin, alpha 5	1.40	2.36
_	44799			small inducible cytokine subfamily A (Cy	1.40	2.29
80	41846	2 BE001596		integrin, beta 4	1.39	2.86 2.28
	45302			serine protease inhibitor, Kunitz type, tasciculation and elongation protein zet	1.38 1.38	2.20 2.24
	41634		Hs.79226	Homo sapiens, Similar to RIKEN cDNA 5830	1.38	2.14
	43341	7 AA587773	3 Hs.8859	CALLED SERVICES COLORED TO LEGISLE COLORED COLOR		

	407815	AW373860	Hs.183860	hypothetical protein FLJ20277	1.36	2.34	
	432894	AW167668	Hs.279772	brain specific protein	1.36	5.09	
	439733	AL365412	Hs.107203	hypothetical protein from EUROIMAGE 1759	1.36	2.00	
-	454478	AW805749		superoxide dismutase 2, mitochondrial	1.35	2.85	
5	423515	AA327017	Hs.176594	ESTs	1.35 1.35	2.45 2.07	
	436663 404246	AW410458	Hs.5258	chromosome 11 open reading frame2 Target Exon	1.34	2.96	
	411939	AI365585	Hs.146246	ESTs	1.33	2.31	
	409178	BE393948	Hs.50915	kallikrein 5	1.33	2.03	
10	427795	BE268268	Hs.180842	ribosomal protein L13	1.33	2.29	
	447299	AF043897	Hs.18075	chromosome 9 open reading frame 3	1.32	2.78 3.37	
	447330	BE279949	Hs.18141	ladinin 1	1.32 1.31	271	
	433399 403986	N46406	Hs.84700	similar to phosphatidylcholine transfer Target Exon	1.31	2.09	
15	407597	AA043925	Hs.339352	Homo sapiens brother of CDO (BOC) mRNA,	1.30	2.28	
••	450796	NM_001988	Hs.25482	envoptakin	1.30	3.45	
	415550	L13720	Hs.78501	growth arrest-specific 6	1.29	2.76	
	415512	Y16270	Hs.78482	paralemmin 050	1.26 1.26	2.49 3.07	
20	430513 422581	AJ012008 NM 016339	Hs.241586 Hs.118562	G6C protein Link guanine nucleotide exchange factor	1.23	2.04	
20	420048	AW206824	Hs.25766	ESTs	1.23	2.01	
	425883	AL137708	Hs.161031	Homo sapiens mRNA; cDNA DKFZp434K0322 (f	1.23	2.72	
	430560	Z28942	Hs.243960	N-myc downstream-regulated gene 2	1.23	2.42	
25	426377	AK001921	Hs.169575	hypothetical protein MGC2550	1.23	2.20 2.01	
25	402218	44004670	11-0046	NM_022165*:Homo sapiens Lin-7b protein ( Homo sapiens mRNA for KIAA1741 protein,	1.23 1.18	2.24	
	413944 414186	AW001579 U33446	Hs.9645 Hs.75799	protesse, serine, 8 (prostasin)	1.16	2.16	
	426068	AF029778	Hs.166154	jagged 2	1.15	2.07	
	431243	U46455	Hs.252189	syndecan 4 (amphiglycan, ryudocan)	1.14	2.33	
30	411388	X72925	Hs.69752	desmocollin 1	1.00	261	
	443672	AA323362	Hs.9667	butyrobetaine (gamma), 2-oxoglutarate di	1.00	263	
	TABLE 63	ıD.					
	Pkey:		ue Eos probeset idea	ntifier number			
35	CAT num		e cluster number				
	Accession	n: Gen	bank accession numi	bers			
	<b></b>	CATALogha	Accession				
	Pkey 412636	CAT Number 1438_1	M77830 NM 004	415 AF139065 RG681115 BG740377 BI712964 BG000	0656 AA128470	BI438324 H27408 BE931630 BE167165 AW370827 AW370813	3
40	412000	1430_1	IOS 211 DC 60886	5 0C740734 BC680618 BC739778 RI765807 RM3534	03 RM353248 A	AW177784 AW205789 AW951576 AW848592 BE182164	
• •			DE1/0266 DE0/0	1187 RIOGOAAS RIOGOAAA RE350983 RE720095 RE7201	069 BE715154 I	BE082584 BE082576 BE004047 AA857316 BIU39774 BE713010	8
			DE7135/8 AW17	0253 RE160423 RI039775 AWRR6475 RM462504 BE9	31734 BF14926	54 AA340777 BF381183 BG621737 AU127200 AW304039	
•			BE713548 AW170	0253 BE160433 BI039775 AW886475 BM462504 BE9 3480 BER19009 BE3R11R4 BE715956 R5R704 AAR522	31734 BF14926 212 AW366566 1	54 AA34U777 BF381183 BG621737 AU127260 AW364639 B1090358 BF087707 BE819046 BE819005 AA377127 BE073467	7
45			BE713548 AW170 BF993352 BG223 BE819069 BE819	0253 BE160433 BI039775 AW886475 BM462504 BE9 3489 BE819009 BF381184 BE715956 F88704 AA8140 888 BI036306 BG990973 BI040954 BF919911 AU140 4784 BI039782 ALIHAMAY BE144243 BE709863 BF88	31734 BF14926 212 AW366566 I 0155 AI951766 / 15642 BF00192	54 AA340777 B7381183 BG827137 AU17720 AW394039 B1090358 BF087707 BE819046 BE819005 AA377127 BE073461 A434518 AW804674 BF752969 BE837009 BE925826 BF149263 3 BF933510 AW265328 BG436319 BE182166 AW365175	7
45			8E713548 AW170 BF993352 BG223 BE819069 BE819 AW995615 BE81	0253 BE160433 BI039775 AW886475 BM462504 BE9 3499 BE819009 BF381184 BE715956 RS8704 AA8522 3048 BI036306 B990973 BI040954 BF919911 AU140 4264 BI039782 AU140407 BE144243 BE709863 BF98 9780 AW177033 BE8773870 AW178000 BF882526 BF-	31734 BF14926 212 AW366566 I 9155 AI951766 / 85642 BE00192 476866 BF0869	34 AA340777 BF381183 BG827137 AU17/20 AW394039 BI090358 BF087707 BE819046 BE819005 AA377127 BE073461 AI434518 AW804674 BF752969 BE837009 BE925826 BF149263 3 BF533510 AW365328 BG436319 BE182166 AW365175 194 BF592276 BE082507 BE082514 BE082505 BF873693	7
45			8E713548 AW17 BF993352 BG223 BE819069 BE819 AW995615 BE81 AW847688 BE81	0253 BE160433 BI039775 AW886475 BM462504 BE9 1489 BE819009 BF381184 BE715956 R58704 AA8522 1048 BI036306 BG990973 BI040954 BF919911 AU140 4264 BI039782 AU140407 BE144243 BE709863 BF98 8280 AW177933 BF873679 AW178000 BE082526 BF98 14578 BE801453 AW385173 BF8173073 AW	31734 BF14926 212 AW366566 I 2155 AI951766 / 25642 BE00192 476866 BF0869 2365153 BF184	54 AA340777 BF381183 BG527137 AU172720 AW356059 BI090358 BF087707 BEB 19046 BEB 1905 AA377127 BE073461 AI434518 AW804674 BF752969 BEB37009 BE925826 BF149261 3 BF933510 AW265328 BG456319 BE182166 AW365175 904 BF592276 BE082507 BE082514 BE082505 BF873693 941 BF749421 BE184920 BF839562 BE184933 BF842254	7
45			BE713548 AW170 BF993352 BG223 BE819069 BE819 AW995615 BE814 AW847688 BE814 AW848840 AW84	0253 BE160433 BI039775 AW886475 BM462504 BE9 1489 BEB19009 BF381184 BE715956 R58704 AA8522 1048 BI036306 BC990973 BI040954 BF919911 AU1404 14264 BI039782 AU140407 BE144243 BE709863 BF98 14267 BE104153 BF873679 AW178000 BE082526 BF- 147678 BF804153 AW365157 BE813930 BE002030 AW	31734 BF14926 212 AW366566 I 2155 AI951766 / 25642 BE00192 476866 BF0869 /365153 BE184 14632 BE18494	54 AA340777 BF381183 BG527137 AUT2720 AW356459 BI090358 BF087707 BE819046 BE819005 AA377127 BE073461 A434518 AW804674 BF752969 BE837009 BE925826 BF149261 3 BF933510 AW265328 BG436319 BE182166 AW365175 194 BF592276 BE082507 BE082514 BE082505 BF87365 941 BF749421 BE184920 BF839562 BE184933 BF842254 8 BG986845 AA131128 AA099891 W39488 C04715 BF096124	7
			BE713548 AW170 BF993352 BG223 BE819069 BE819 AW995615 BE814 AW068840 AW847688 BE814 AW068840 AW8470 BE93470 BE93470 BE9341	0253 BE160433 BI039775 AW886475 BM462504 BE9 3489 BE819009 BF381184 BE715956 R58704 AA8522 3489 BE819009 BF381184 BE715956 R58704 AA8522 4264 BI039782 AU140407 BE144243 BE709863 BF98 8280 AW177933 BF873679 AW178000 BE082526 BF 47678 BF804153 AW365157 BE813930 BE002030 AW 1048 BF993889 BF368816 BE184924 BE159646 BE71	31734 BF14926 212 AW366566 1 3155 AI951766 / 35642 BE00192 476866 BF0869 7365153 BE184 365153 BE184 365163 AW8487	54 AA340777 BF381183 BG527137 AUT2720 AW39-0493 BI090358 BF087707 BE819046 BE819005 AA377127 BE073461 AI434518 AW804674 BF752969 BE837009 BE925826 BF149261 3 BF933510 AW265328 BG436319 BE182166 AW365175 194 BF592276 BE082507 BE082514 BE082505 BF873693 941 BF749421 BE184920 BF839562 BE184933 BF842593 941 BF749421 BE184920 BF839562 BE184933 BF842526 8 BG986845 AA131128 AA099891 W39488 CO4715 BF096124 23 AW376699 AW376817 AW376697 BG005097 BF751115	7
45			BE713548 AW17 BF993352 BG223 BE819069 BE819 AW995615 BE81 AW847688 BE81 AW068840 AW84 BE698470 BE931 BE865084 AW84	0253 BE160433 BI039775 AW886475 BM462504 BE9 4889 BEB19009 BF381184 BE715956 R58704 AA8522 4048 BI036306 BG990973 BI040954 BF919911 AU140 4264 BI039782 AU140407 BE144243 BE708863 BF88 8280 AW177933 BF873679 AW178000 BE082526 BF- 41678 BF804153 AW365157 BE813930 BE002030 AW 1048 BF999889 BF368816 BE184924 BE159646 BE71 9304 AL603116 BE149760 BE705967 BE705966 BE7-	31734 BF14926 212 AW366566 3155 AI951766 315642 BE00192 476866 BF0869 7365153 BE184 4632 BE18494 05968 AW8487 F927725 BF094	54 AA340777 BF-381183 BG52/137 AUT-2720 AW356-89-8 BIO90358 BF-087707 BEB 19046 BEB 37009 BE925826 BF14926: 3 BF933510 AW256328 BG435319 BE182166 AW355175 948 BF592276 BE082507 BE082514 BE082505 BF673693 941 BF749421 BE184920 BF639562 BE184933 BF842254 8 BG986845 AA131128 AA099891 W39488 CO4715 BF096124 23 AW376699 AW376817 AW376697 BG005097 BF751115 8271 AW997139 BE865474 BE185187 BE156621 BE715089	7
			BE713548 AW177 BF993352 BE91969 BE819 AW995615 BE81 AW947688 BE81 AW068840 AW84 BE685341 AW79 BE696084 AW84 BE713227 BE713227 BE713227 BE713227 BE713227 BE713227 BE71	0253 BE160433 BI039775 AW886475 BM462504 BE9 3489 BE819009 BF381184 BE715956 R58704 AA8522 3048 BI036306 BC990973 BI040954 BF919911 AU1404 4264 BI039782 AU140407 BE144243 BE709863 BF98 8280 AW177933 BF873679 AW178000 BE082526 BF- 47678 BF804153 AW365157 BE813930 BE002030 AW 1048 BF999889 BF368816 BE184394 BE159546 BE7 19304 AL603116 BE149760 BE705967 BE705966 BE7 8371 AW376782 AW848789 AW649074 AW361413 B 2293 BE179915 AW799309 BF872345 BF08867 BE7 1190 BF752409 BF06551 BC959922 BF008483 BF0	31734 BF14926 212 AW366566 1155 AI951766 / 15642 BE00192 476866 BF0869 /365153 BE184 14632 BE18494 05968 AW8487 F927725 BF094 05939 AW7525	54 AA340777 BF381183 BG52/137 AU17/20 AW356936 BI090358 BF087707 BE819046 BE819005 AA377127 BE073461 AI434518 AW804674 BF752969 BE837009 BE925826 BF149261 33 BF933510 AW265328 BG436319 BE182166 AW365175 944 BF7592276 BE082507 BE082514 BE082505 BF873693 941 BF749421 BE184920 BF839562 BE184933 BF842254 88 BG986845 AA131128 AA099891 W39488 CO4715 BF096124 23 AW376699 AW376817 AW376697 BG005097 BF751115 4211 AW997139 BE865474 BE185187 BE156621 BE715089 99 BG005197 BF350086 BE715196 BE715155 BF752396 33 AW377699 AW607238 BE082519 AW377700 BF349467	7
			BE713548 AW176 BF993352 BE993352 BE819069 BE819 AW995615 BE81 AW368840 AW84 BE685341 AW79 BE695084 AW84 BE713297 BE713	0253 BE160433 BI039775 AW886475 BM462504 BE9 3489 BEB19009 BF381184 BE715956 R58704 AA8522 3648 BI036306 BG99073 BI040954 BF919911 AU140 4264 BI039782 AU140407 BE144243 BE709863 BF98 8280 AW177933 BF873679 AW178000 BE082526 BF 47678 BF804153 AW365157 BEB13930 BE002030 AW 1048 BF999889 BF368816 BE184924 BE159646 BE7 19304 AL603116 BE149760 BE705967 BE705966 BE7 8371 AW376782 AW848789 AW849074 AW361413 B 3298 BE179915 AW798309 BF872345 BF088676 BE7 1013 AL39396 AU158477 BL67252 AU159919 AU7608	31734 BF14922 31734 BF14926 1155 AI951766 / 15642 BE00192 476866 BF0859 /365153 BE184 14632 BE18494 05968 AW8487 F927725 BF094 05939 AW7525 164748 BF09458 16 BF08458	54 AA340777 BF381183 BG52/137 AU17/20 AW396493 BI090358 BF087707 BE819046 BE819005 AA377127 BE073461 AI434518 AW804674 BF752969 BE837009 BE925826 BF149261 33 BF933510 AW265328 BG436319 BE182166 AW365175 944 BF759276 BE082507 BE082514 BE082505 BF873693 941 BF749421 BE184920 BF839562 BE184933 BF842254 8 BG986845 AA131128 AA099891 W39488 CO4715 BF096124 23 AW376699 AW376817 AW376697 BG005097 BF751115 4211 AW997139 BE865474 BE185187 BE156621 BE715089 99 BG005197 BF350086 BE715196 BE715155 BF752396 3 AW377699 AW607238 BE082519 AW3777700 BF349467 4439101 AA451923 AI340326 AI590975 BI791553 AI700963	7
50			BE713548 AW171 BF993352 BG223 BE819069 BE819 AW995615 BE81 AW947688 BE811 AW68840 AW84 BE6538470 BE93 BE865341 AW79 BE695084 AW84 BE713297 BE715 BF093817 BF831 A1190590 A564	0253 BE160433 BI039775 AW886475 BM462504 BE5 4889 BE819009 BF381184 BE715956 R58704 AA8522 3048 BI036306 BG990973 BI040954 BF919911 AU140 4264 BI039782 AU140407 BE144243 BE709863 BF88 8280 AW177933 BF873679 AW178000 BE082526 BF7 67678 BF804153 AW385157 BE813930 BE002303 AW 1048 BF993889 BF368816 BE184924 BE159646 BE71 9304 AL603116 BE149760 BE705967 BE705966 BE7 8371 AW376782 AW848789 AW849074 AW361413 B 3298 BE179915 AW799309 BF872345 BF088676 BE7 1190 BF752409 BE006561 BG959922 BF094833 BF09 103 AJ32926 AU158477 BI467252 AU159919 AJ76081	31734 BF14922 1155 AI951766 A 15642 BE00192: 476866 BF0869 7365153 BE1844 16532 BE18494 05968 AW8487 F927725 BF094 05939 AW7525 14748 BF09458. 166 BF082516 AI 7612 AW19055:	34 AA340777 BF381183 BG52/137 AUT-20 AWN396398 BIO90358 BF087707 BEB1 9046 BEB 18005 AA377127 BE073461 AI434518 AW804674 BF752969 BEB37009 BE925826 BF149263 3 BF933510 AW265328 BG456319 BE182166 AW365175 904 BF592276 BE082507 BE082514 BE082505 BF873693 904 BF7949421 BE184920 BF839562 BE184933 BF842254 8 BG986845 AA131128 AA099891 W39488 CO4715 BF096124 23 AW376699 AW376817 AW376697 BG005097 BF751115 4211 AW997139 BE865474 BE185187 BE156621 BE715089 99 BG005197 BF350086 BE715196 BE715155 BF752396 3 AW3777699 AW507238 BE082519 AW377700 BF349467 AW3717699 AW507238 AS052545 BY3553 AI700963 5 AI220573 A3304772 AI270345 AI627383 AA552300 AI911702	7
			BE713548 AW17: BF993352 BG223 BE819069 BE819 AW995615 BE81 AW947688 BE81 AW668840 AW84 BE665341 AW79 BE695084 AW84 BE713297 BE713 BF0933817 BE731 A1190590 AI5544 A1142882 AA073 AW168807 A1394	0253 BE160433 BI039775 AW886475 BM462504 BE9 4889 BE819009 BF381184 BE715956 R58704 AA8522 3048 BI036306 BG990973 BI040954 BF919911 AU1404 4264 BI039782 AU140407 BE144243 BE709863 BF98 8280 AW177933 BF873679 AW178000 BE082526 BF- 47678 BF804153 AW365157 BE813930 BE002030 AW 1048 BF999889 BF386816 BE184924 BE159646 BE7 19304 AL603116 BE149760 BE705967 BE705966 BE7 8371 AW376782 AW848789 AW649074 AW361413 B 3298 BE179915 AW799309 BF872345 BF088676 BE7 1190 BF752409 BE006561 BG959922 BF094833 BF0 103 AJ392926 AU158477 BI467252 AU159919 AI76081 1975 AA946936 AA644381 BM314884 AA702424 A415 1978 W956770 AA149191 AA076864 AIR30049 AW780	31734 BF14925 1112 AW366566 1 1155 A1951766 / 15642 BE00192: 476856 BF0859 1365153 BE184 14632 BE18494 105968 AW8487 F927725 BF094 105939 AW7525 14748 BF09458 16 BF082516 AI 7612 AW19055 313 AU784449 A	54 AA340777 BF381183 BG52/137 AU17-20 AW39-68-98 BIG90358 BF087707 BB1 9046 BEB19005 AA377127 BE073461 AI434518 AW804674 BF752969 BE837009 BE925826 BF149261 3 BF933510 AW265328 BG436319 BE182166 AW365175 994 BF592276 BE082507 BE082514 BE082505 BF873693 9941 BF749421 BE184920 BF839562 BE184933 BF842254 8 BG986845 AA131128 AA099891 W39488 C04715 BF096124 23 AW376699 AW376817 AW376697 BG005097 BF751115 4211 AW997139 BE865474 BE185187 BE156621 BE715089 99 BG005197 BF350086 BE715196 BE715155 BF752396 3 AW377699 AW507238 BE082519 AW377700 BF349467 1439101 AA451923 AI340326 AI\$50975 BI791553 AI700963 5 AI220573 AI304772 AI270345 AI627383 AA552300 AI911702 U819984 AI858282 B1468588 AI860584 AI025932 AA026047	7
50			BE713548 AW171 BF993352 BE619069 BE819 AW995615 BE81 AW9668840 AW84 BE685341 AW79 BE695084 AW84 BE713297 BE713 AH90590 AI5544 A1142882 AA039 AW166807 AJ344	0253 BE160433 BI039775 AW886475 BM462504 BE2 3489 BE819009 BF381184 BE715956 R58704 AA852 3489 BE036306 BC990973 BI040954 BF919911 AU1404 4264 BI039782 AU140407 BE144243 BE709863 BF98 8280 AW177933 BF873879 AW178000 BE082526 BF- 47678 BF804153 AW365157 BE813930 BE002030 AW 1048 BF999889 BF368816 BE184394 BE159646 BE7 19304 AL603116 BE149760 BE705967 BE705966 BE7 8371 AW376782 AW848789 AW849074 AW361413 B 3298 BE179915 AW799309 BF72345 BF088676 BE7 1190 BF752409 BE006561 BC959922 BF094833 BF08 103 AI392926 AU158477 BI467252 AU159919 AI7608 1975 AA946936 AA64381 BM314884 AA702424 A41 5078 W95070 AM149191 AA026864 AI830049 AW780 1154 AA515500 AW192085 AA918281 T77861 AB977	31734 BF14926 1112 AW366566 1 1155 A1951766 / 15642 BE00192 476866 BF0859 7365153 BE184 41632 BE18494 05968 AW8487 F927725 BF094 05939 AW7525 14748 BF09458 16 BF082516 AI 7612 AW19055 435 AW78449 A	34 AA340777 BF381183 BG52/137 AUT2720 AW396393 BI090338 BF087707 BE819046 BE819005 AA377127 BE073461 AI434518 AW804674 BF752969 BE837009 BE925826 BF149261 33 BF933510 AW265328 BG436319 BE182166 AW365175 941 BF749421 BE184920 BF839562 BE184933 BF842254 88 BG986845 AA131128 AA099891 W39488 CO4715 BF096124 23 AW376699 AW376817 AW376697 BG005097 BF751115 4211 AW997139 BE865474 BE185187 BE156621 BE715089 99 BG005197 BF350086 BE715196 BE715155 BF752396 33 AW377699 AW607238 BE082519 AW377700 BF349467 1439101 AA451923 AI340326 AI590975 BI791553 AI700963 5 AIZ20573 AJ304772 AI270345 AI627383 AA552300 AI911702 W819984 AI858282 BI468588 AI860584 AI025932 AA026047 F082491 AW021347 AI558096 BE939862 AA0888866 O12062	7
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50 55 60 65 70	456034 432222 459702 444726 444105 455797	685586_1 539529_1 539529_1 3503_2 649788_1 1511159_1	BE713548 AW17: BF993352 BG223 BE819069 BE819 AW995615 BE81- AW96868 BE81: AW68840 AW84 BE698470 BE931 BE865341 AW79 BE696084 AW84 BE713297 BE71: BF093817 BF831 AI190590 AI524 AI412882 AA039 AW166807 AI346 AA705232 AA655 AA705232 AA655 AA705232 AA655 AA705232 AA655 AW799118 BF09 AW799118 BF09 AW866978 BE93 AW365148 AI900 BI089463 BE706 BG981498 BG67 BG9949393 BE71 BE001925 AW36 BG940393 BE71 BE001925 AW36 BG940393 BE93 AW16664668 AW2 AW18320 AI59	0253 BE160433 BI039775 AW886475 BM462504 BE5 4889 BEB19009 BF381184 BE715956 R58704 AA8522 3048 BI036306 BG990973 BI040954 BF919911 AU140 4264 BI039782 AU140407 BE144243 BE70863 BF88 8280 AW177933 BF873679 AW178000 BE082526 BF- 41678 BF804153 AW365157 BE813930 BE002030 AW 1048 BF999889 BF368816 BE184924 BE159646 BE71 9304 AL603116 BE149760 BE705967 BE705966 BE7- 8371 AW376782 AW848789 AW849074 AW361413 B 3371 AW376782 AW848789 AW849074 AW361413 B 3293 BE179915 AW799309 BF872345 BF088676 BE7- 1190 BF752409 BE006551 BG959922 BF094833 BF05 103 AL392926 AU158477 B1467252 AU159919 AI76081 1975 AA946936 AA644381 BM314884 AA702424 A41: 5078 W95070 AA149191 AA026664 AI830049 AW780- B154 AA515500 AW190085 AA918281 T77861 AI9272- 2109 W19287 W02156 AW15038 AA022701 T87181 16078 R20904 BG680059 BG676647 BF764409 AA026 17996 BE002273 AW879451 AL571075 BE067786 AW7 1892 A1915596 AW106614 AI887258 AIS38577 BE926 18970 BE185750 BE714064 BE713903 BE713868 BE7 1873 BE872225 AW391912 BE925515 BG677012 BG7 18938 BB194444 AW96663 BF763109 BE931637 B6 18489 AA715880 BF001091 BF880066 AA666102 AA 18659 A124095 BG199355 AW969908 AA528756 AW 186299 A1204995 BG199355 AW969908 BC64323 BE7 189396 AW849173 BE673179 A1611327 AA705753 BE 1874 A1744241 BE717113 BE717108 BE715564 AI8726 1871 AA152097 W84430 A1304351 BE670780 BF003 18874 BE091871 18719 AA152097 W84430 A1304351 BE670780 BF003	31734 BF14925 112 AW366566 1155 AI951766 / 15642 BE00192 476866 BF0869 37365153 BE184 14632 BE18494 05986 AW8487 05986 AW8487 15072 AW19055 14072 AW1905 14072 AW1906 14072 A	54 AA310777 BF381183 BG5C1373 AUT-1270 AWN39-68-8 BIG90358 BF087707 BE819046 BE819005 AA377127 BE073461 AIA34518 AW804674 BF752969 BE837009 BE925826 BF149261 30 BF333510 AW265328 BG436319 BE182166 AW365175 948 BF592276 BE082507 BE082514 BE082505 BF673693 941 BF749421 BE184920 BF639562 BE184933 BF842254 88 BG986845 AA131128 AA099891 W39488 CO4715 BF096124 233 AW376699 AW376817 AW376697 BG005097 BF751115 2211 AW997139 BE865474 BE185187 BE166621 BE715089 99 BG005197 BF350086 BE715196 BE715155 BF752396 3 AW377699 AW607238 BC602519 AW377700 BF7349563 3 AW377699 AW607238 BC602519 AW377700 BF7349563 5 AI220573 AJ304772 AI270345 AI627383 AA552300 AI911702 B819984 AI858282 B1468588 AI860584 AI025932 AA026047 F082491 AW021347 AI5568096 BE9339862 AA088866 D12062 I349 BF082513 AI494069 AI270027 AI635878 AA128330 BI762796 BG287391 AW798780 BE706045 BE926470 I2 N29754 CO3378 N84767 AA131077 H30146 BE714290 I2 N29754 CO3378 N84767 AA131077 H30146 BE714290 I2 N29754 CO3378 N84767 AA131077 H30146 BE714290 I2 N29754 CO3378 N84767 BA131077 H30146 BE714290 I2 N29754 CO3378 N84767 BA191878 AW103521 BF989173 I2 BG681087 BC688430 AA455100 T8726 BE695209 BE6962 BB E700599 BC677157 BE050909 BC6861378 BE712291 65 W95048 W25458 AW177786 AA025851 BE931733 BF15483 48 BG991212 BF375714 BF349522 BC996267 T48783 BI01329 BR79 BF354008 BF678726 H90899 AW365145 W38382 AM9848 I4 A4849399 AI085759 AI140849 T67412 AI889885 AW1046 CO0338 AI469558 BE715577 AA045413 BF843813	7 5 7 7 7 12 17 7 7 7
50 55 60 65 70	456034 432222 459702 444726 444105 455797	685586_1 539529_1 539529_1 3503_2 649788_1 1511159_1	BE713548 AW17: BF993352 BG223 BE819069 BE819 AW995615 BE81- AW96840 AW84 BE658470 BE931 BE865341 AW79 BE696084 AW84 BE713297 BE71: BF093817 BF831 A1190590 AS524 A4142882 AA039 AW168807 AB28 AW365148 AB90 BG81425 BE70 AW799118 BF08 AW868689 AB5686 AW860878 BE31 BE01925 AW38 BG941939 BE71 BE01925 AW38 BG941939 AB71 BE01925 AW38 BG940189 AW188320 AW5 AW188320 AW5 AW188320 AW5 AW189097 A112 BE091833 BE05 AL110199 AL59 AA358674 A113 AA258674 AH3	0253 BE160433 BI039775 AW886475 BM462504 BE5 4889 BEB19009 BF381184 BE715956 R58704 AA8522 3048 BI036306 BG990973 BI040954 BF919911 AU140 4264 BI039782 AU140407 BE144243 BE709863 BF38 8280 AW177933 BF873673 AW178000 BE082356 BF- 41678 BF804153 AW365157 BE813930 BE002303 AW 1048 BF993889 BF368816 BE184924 BE159646 BE71 9304 AL603116 BE149760 BE705967 BE705966 BE7- 8371 AW376782 AW848789 AW849074 AW361413 B 3298 BE179915 AW799309 BF872345 BF088676 BE7- 1190 BF752409 BE006561 BG959922 BF094833 BF00 103 AJ39226 AU188477 BI467252 AU159919 AJ76081 975 AA946936 AA644381 BW314884 AA702424 A41- 5078 W95070 AA149191 AA026864 AI830049 AW780- 8154 AA515500 AW192085 AA918281 T77661 AB272- 2109 W19287 W02156 AW150038 AA022701 T87181 6078 R29004 BG680059 BG676647 BF764409 AA026 17996 BE002273 AW879451 AL571075 BE067786 AV7 9892 AI915596 AW105614 AI887258 AI538577 BE9264 189707 BE1887520 BE714064 BE713903 BE713868 BE7 1892 AI915596 AW106614 AI887258 AI538577 BE9268 189707 BE1887520 BE714064 BE713903 BE713868 BE7 18934 BI040941 AA337270 AW38471 AW7847442 BI0 18934 BI040941 AA337270 AW38471 AW7847442 BI0 18934 BI040941 AA337270 AW3849171 AW7847442 BI0 18934 BI040941 AA337270 AW3849171 AW7847442 BI0 18043356 AW365154 AW506653 BF763109 BE931637 B 18934 BI040941 AA337270 AW3849171 AW7847442 BI0 18043356 AW369193455 AW969908 AA528756 AW 180573 BG432524 BE157554 BG676890 AU144284 AI7 18043936 AW849173 BE673179 AI611327 AA75753 BE 1814 AI744241 BE717113 BE717108 BE715564 AI872 18191 AA351091 AU4987333 AI039345 AI6593 AI147288 BI191 AA152097 W84430 AI304351 BE670780 BF003 18184 BE091871 18191 AA55097 W84430 AI304351 BE670780 BF003 18184 BE091871 18191 AA55097 W84430 AI304351 BE670780 BF003 18184 BE091871 18191 AA55097 W84430 AI304351 BE670780 BF003 18184 BE091871	31734 BF14925 112 AW366566 1155 AI951766 J 15642 BE00192 476866 BF0869 3/365153 BE184 14632 BE18494 05988 AW8487 15927725 BF094 05939 AW7525 94748 BF09458 16 BF082516 AI 1	54 AA340777 BF381183 BG52/137 AUT1-720 AWN39-693- BIO90358 BF087707 BEB19046 BEB19005 AA377127 BE073461 AI434518 AW804674 BF752969 BEB37009 BE925826 BF149263 3 BF933510 AW265328 BG456319 BE182166 AW365175 941 BF749421 BE184920 BF839562 BE184933 BF842254 8 BG986845 AA131128 AA099891 W39488 CO4715 BF096124 23 AW376699 AW376817 AW376697 BG005097 BF751115 4211 AW997139 BE665474 BE185187 BE156621 BE715089 99 BG005197 BF350086 BE715196 BE715155 BF752396 3 AW377699 AW507238 BE082519 AW377700 BF349467 439101 AA451923 AJ340326 AI590975 BI791553 AI700963 5 AI220573 AJ304772 AI270345 AI627383 AA552300 AI911702 4819984 AI858282 BI468588 AI860584 AI025932 AA026047 F082491 AW021347 AI568096 BE939862 AA088866 D12062 134 BF082513 AJ494069 AI270027 AI635878 AA128330 181762736 BG287391 AW798780 BE706045 BE926470 12 N29754 CO3378 N84767 AA131077 H30148 BE714290 16319486 AA247685 AW798883 AW103521 BF989173 32 BG681087 BG698430 AA455100 T87267 BE696209 BE6962 80 BE705999 BG677157 BE005090 BG681378 BE712291 65 W95048 W25458 AW177786 AA025851 BE931733 BF15833 48 BG991212 BF375714 BF349522 BG999267 T48793 BI01329 8879 BF354008 BF678726 H90899 AW365145 W38382 A449848 54 44 454 AI693500 AW293668 AW371408 BE856107 AI338042 1 A1184302 AA857671 BE857018 AI307420 AI318157 AW20432 731 BF718413 AA877495 BF001575 AI824693 AW849604 2414 AW849399 AI086759 AI140849 T67412 AI889885 AW1046 C00338 AI469558 BE715577 AA045413 BF843813	7 5 7 7 7 12 17 7 7 7

5		BF960659 AA987907 Z41449 BF908059 BF9908053 BF908049 BE699424 BF908060 BF905402 BF950708 BF505020 BF950708 BF090026 BF943158 AI632924 BF512340 BF952021 BF960776 BF943437 BF942847 A1768015 F09778 F04816 F02721 AA102645 AI633838 AA617929 BF947001 BI035448 BE935876 AW890804 BF957405 BF963433 BG704815 AF284421 AL137646 BG542551 AI278088 AI423919 AI274095 BE638965 BE839174 BE839102 BF924520 BI913343 AW238809 AL134380 AW793289 AL534638 T97116 AW855182 C02210 A1783480 AW024874 AL534638 T97116 AW855182 C02210 A1783480 AW024874									
	454478	4273_16 <i>F</i>	UL534638 19/116 A W/796921 AW/7981	02 AW805749 AW805872 BF985060 AW794380 BF3	80449 AW794466 AW794538						
10	404470	4213_10 r	(11730321711730	<b>52.</b>							
	TABLE 63C:										
	Pkey: Ref:	Contract	ne source The 7 d	ting to an Eos probeset igit numbers in this column are Genbank Identifier (GI)	numbers. "Dunham, et al." refe	rs to the publication entitled 'The DNA					
	ruei.	sequen	ce of human chrom	osome 22" Dunham, et al. (1999) <u>Nature</u> 402:469-495.							
15	Strand:	Indicate	s DNA strand from	which exons were predicted.							
	Mt_position:	Indicate	s nucleotide position	ns of predicted exons.							
	Pkey	Ref :		osition							
20	401781			5-83435,83531-83656,83740-83901,8423 7-28617,28920-29045,29135-29296,2941							
20				76-165996,166189-166314,166408-16656							
	401765		Minus 1974	8-20683							
	401760	9929699		6-83250,85320-85540,94719-95287							
25	402880			5-41865 29-116371,117512-117651							
25	406387 403828			5-32148							
	403628		Plus 5138	2-51521							
	404246	7406725		7-82628,82721-82817,82910-83071,8314							
20	403986	•••••		12-91238 277 127996							
30	402218	7689783	Plus 1276	577-127886							
35	TABLE 64A: ABOUT 929 GENES DOWNREGULATED IN PRIMARY MELANOMAS AND/OR MELANOMA METASTASES RELATIVE TO NORMAL SKIN Table 64A lists about 929 genes downregulated in primary melanomas and/or melanoma metastases relative to normal skin. Genes were selected from 59680 probesets on the Eos/Affymetrix Hud3 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.  Pkey: Unique Eos probeset identifier number ExAcon: Exemplar Accession number, Genbank accession number										
40	UnigenelD		ne number								
40	Unigene Ti R1		ne gene title rementile of normal	skin Als divided by the 90th percentile of primary mela	noma and melanoma metastasi	s Als					
	R2	90th r	sercentile of normal	skin Als divided by the 90th percentile of primary mela	inoma and metanoma metastasi	s Als, where the 15th percentile or normal ussue					
		Als w	as subtracted from	both the numerator and denominator							
45	Pkey	ExAcon	UnigenelD	Unigene Title	R1	R2					
40	420813	X51501	Hs.99949	prolactin-induced protein	27.72	20.12					
	408591	AF015224	Hs.46452	mammaglobin 1	26.40 26.16	24.26 20.45					
	431360	NM_000427	Hs.251680	loricrin Target Exon	19.68	19.56					
50	401781 412636	NM_004415		desmoplakin (DPI, DPII)	18.12	10.36					
30	429441	AJ224172	Hs.204096	tipophilin B (uteroglobin family member)	16.61	18.06 25.32					
	418067	A1127958	Hs.83393	cystatin E/M	16.00 15.64	11.81					
	409632	W74001	Hs.55279 Hs.80828	serine (or cysteine) proteinase inhibito keratin 1 (epidermolytic hyperkeratosis)	15.03	37.51					
55	409601 401780	AF237621	ns.00020	NM_005557*:Homo sapiens keratin 16 (foca	14.20	14.86					
55	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	13.95 13.52	28.08 18.85					
	420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7 collagen, type XVII, alpha 1	13.14	13.81					
	422511	AU076442 L22524	Hs.117938 Hs.2256	matrix metalloproteinase 7 (matritysin,	12.78	6.35					
60	428330 421733	AL119671	Hs.1420	fibroblast growth factor receptor 3 (ach	12.78	15.22					
00	428824	W23624	Hs.173059	ESTs	12.67	13.24 12.42					
	453309	AI791809	Hs.32949	defensin, beta 1	12.02 11.79	12.32					
	446227	A1281459	Hs.270114 Hs.334309	ESTs keratin 6A	11.58	9.02					
65	421948 432877	L42583 AW974111	Hs.292477	ESTs	11.18	11.30					
0,5	412047	AA934589	Hs.49696	ESTs	11.04 10.79	11.07 11.40					
	407230	AA157857	Hs.182265	keratin 19	10.73	7.94					
	421296	NM_002666	Hs.103253 Hs.57771	perilipin kallikrein 11	10.72	10.70					
70	410001 418026	AB041036 BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	10.33	7.16					
70	447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	10.09	9.67					
	401203			Target Exon	9.95 9.71	7.37 20.05					
	452308	AI167560	Hs.61297	ESTs	9.66	8.41					
75	425580 433124	L11144 U51712	Hs.1907 Hs.13775	galanin hypothetical protein SMAP31	9.50	4.96					
, ,	420919	M57892	Hs.100322	carbonic anhydrase VI	9.41	6.34					
	443162	T49951	Hs.9029	DKFZP434G032 protein	9.36	10.58 11.73					
	427666	A1791495	Hs.180142	calmodulin-like skin protein (CLSP)	9.19 8.85	11.73 17.76					
80	431369	BE184455	Hs.251754 Hs.135188	secretory leukocyte protease inhibitor ( ESTs	8.82	26.43					
٥U	408536 430686			desmoglein 1	8.73	6.58					
	436895		Hs.5338	carbonic anhydrase XII	8.69	6.81					
	418663		Hs.41690	desmocollin 3	8.61	9.15					

	*****			and the state of t	8.51	13.13
	429852 424012	AB010445 AW368377	Hs.225948 Hs.137569	small inducible cytokine subfamily A (Cy tumor protein 63 kDa with strong homolog	8.44	9.61
	430130	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (	8.39	5.13
	442577	AA292998	Hs.163900	ESTs	8.34	7.92
5	437191	NM_006846	Hs.331555	serine protease inhibitor, Kazal type, 5	8.16	10.68
_	420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	8.04	7.55
	413859	AW992356	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	7.68	7.81
	452240	AI591147	Hs.61232	ESTs	7.63	9.39
• •	442757	A1739528	Hs.28345	ESTs	7.62	7.31
10	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	7.51	6.17
	456525	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	7.49 7.35	7.12
	407328	AA508857		ESTs, Weakly similar to ALU1_HUMAN ALU S	7.35 7.16	7.20 8.39
	414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	7.13	15.05
15	417240	N57568	Hs.48028	EST Homo sepiens cDNA FLJ14462 fis, clone MA	7.13	7.28
13	410052 431842	AA525225 NM_005764	Hs.334630 Hs.271473	epithelial protein up-regulated in carci	7.06	6.93
	426488	X03350	Hs.4	alcohol dehydrogenase 1B (class I), beta	7.03	7.85
	439394	AA149250	Hs.56105	ESTs	7.00	4.53
	422963	M79141	Hs.13234	ESTs	6.99	5.30
20	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	6.97	20.68
	410530	M25809	Hs.64173	ATPase, H transporting, lysosomal (vacuo	6.96	7.04
	446989	AK001898	Hs.16740	hypothetical protein FLJ11036	6.96	6.68
	427890	AA435761		ESTs	6.94	6.68
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	6.84	8.44
25	429624	AA458648	Hs.99476	ESTs, Wealthy similar to 1313184B alpha1	6.83	6.37
	451029	AAB52097	Hs.25829	ras-related protein	6.81	8.96 7.68
	408000	L11690	Hs.198689	bullous pemphigoid antigen 1 (230/240kD)	6.80 6.77	14.06
	439496	BE616501	Hs.32343	Homo sapiens, Similar to RIKEN cDNA 1110	6.72	7.11
30	431713	AK000388	Hs.267997	EHM2 gene - claudin 10	6.71	7.17
30	451253 414987	H48299 AA524394	Hs.26126 Hs.294022	hypothetical protein FLJ 14950	6.67	11.68
	400304	AF005082	Hs.113261	Homo sapiens skin-specific protein (xp33	6.64	7.90
	408063	BE086548	Hs.42346	calcineurin-binding protein calsarcin-1	6.60	7.29
	424364	AW383226	Hs.163834	ESTs, Weakly similar to G01763 atrophin-	6.58	6.78
35	421773	W69233	Hs.112457	ESTs	6.55	17.59
	425280	U31519	Hs.1872	phosphoenolpyruvate carboxykinase 1 (sol	6.55	6.79
	411388	X72925	Hs.69752	desmocollin 1	6.55	8.97
	401785			NM_002275*:Homo sapiens keratin 15 (KRT1	6.51	9.94
4.0	406867	AA157857	Hs.182265	keratin 19	6.50	6.23
40	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3) (NGAL)	6.43	6.79
	426106	AI678765	Hs.21812	ESTs	6.41	7.69 7.09
	413172	M38180	Hs.38586	hydroxy-delta-5-steroid dehydrogenase, 3	6.39 6.39	7.71
	407395	AF005082	14- 440405	gb:Homo sapiens skin-specific protein (x	6.36	9.23
45	422166	W72424	Hs.112405	S100 calcium-binding protein A9 (calgran	6.30	5.45
43	437176	AW176909	Hs.42346	catcineurin-binding protein catsarcin-1 ESTs	6.26	6.25
	440383	AA884208 AY007220	Hs.30484 Hs.288998	S100-type calcium binding protein A14	6.22	10.13
	419329 418686	Z36830	Hs.87268	annexin A8	6.19	6.14
	440116	A1798851	113.01200	hemoglobin, gamma G	6.18	4.28
50	424049	AB014524	Hs.138380	KIAA0624 protein	6.18	6.91
•	417366	BE185289	Hs.1076	small profine-rich protein 1B (comifin)	6.17	7.42
	432543	AA552690	Hs.152423	Homo sapiens cDNA: FLJ21274 fis, clone C	6.16	6.86
	414449	AA557660	Hs.76152	decorin	6.15	3.93
	441188	AW292830	Hs.255609	ESTs	6.12	6.68
55	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	6.12	5.33
	431319	AA873350	Hs.302232	ESTs	6.11	6.84
	444105	AW189097		ESTs	5.97 5.94	6.20 5.15
	428358	AA993222	Hs.101915	Stargardt disease 3 (autosomal dominant)	5.71	5.83
60	407788	BE514982	Hs.38991	S100 calcium-binding protein A2 ESTs, Weakly simitar to DAP1_HUMAN DEATH	5.69	4.49
OU	439706	AW872527 ALORO 190	Hs.59761 Hs.189242	Homo sapiens mRNA; cDNA DKFZp434A202 (fr	5.65	5.16
	428666	712000100	Hs.64179	syntenin-2 protein	5.62	5.84
	410541	AA065003 AW972724	113.04173	gb:EST384816 MAGE resequences, MAGL Homo	5.61	5.75
	431926 430332	R51790	Hs.239483	Human clone 23933 mRNA sequence	5.60	5.76
65	444946	AW139205	Hs.156457	hypothetical protein FLJ22408	5.53	9.25
05	430714	AA484757	Hs.287601	Homo sapiens cDNA FLJ13830 fis, clone TH	5.48	5.38
	435538	AB011540	Hs.4930	low density lipoprotein receptor-related	5.46	3.19
	414407	AA147026	Hs.76704	ESTs	5.43	5.29
	417035	AA192455	Hs.22968	Homo sapiens clone IMAGE:451939, mRNA se	5.40	5.40
70	442315	AA173992	Hs.7956	ESTs, Moderately similar to ZN91_HUMAN Z	5.40	3.87
	416931	D45371	Hs.80485	adipose most abundant gene transcript 1	5.39 5.30	9.12
	431048	R50253	Hs.249129	cell death-inducing DFFA-like effector a	5.39 5.37	6.06 5.33
	436090		Hs.332879	EST	5.37 5.37	5.33 5.97
76	411274	NM_002776		kallikrein 10	5.37 5.36	9.35
75	418394	AF132818	Hs.84728	Kruppel-like factor 5 (intestinal)	5.34	4.08
	406706	X03740 AF086289	Hs.231581	myosin, heavy polypeptide 1, skeletal mu skin-specific protein	5.32	10.40
	430171 452747		Hs.234766 Hs.61460	to superfamily receptor UNIR	5.31	6.01
	452/4/ 426451		Hs.169946	GATA-binding protein 3 (T-cell receptor	5.31	3.81
80	414502		Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (I	5.26	5.92
00	424399			AI905687:IL-8T095-190199-019 BT095 Homo	5.25	16.94
	430071		Hs.232068	transcription factor 8 (represses interf	5.20	5.01
	431416		Hs.178604	ESTs	5.18	5.38

Authority				U- 04P04	and the boson facility of the St. 1970	5.17	5.72
1985   AMS99887   th. 292718   ESTs. Weakly similar to RET2_HUMAN RETIN   5.14   4.97   4.97   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.98   4.9		420039	NM_004605	Hs.94581	sulfotransferase family, cytosolic, 2B,		
14868   173651   14.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987   18.5987							
Additional							
1966   173661   16.91877   19   19   19   19   19   19   19	5						3.79
ASSEST   BEMSSSS   BEMSSSS   H1902   H2050	-			Hs.91877		5.08	
10			BE046594				
ASSISTANCE   ASS			AF249745				
442733 AA045144	• •						
March   Marc	10						
MAY							
15   16.57   AAA26174   14.57680   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   16.04   1							
15							
Assessment   Ass	15						
1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875   1875	13			115.70700			
417833				Hs 99249			
August   A						4.90	11.71
A008863						4.85	4.88
## # # # # # # # # # # # # # # # # # #	20					4.80	
April				Hs.145582	DKFZP43411735 protein		
25.5 44393 BE18555 Hs.3118804 M97852 W97826 Hs.55412 ls.55412 ls.5		407102	AA007629		glycerol-3-phosphate dehydrogenase 1 (so		
August							
439552 W67826 Hs.1508	0.0						
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Assession   Asse							
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### ### ### ### ### ### ### ### ### ##	30			He 79103			
1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979   1979	50						
April							
A							3.19
ASSTRICT   AB011792							3.57
424046 AF027866 Hs.138202 serine (or cysteina) problemase inhibitio 4.61 6.89 45525 AW967069 Hs.211556 hypothetical protein MGC5467 4.59 2.45 402234 445235 AW967069 Hs.211556 hypothetical protein MGC5467 4.59 2.45 402234 42798 AF077374 Hs.138322 smell protein MGC5467 4.57 5.47 476 478021 Ms.201	35				extracellular matrix protein 2, female o		
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402294 AF077374 Hs.139322 small proline-rich protein 3 A57 5.12 42098 M93774 Hs.199336 keratin 10 (epidemolyfic hyperkeratosis 4.57 4.76 42098 M93774 Hs.199336 keratin 10 (epidemolyfic hyperkeratosis 4.57 4.76 42008 A807519 Hs.104520 hrom sepiens CMNA FL13998 Hs. chan PL 4.54 4.32 414798 M328323 Hs.97411 hypothetical protein MGC12335 4.53 3.04 416798 M18728 Hs.300346 Misrofibni-associated glycoprotein-2 4.53 2.91 400109 M18728 Hs.300946 Misrofibni-associated glycoprotein-2 4.53 3.94 400109 M18728 Hs.300946 Misrofibni-associated glycoprotein-2 4.50 3.94 439991 Al033229 Hs.118317 Homo sepiens CDNA Full 2088 fis, chone HE 4.50 4.16 439992 Misrofibni-associated sprotein Full 20221 4.49 449785 A1225235 Hs.288300 hypothetical protein Full 20221 4.49 449785 A1225235 Hs.288300 hypothetical protein Full 20221 4.49 42620 A101043 Hs.151264 killsrein 7 (Phymothypic, stratum com 4.47 5.43 432599 MW05494 Hs.257631 ESTs 4.47 3.10 415305 AU076628 Hs.79187 consactic virus and adenovirus receptor 4.45 5.07 42213 AF045941 Hs.112242 normal mucosa of esophagus specific 1 4.43 3.52 441633 AW958544 Hs.112242 normal mucosa of esophagus specific 1 4.43 2.64 441633 AW958544 Hs.112242 normal mucosa of esophagus specific 1 4.43 4.29 44091 Misrofila Hs.33038 Hs.23071 ESTs 4.41 3.77 43040 A13338 Hs.23071 ESTs 4.43 43040 A13338 Hs.23071 ESTs 4.44 43040 A13339 A1902298 Hs.33031 Ks.23041 ESTs 4.43 43040 A133339 A190226 Hs.23046 Hs.39174 ESTs 4.3040 A133339 A190226 Hs.30368 Hs.50369 Hs.30394 Hs.50394 Hs.50394 Hs.50394 Hs.50394 Hs.50394 Hs.50396 Hs.50394 Hs.50396 Hs.503996 Hs.50396 Hs.503996 Hs.50396 Hs.503996 Hs.503996 Hs.50396 Hs.5			D81448	Hs.339352	Homo sapiens brother of CDO (BOC) mRNA,		
40 42498 AF077374 Hs. 139322 small profiles-rich protein 3 4.57 5.12 420788 W93774 Hs. 99336 keratin 10 (epidemolyfic hyperkeratosis 4.57 4.76 48921 M15981 Hs. 11377 unroundulin furromodulin furromodu		446525	AW967069	Hs.211556			
## 420798   W93774   Hs. 99936   keratin 10 (epidemotyfic hypertecratosis   4.57   4.76   ## 42068   A807579   Hs. 104520   more spiens cDNA F L13598   Ks. John P L   ## 42068   A807579   Hs. 104520   hypothetical protein MCC12335   4.54   4.32   ## 4378   A1286323   Hs. 97411   hypothetical protein MCC12335   4.53   3.04   ## 40103   Muray 25059   Hs. 272023   transforming, acidic colled-coll contain   4.52   3.94   ## 407424   Mi18728   dynamic more spiens cDNA F L13598   Ks. John P L   ## 43992   A103229   Hs. 118317   Homo sapiens cDNA F L12688 fs. chone HE   4.50   4.77   ## 43785   B1383676   Hs. 334   Homo sapiens cDNA F L12688 fs. chone HE   4.50   4.77   ## 43785   A128533676   Hs. 283300   hypothetical protein F L123231   4.93   ## 449785   A1225235   Hs. 288300   hypothetical protein F L123231   4.93   ## 449785   A1225235   Hs. 288300   hypothetical protein F L123231   4.94   4.02   ## 449785   A1225235   Hs. 283300   hypothetical protein F L123231   4.93   4.02   ## 45260   AU07628   Hs. 257631   ESTs   4.47   5.43   ## 45200   Mu D11646   Hs. 34853   inhibitor of DNA binding 4, dominant neg   4.45   3.17   ## 46305   AU07628   Hs. 115166   soicillin   4.45   3.12   ## 46303   AU07628   Hs. 112242   normal mucosa of esophagus specific 1   4.43   3.52   ## 46304   A433338   Hs. 12321   soicillin   4.45   4.27   ## 46304   A433338   Hs. 12321   soicillin   4.45   4.27   ## 4780470   Mc1275   Hs. 13305   KIAA0300 protein   4.35   4.99   ## 47974   A4978531   Hs. 337194   ESTs   4.31   4.35   ## 4780470   A4767947   Hs. 337195   ESTs   4.31   4.35   4.99   ## 4780470   A4767947   Hs. 3337194   ESTs   4.35   4.99   ## 4780470   A4767947   Hs. 337195   Hs. 33806   Hs. 33773   4.35068   Hs. 33330   A4702766   Hs. 33737   A4767947   Hs. 53964   Hs. 53074   Hs. 53084   Hs. 53096	40						
## 18027 M15881 Hs.1137 brown of the control of the	40						
4208 AB07519 Hs.104520 Homo sapiens cDNA FLJ13694 fis, clone PL 4.54 4.32 4.4788 AI286323 Hs.97411 hypothetical protein MCCI2335 4.53 3.04 4.00109 4.00109 Hs.300946 Ms.003480 Hs.300946 Ms.00109 Eos Control 4.52 3.94 4.52 4.53 4.59 4.51 4.07 4.59 4.59 4.59 4.59 4.59 4.59 4.59 4.59							
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Society						4.50	4.77
44985   A1225235   Hs. 288300   hypothetical protein FL/23/231   4.49   4.02     424620   AA101043   Hs. 151254   kalilkrein 7 (chymotryptic, stratum com   4.47   5.43     432599   AW452948   Hs. 257631   ESTs   inhibitor of DNA binding 4, dominant neg   4.45   3.17     459290   NM, 001546   Hs. 34853   inhibitor of DNA binding 4, dominant neg   4.45   3.17     416305   AU076628   Hs. 19187   coxsackie virus and adenovirus receptor   4.44   5.25     432314   AA533447   Hs. 312889   ESTs   4.44   3.52     424670   W61215   Hs. 116651   epithetial V-fike antigen 1   4.42   4.27     424670   W61215   Hs. 116651   epithetial V-fike antigen 1   4.42   4.27     413040   AA193338   Hs. 12321   sodium exchanger   4.36   4.58     426974   AB002298   Hs. 173035   KIAA0300 protein   4.35   4.97     48249   AW655331   Hs. 337124   ESTs   4.36   4.49     422305   A173942   Hs. 326416   Homo sapiens mRNA; cDNA DKFZp564H1916 (f   4.33   3.94     422305   A1928242   Hs. 293438   ESTs, Highly similar to AF198488 1 trans   4.32   7.20     439349   A660898   Hs. 6834   ESTs   4.36   4.99     427074   AA527435   Hs. 178589   hepatocellular carcinoma antigen gene 52   4.28   4.97     42833   NM, 003894   Hs. 153405   period (Drosophila) homolog 2   4.22   3.13     406805   A1686003   Hs. 29368   ESTs   4.29   4.16     42833   NM, 003894   Hs. 153405   period (Drosophila) homolog 2   4.22   3.13     406805   A1686003   Hs. 293688   ESTs   4.29   4.16     43806   A1686894   Hs. 153405   period (Drosophila) homolog 2   4.22   3.13     401480   RS7457   Hs. 60841   ESTs   4.19   3.87     401480   RS7457   Hs. 53884   cadherin 13, H-cadherin (heart)   4.19   3.87     401480   RS7457   Hs. 60841   ESTs   4.19   3.87     401	50					4.50	
A32559				Hs.288300	hypothetical protein FLJ23231		
55         459290         NM_001546         Hs.34853         Inhibitor of DNA binding 4, dominant neg         4.45         3.17           416305         AU076628         Hs.115166         sciellin         4.45         5.07           416305         AU076628         Hs.79187         coxsackie virus and adenovirus receptor         4.44         5.25           422314         AA53347         Hs.312989         ESTs         4.44         3.52           41633         AW958544         Hs.112242         normal mucosa of esophagus specific 1         4.43         2.64           424670         W61215         Hs.116651         epithelial V-like antigen 1         4.42         4.27           413040         A4193338         Hs.12321         sodium catchium exchanger         4.36         4.58           48249         AW855331         Hs.137035         KIAA0300 protein         4.35         4.49           487143         AW074266         Hs.23071         ESTs         4.34         4.52           427919         AA173942         Hs.23071         ESTs         4.33         4.92           427919         AA173942         Hs.293438         ESTs, Highty similar to AF198488 1 trans         4.32         7.20           408104         AW9729		424620	AA101043	Hs.151254	kallikrein 7 (chymotryptic, stratum com		
5.5         422313         AF045941         Hs. 115166         sciellin         4.45         5.07           416305         AU076628         Hs. 79167         coxsackie virus and adenovirus receptor         4.44         5.25           432314         AA533447         Hs. 312989         ESTs         4.44         3.52           441633         AW958544         Hs. 112242         normal mucosa of esophagus specific 1         4.43         2.64           424670         W61215         Hs. 116651         epithetial V-like antigen 1         4.42         4.27           413040         AA193338         Hs. 173035         ESTs         4.36         4.58           426974         AB002298         Hs. 173035         KIAA0300 protein         4.35         4.97           48249         AW655331         Hs. 337124         ESTs         4.34         4.52           451743         AW074266         Hs. 23071         ESTs         4.34         4.52           427919         AA173942         Hs. 293438         ESTs, Highly similar to AF198488 1 trans         4.32         7.20           408104         AW972927         Hs. 293368         ESTs         4.31         3.53         3.72           433339         AI660898 <td< td=""><td></td><td>432559</td><td></td><td></td><td></td><td></td><td></td></td<>		432559					
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65       427919       AA173942       Hs.326416       Home sapiens mRNA; cDNA DKFZp564H1916 (f       4.33       3.94         422305       AI922824       Hs.293438       ESTs, Highly similar to AF198488 1 trans       4.32       7.20         408104       AW972927       Hs.293968       ESTs       4.31       3.53         447945       AI922838       Hs.8670       ESTs, Wealdy similar to ALU1_HUMAN ALU S       4.30       3.72         433339       AF019226       Hs.8036       glioblastoma overexpressed       4.29       4.16         427074       AA527435       Hs.178589       hepatocellular carcinoma antigen gene 52       4.28       4.97         453574       AI767947       Hs.50841       ESTs       4.25       3.66         410677       NM_003278       Hs.65424       tetranectin (plasminogen-binding protein       4.25       3.66         424833       NM_003894       Hs.153405       period (Drosophila) homotog 2       4.22       3.13         75       426248       718988       Hs.293668       ESTs       4.21       4.09         406805       AIGB6003       Hs.293668       ESTs       4.21       4.09         406805       AIGB6003       Hs.170673       ESTs, Wealdy similar to T24832 hypoth						4.34	4.52
42305 Al928242 Hs.293438 ESTs, Highly similar to AF198488 1 trans 4.32 7.20 408104 AW972927 Hs.293968 ESTs 447945 Al922838 Hs.9670 ESTs, Weakly similar to ALU1_HUMAN ALU S 4.30 3.72 439349 Al660898 Hs.6834 ESTs 429 4.16 433339 AF019226 Hs.8036 glioblastoma overexpressed 4.29 3.94 427074 AA527435 Hs.178589 hepatocellular carcinoma antigen gene 52 4.28 4.97 453574 AJ767947 Hs.50841 ESTs 410677 NM_003278 Hs.65424 tetranectin (plasminogen-binding protein 4.25 3.66 410677 NM_003278 Hs.65424 tetranectin (plasminogen-binding protein 4.25 17.64 424833 NM_003894 Hs.153405 period (Drosophila) homolog 2 4.22 3.13 42648 T18988 Hs.293668 ESTs 4.21 4.09 406805 Al685003 Hs.296031 ESTs 406805 Al685003 Hs.296031 ESTs 43853 Al440266 Hs.170673 ESTs, Weakly similar to T24832 hypotheti 4.18 5.93 451831 NM_001674 Hs.460 activating transcription factor 3 4.18 4.74 431211 M85849 Hs.232733 gap function protein, beta 2, 26kD (conn 4.17 2.83 430361 AJ033965 Hs.239926 sterol-C4-methyl oxidase-like	65					4.33	3.94
447945 AI922838 Hs.9670 ESTs, Wealdy similar to ALU1_HUMAN ALU S 4.30 3.72 439349 AI660898 Hs.8834 ESTs 4.29 4.16 433339 AF019226 Hs.8036 glioblastorna overexpressed 4.29 3.94 427074 AA527435 Hs.178589 hepatocellular carcinoma antigen gene 52 4.28 4.97 453574 AI767947 Hs.50841 ESTs 4.25 3.66 410677 NM_003278 Hs.153405 period (Drosophita) homolog 2 4.22 3.13 42833 NM_003894 Hs.153405 period (Drosophita) homolog 2 4.22 3.13 426248 718988 Hs.293668 ESTs 4.21 4.09 410480 R97457 Hs.63984 cadherin 13, H-cadherin (heart) 4.19 2.76 406805 AI685003 Hs.296031 ESTs 4.19 3.87 406805 AI685003 Hs.170673 ESTs, Wealdy similar to T24832 hypotheti 4.18 5.93 451831 NM_001674 Hs.460 activating transcription factor 3 4.18 4.74 431211 M85849 Hs.323733 gap junction protein, beta 2, 26kD (conn 4.17 2.83 430361 AI033965 Hs.239926 sterol-C4-methyl oxidase-like			AI928242	Hs.293438	ESTs, Highly similar to AF198488 1 trans		
439349         Al660898         Hs.6834         ESTs         4.29         4.16           433339         AF019226         Hs.8036         glioblastoma overexpressed         4.29         3.94           427074         AA527435         Hs.178589         hepatocellular carcinoma antigen gene 52         4.28         4.97           453574         AJ767947         Hs.50841         ESTs         4.25         3.66           410677         NM_003278         Hs.65424         tetranectin (plasminogen-binding protein         4.25         3.66           424833         NM_003894         Hs.153405         period (Drosophila) homolog 2         4.22         3.13           456248         T18989         Hs.293668         ESTs         4.21         4.09           406805         Al685003         Hs.296031         ESTs         4.19         2.76           406805         Al685003         Hs.196031         ESTs         4.19         3.87           451831         NM_001674         Hs.460         activating transcription factor 3         4.18         4.74           40         431211         M85849         Hs.323733         gap junction protein, beta 2, 26kD (conn         4.17         2.83           430361         AL033965         <		408104	AW972927	Hs.293968	ESTs		
70 433399 AF019226 Hs.8036 glioblastoma overexpressed 4.29 3.94 427074 AA527435 Hs.178589 hepatocellular carcinoma antigen gene 52 4.28 4.97 453574 AI767947 Hs.50841 ESTs 4.25 3.66 4.26 116677 NM_003278 Hs.65424 tetranectin (plasminogen-binding protein 4.25 17.64 424833 NM_003894 Hs.153405 period (Drosophila) homolog 2 4.22 3.13 75 426248 T18988 Hs.293668 ESTs 4.21 4.09 410480 R97457 Hs.63984 cadherin 13, H-cadherin (heart) 4.19 2.76 406805 AI686003 Hs.296031 ESTs 4.19 3.87 438533 AI440266 Hs.170673 ESTs, Wealdy similar to T24832 hypotheti 4.18 5.93 451831 NM_001674 Hs.460 activating transcription factor 3 4.18 4.74 43143436 AI285970 Hs.183817 ESTs 4.17 2.83 430361 AI033965 Hs.239926 sterol-C4-methyl oxidase-like		447945	A1922838	Hs.9670	ESTs, Weakly similar to ALU1_HUMAN ALU S		
427074 AA527435 Hs.178589 hepatocellular carcinoma antigen gene 52 4.28 4.97 453574 A1767947 Hs.50841 ESTs 4.25 3.66 410677 NM_003278 Hs.655424 tetranectin (plasminogen-binding protein 4.25 17,64 424833 NM_003894 Hs.153405 period (Drosophila) homolog 2 4.22 3.13 75 426248 T18988 Hs.293668 ESTs 4.21 4.09 410480 R97457 Hs.63984 cadherin 13, H-cadherin (heart) 4.19 2.76 406805 A1686003 Hs.296031 ESTs 4.19 3.87 438533 A1440266 Hs.170673 ESTs, Wealdy similar to T24832 hypotheti 4.18 5.93 451831 NM_001674 Hs.460 activating transcription factor 3 4.18 4.74 431211 M86849 Hs.323733 gap junction protein, beta 2, 26kD (conn 4.17 2.83) 430361 A1033965 Hs.239926 sterol-C4-methyl oxidase-like	70						
453574 A1767947 Hs. 50841 ESTs 4.25 3.66 410677 NM_003278 Hs. 55424 tetranectin (plasminogen-binding protein 4.25 17.64 424833 NM_003894 Hs. 153405 period (Drosophila) homolog 2 4.22 3.13 75 426248 718989 Hs. 293668 ESTs 4.21 4.09 410480 R97457 Hs. 63984 cadherin 13, H-cadherin (heart) 4.19 2.76 406805 A1686003 Hs. 296031 ESTs 4.19 3.87 438533 A1440266 Hs. 170673 ESTs, Weakly similar to 1724832 hypotheti 4.18 5.93 451831 NM_001674 Hs. 460 activating transcription factor 3 4.18 4.74 431211 M85849 Hs. 323733 gap junction protein, beta 2, 26kD (conn 4.17 2.83 434936 A1285970 Hs. 183817 ESTs 4.19 4.39 430361 A1033965 Hs. 239926 sterol-C4-methyl oxidase-like 4.17 2.38	70						
410677 NM_003278 Hs.65424 tetranectin (plasminogen-binding protein 4.25 17.64 424833 NM_003894 Hs.153405 period (Drosophita) homolog 2 4.22 3.13 426248 T18988 Hs.293668 ESTs 4.21 4.09 410480 R97457 Hs.63984 cadherin 13, H-cadherin (heart) 4.19 2.76 406805 Al686003 Hs.296031 ESTs 4.19 3.87 438533 Al440266 Hs.170673 ESTs, Wealdy similar to T24832 hypotheti 4.18 5.93 451831 NM_001674 Hs.460 activating transcription factor 3 4.18 4.74 431211 M86849 Hs.323733 gap junction protein, beta 2, 26kD (conn 4.17 2.83) 430361 Al033965 Hs.239926 sterol-C4-methyl oxidase-like 4.17 2.38							
75 42833 NM_003894 Hs.153405 period (Drosophila) homolog 2 4.22 3.13 75 426248 T18988 Hs.293668 ESTs 4.21 4.09 410480 R97457 Hs.63984 cadherin 13, H-cadherin (heart) 4.19 2.76 406805 A1686003 Hs.296031 ESTs 4.19 3.87 438533 A1440266 Hs.170673 ESTs, Wealdy similar to T24832 hypotheti 4.18 5.93 451831 NM_001674 Hs.460 activating transcription factor 3 4.18 4.74 431211 M86849 Hs.323733 gap junction protein, beta 2, 26kD (conn 4.17 2.83 430361 A1033965 Hs.239926 sterol-C4-methyl oxidase-like 4.17 2.38							
75 426248 T18988 Hs.293668 ESTs 4.21 4.09 410480 R97457 Hs.63984 cadherin 13, H-cadherin (heart) 4.19 2.76 406805 Al6856003 Hs.296031 ESTs 4.19 3.87 438533 Al440266 Hs.170673 ESTs, Weakly similar to T24832 hypotheti 4.18 5.93 451831 NM_001674 Hs.460 activating transcription factor 3 4.18 4.74 431211 M85849 Hs.323733 gap junction protein, beta 2, 26kD (conn 4.17 2.83 434936 Al285979 Hs.183817 ESTs 4.17 4.39 430361 Al033965 Hs.239926 sterot-C4-methyl oxidase-like 4.17 2.38							
410480 R97457 Hs.63984 cadherin 13, H-cadherin (heart) 4.19 2.76 406805 Al685603 Hs.296031 ESTs 4.19 3.87 438533 Al440266 Hs.170673 ESTs, Weakly similar to T24832 hypotheti 4.18 5.93 451831 NM_001674 Hs.460 activating transcription factor 3 4.18 4.74 431211 M85849 Hs.323733 gap junction protein, beta 2, 26kD (conn 4.17 2.83 434936 Al285979 Hs.183817 ESTs 4.17 4.39 430361 Al033965 Hs.239926 sterok-C4-methyl oxidase-like 4.17 2.38	75						
406805 A1685003 Hs.296031 ESTs 4.19 3.87 438533 A1440266 Hs.170673 ESTs, Weakly similar to T24832 hypotheti 4.18 5.93 451831 NM_001674 Hs.4600 activating transcription factor 3 4.18 4.74 431211 M86849 Hs.323733 gap junction protein, beta 2, 26kD (conn 4.17 2.83 434936 A1285970 Hs.183317 ESTs 4.17 4.39 430361 A1033965 Hs.239926 sterol-C4-methyl oxidase-fike 4.17 2.38	13						
438533 Al440266 Hs. 170673 ESTs, Wealdy similar to T24832 hypotheti 4.18 5.93 451831 NM, 001674 Hs. 460 activating transcription factor 3 4.18 4.74 431211 M86849 Hs. 323733 gap junction protein, beta 2, 26kD (conn 4.17 2.83 434936 Al285970 Hs. 183917 ESTs 4.17 4.39 430361 Al033965 Hs. 239926 sterol-C4-methyl oxidase-like 4.17 2.38							
451831 NM_001674 Hs.460 activating transcription factor 3 4.18 4.74 80 431211 M86849 Hs.323733 gap junction protein, beta 2, 26kD (conn 4.17 2.83 434936 AJ285970 Hs.183817 ESTs 4.17 4.39 430361 AJ033965 Hs.239926 sterol-C4-methyl oxidase-fike 4.17 2.38							
80 431211 M86849 Hs.323733 gap junction protein, beta 2, 26kD (conn 4.17 2.83 434936 AJ285970 Hs.183817 ESTs 4.17 4.39 430361 AJ033965 Hs.239926 sterol-C4-methyl oxidase-like 4.17 2.38							
434936 AJ285970 Hs.183817 ESTs 4.17 4.39 430361 AJ033965 Hs.239926 sterol-C4-methyl oxidase-like 4.17 2.38	80						
430361 A1033965 Hs.239926 sterol-C4-methyl oxidase-fike 4.17 2.38							
			AI033965	Hs.239926			
				Hs.21223	calponin 1, basic, smooth muscle	4.16	5.15

	424070	A 1040000	U- 11010C	AUCC A		0.07
	421978	AJ243662	Hs.110196	NICE-1 protein	4.15	8.07
	437135	AL038624	Hs.208752	ESTs, Wealty similar to ALU8_HUMAN ALU S	4.14	4.92
	442554	AW467376	Hs.129640	ESTs	4.12	4.00
-	451814	AA847992	Hs.137003	ESTs .	4,11	4.58
5	410023	AB017169	Hs.57929	slit (Drosophila) hornolog 3	4.10	3.92
	457121	A1743770	Hs.180513	ESTs, Wealthy similar to KIAA0822 protein	4.09	3.19
	426539	AB011155	Hs.170290	discs, large (Drosophila) homolog 5	4.09	3.69
	430191	Al149880	Hs.188809	EST8	4.07	4.49
	430433	AA478883	Hs.273766	ESTs	4.07	3.74
10	425992	AA367069	Hs.100636	ESTs	4.06	4.37
	428931	AA994979	Hs.98967	ATPase, H()-transporting, lysosomal, non	4.05	4.15
	452392	L20815	Hs.507	comeodesmosin	4.04	11.00
	402845			ENSP00000246267:KIAA0444 PROTEIN (FRAGME	4.03	4.18
	439873	BE159253	Hs.300638	ESTs	4.03	3.86
15	432305	M62402	Hs.274313	Insulin-like growth factor binding prote	4.02	8.79
	420789	AI670057	Hs.199882	ESTs	4.02	4.34
	453560	AA348626	Hs.5890	hypothetical protein FLJ23306	4.02	5.13
	428957	NM_003881	Hs.194679		4.01	4.29
	429556	AW139399		WNT1 inducible signaling pathway protein		
20	448585	AB020676	Hs.98988	ESTs	4.01	4.59
20	403710	ABUZUOTO	Hs.21543	KIAA0869 protein	4.01	4.52
	423634	*******	11. 1500	C4000160:gi]12735793(ref)XP_011928.1  pr	4.00	3.31
		AW959908	Hs.1690	heparin-binding growth factor binding pr	3.98	6.61
	421485	AA243499	Hs.104800	hypothetical protein FLJ 10134	3.98	3.79
25	437611	AA897108		gb:am08a06.s1 Soares_NFL_T_GBC_S1 Homo s	3.97	4.24
25	426500	NM_014638	Hs.170156	KIAA0450 gene product	3.96	4.93
	448710	T62926	Hs.304184	ESTs	3.96	4.54
	408199	AA132637	Hs.15396	Homo sapiens, clone IMAGE:3948909, mRNA,	3.95	5.57
	428340	AF261088	Hs.154721	aconitase 1, soluble	3.94	3.24
20	410197	NM_005518	Hs.59889	3-hydroxy-3-methylglutaryl-Coenzyme A sy	3.94	9.16
30	456972	AI054347	Hs.2017	ribosomal protein L38	3.93	4.37
	418381	AA682393	Hs.119237	ESTs	3.93	3.45
	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	3.92	15.00
	456332	AA228357		gb:nc39d05.r1 NCI_CGAP_Pr2 Homo sapiens	3.91	4.88
	445607	AA488107	Hs.30156	ESTs, Weakly similar to unnamed protein	3.91	3.19
35	426411	AK000708	Hs.169764	hypothetical protein FLJ20701	3.90	4.50
	446733	AA863360	Hs.26040	ESTs, Wealdy similar to fatty acid omega	3.90	3.89
	442498	U54617	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	3.89	5.11
	452894	AI598065	Hs.61558	ESTs	3.88	3.73
	430570	AJ417881	Hs.292464	ESTs	3.87	4.47
40	439625	AF086453	Hs.58611	ESTs	3.86	4.81
70						
	418793	AW382987	Hs.88474	prostaglandin-endoperoxide synthase 1 (p	3.85	3.01
	431247	AL021578	Hs.278489	matriin 4	3.85	3.35
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	3.85	5.15
45	441319	AI354869	Hs.133081	ESTs, Wealthy similar to T08700 hypotheti	3.84	5.03
43	452877	AI250789	Hs.32478	ESTs	3.84	3.26
	444252	R21135	Hs.54985	ESTs	3.83	5.58
	416265	AA177088	Hs.190065	ESTs	3.82	3.87
	418875	W19971	Hs.233459	ESTs	3.80	2.92
50	440509	BE410132	Hs.134202	ESTs, Weakly similar to T17279 hypotheti	3.80	4.36
50	442503	AF147078	Hs.150853	p53-responsive gene 5	3.80	7.53
	427081	AI474533	Hs.170528	ESTs, Moderately similar to ALUC_HUMAN!	3.77	4.81
	458222	AW139592		hypothetical protein DKFZp434K1421	3.77	3.56
	445107	Al208121	Hs.147313	ESTs, Weakly similar to 138022 hypotheti	3.77	3.20
	436283	AJ480319	Hs.120058	ESTs	3.76	3.76
55	436557	W15573	Hs.5027	ESTs, Wealdy similar to A47582 B-cell gr	3.76	2.65
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	3.75	7.59
	434206	AW136973		ESTs, Weakly similar to \$69890 mitogen i	3.72	3.96
	424824	AJ217440	Hs.143873	ESTs	3.72	3.52
	457411	AW085961	Hs.130093	iroquois-class homeobox protein IRX2	3.71	3.05
60	452241	AL050204	Hs.28540	Homo sapiens mRNA; cDNA DKFZp586F1223 (f	3.70	4.84
-	421845	AW021631	Hs.16515	ESTs	3.69	3.59
	413922	AI535895	Hs.221024	ESTs	3.68	4.22
	422746	NM_004484	Hs.119651	glypican 3	3.68	4.29
	433934	AW273261	Hs.216292	ESTs	3.68	4.39
65	452547	AA335295	Hs.74120	adipose specific 2	3.66	12.23
	400295	W72838	10.17120	AJ905687:IL-BT095-190199-019 BT095 Homo	3.66	9.25
	419098	AA234041	Hs.87271	ESTs	3.66	4.94
	417054	AF017060	1.0.01 2.1	aldehyde oxidase 1	3.65	4.51
	423974	AL118754		gb:DKFZp761P1910_r1 761 (synonym: harny2)	3.65	4.32
70	431362	AJ874223	Hs.293560	ESTs	3.65	3.73
. •	420506	AW977779	Hs.194613	ESTs	3.65	3.25
	448065	A1459177	Hs.172759			
				ESTs, Moderately similar to ALU7_HUMAN A	3.64	4.62
	437457	AA757900	Hs.270823	ESTs, Weakly similar to S65657 alpha-1C-	3.64	4.54
75	451951	AW082870	Hs.210954	ESTs	3.64	3.69
,,	436679	AJ127483	Hs.120451	ESTs, Weakly similar to unnamed protein	3.64	3.39
	412676	NM_000165	Hs.74471	gap junction protein, alpha 1, 43kD (con	3.62	3.62
	412668	AA456195	U- 30000	hypothetical protein FLJ14621	3.62	4.22
	413899	AF083892	Hs.75608	tight junction protein 2 (zona occludens	3.62	3.06
80	444726	NM_006147	U- 400707	interferon regulatory factor 6	3.59	10.65
οU	428722	U76456	Hs.190787	tissue inhibitor of metalloproteinase 4	3.59	3.31
	429973	AI423317	Hs.164680	ESTs	3.59	3.71
	452413	AW082633	Hs.215030	ESTs	3.58	4.66
	416157	NM_003243	Hs.342874	transforming growth factor, beta recepto	3.58	4.44

				his advanta brossmantas solutad destain	3.57	3.74
	430397 411939		Hs.105607 Hs.146246	bicarbonate transporter related protein ESTs	3.57	12.42
	450353		Hs.103296	ESTs, Weakly similar to S65657 alpha-1C-	3.57	4.11
_	432406	AI340571	Hs.343666	KIAA0969 protein	3.57 3.56	2.84 3.14
5	439609		Hs.293236	ESTs ESTs	3.56	3.48
	435381 410173	AW136397 AA706017	Hs.175382 Hs.119944	ESTs	3.56	3.37
	414002	NM_006732	Hs.75678	FBJ murine osteosarcoma viral oncogene h	3.56 3.55	9.93 4.24
10	413305	NM_000426	Hs.323511	Homo sapiens cDNA: FLJ23176 fis, clone L	3.55	4.77
10	434360	AW015415	Hs.127780 Hs.136574	ESTs arachidonate 12-lipoxygenase, 12R type	3.53	5.65
	423973 425681	AF038461 AB018297	Hs.159183	KIAA0754 protein	3.52	4.79
	428382	AF007132	Hs.184019	Homo sapiens clone 23551 mRNA sequence	3.51 3.51	4.46 3.63
	451184	T87943		transcription factor 7-like 2 (T-cell sp	3.51	3.30
15	448496	BE379077	Hs.130849 Hs.159608	ESTs, Weakly similar to I38022 hypotheti aldehyde dehydrogenase 3 family, member	3.48	8.66
	425831 428232	U46689 BE272452	Hs.183109	monoamine oxidase A	3.48	9.54
	425483	AF231022	Hs.158159	FAT turnor suppressor (Drosophila) homolo	3.48	6.05 7.86
••	401760			Target Exon	3.48 3.47	3.67
20	427899	AA829286	Hs.332053	serum amyloid A1 ESTs	3.46	3.85
	451767 452849	A1625014 AF044924	Hs.187328 Hs.30792	hook2 protein	3.45	5.66
	427408	AA583206	Hs.2156	RAR-related orphan receptor A	3.45	5.02 3.61
	447165	AL042400	Hs.75668	Homo sapiens, Similar to RIKEN cDNA 1700	3.45 3.45	7.71
25	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ ESTs	3.44	8.46
	420876 421114	AA918425 AW975051	Hs.177744 Hs.293156	ESTs. Weakly similar to 178885 serine/th	3.44	4.47
	426233	AA372796	Hs.269339	ESTs, Weakly similar to AF161356 1 HSPC0	3.44	3.96 4.32
	428221	U96781	Hs.183075	ATPase, Ca transporting, cardiac muscle,	3.42 3.42	6.35
30	403593		U= 100014	Target Exon hypothetical protein FLJ20207	3.42	3.34
	423467 447731	AK000214 AA373527	Hs.129014 Hs.19385	CGI-58 protein	3.41	2.44
	456327	H68741	Hs.38774	ESTs	3.40	3.46 3.61
	413880	AI660842	Hs.110915	interleukin 22 receptor	3.37 3.37	3.44
35	429501	A1700588	Hs.293388	ESTs, Weakly simitar to A34612 zinc fing hypothetical protein MGC11242	3.36	4.87
	437575 420231	AW954355 R06866	Hs.36529 Hs.19813	ESTs	3.36	8.60
	424010	AL080188	Hs.137556	Homo sapiens mRNA; cDNA DKFZp434A132 (fr	3.36	6.20
	426789	F06596	Hs.23837	Homo sapiens cDNA FLJ11812 fis, clone HE	3.34 3.34	3.40 3.35
40	434274	AA628539	Hs.116252	ESTs, Moderately similar to ALU1_HUMAN A elastase 2, neutrophil	3.34	4.06
	420693 418318	NM_001972 U47732	Hs.99863 Hs.84072	transmembrane 4 superfamily member 3	3.33	4.36
	413163	Y00815	Hs.75216	protein tyrosine phosphatase, receptor t	3.32	9.47
	428496	AA769986	Hs.185802	ESTs	3.32 3.31	3.88 4.01
45	416349	X69089	Hs.79227	myomesin (M-protein) 2 (165kD) ESTs, Moderately similar to S72481 proba	3.31	3.31
	409095	AW337272 AI937532	Hs.293656	gb:wp78d02.x1 NCI_CGAP_Bm25 Homo sapien	3.31	4.40
	443072 437596	AA761490		ESTs, Moderately similar to \$65657 alpha	3.30	5.31
	444094	A1695764	Hs.202394	ESTs	3.29 3.29	3.47 3.76
50	437150	R51407	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	3.28	4.30
	407334	AA494411	Hs.296031 Hs.227948	ESTs serine (or cysteine) proteinase inhibito	3.28	3.78
	423017 447875	AW178761 R22029	Hs.13905	ESTs	3.28	3.44
	418969	W33191	Hs.28907	hypothetical protein FLJ20258	3.27 3.27	3.71 4.28
55	411962	AA099050		gb:zk85d12:r1 Soares_pregnant_uterus_NbH	3.27	3.82
	424395	AA165082	Hs.146388	microtubule-associated protein 7 ENSP00000238970*:CIG30 (Fragment).	3.27	2.60
	400494 430418	R98852	Hs.36029	heart and neural crest derivatives expre	3.26	6.19
	409231		Hs.692	GA733-2 antigen; epithelial glycoprotein	3.26 3.26	4.24 5.17
60	434952		Hs.4285	Homo sapiens cDNA: FLJ22505 fis, clone H	3.25	5.59
	445234			ESTs BarH-like homeobox 2	3.25	5.21
	426150 400076		6 H5.10/210	Eos Control	3.25	3.60
	421462		Hs.104624	aquaporin 9	3.25	3.93 3.53
65	420677	AW086215		ESTs	3.25 3.24	3.88
	424125		Hs.1735 Hs.9667	inhibin, beta B (activin AB beta polypep butyrobetaine (gamma), 2-oxoglutarate di	3.24	5.64
	443672 420682		Hs.88602	ESTs	3.24	4.13
	42372			hypothetical protein LOC57822	3.23	4.90
70	43115	7 AI823969	Hs.132678	ESTs	3.23 3.23	3.97 3.39
	44046			gb:ny40e07.s1 NCI_CGAP_Pr12 Homo sapiens ESTs	3.21	5.36
	44996 40794			ICEBERG caspase-1 inhibitor	3.21	4.61
	40083			chromosome 2 open reading frame 2	3.21	3.62
75	41332	9 A1056885		ESTs	3.21 3.21	3.43 3.72
	41482		, Hs.77432	epidermal growth factor receptor (avian integrin, beta 8	3.20	5.89
	45086 44481		r Hs.283742	H.sapiens mRNA for retrotransposon	3.19	6.84
	45385			ESTs, Weakly similar to ALUB_HUMAN !!!!	3.19	3.59
80	43227	8 AL137506	Hs.274256	hypothetical protein FLJ23563	3.19 3.18	3.51 5.50
	42007		5 Hs.190074	ESTs CO34 antigen	3.18	3.65
	41848 40852		Hs.46320	Small proline-rich protein SPRK (human,	3.18	7.43
				***		

				FOT. W. III. I . 7-1- DOI 1000 6-75-	3.17	3.51
	435337	AI078307	Hs.134317	ESTs, Weakly similar to PC4259 ferritin DKFZP434J214 protein	3.17	3.62
	445502	AW379160 AA150864	Hs.12813	microsomal glutathione S-transferase 1	3.17	5.39
	412477 421757	Z20897	Hs.296259	paraoxonase 3	3.16	3.60
5	413835	A1272727	Hs.249163	fatty acid hydroxylase	3.16	5.56
,	420309	AW043637	Hs.21766	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.15	1.99
	444895	AI674383	Hs.22891	solute carrier family 7 (cationic amino	3.15	4.45
	414869	AA157291	Hs.21479	ubinuclein 1	3.13	4.40
	412947	AA122277		gb:zk97e09.s1 Soares_pregnant_uterus_NbH	3.13	3.30
10	443265	AI916207	Hs.9167	SH3 domain binding glutamic acid-rich pr	3.12	4.62
	421335	X99977	Hs.103505	ARS component B	3.11	11.54
	401905			ENSP00000252232":Sterol regulatory eleme	3.10	2.85
	443514	BE464288	Hs.141937	ESTs	3.09	3.66
1.	418817	AA913229	Hs.19339	ESTs	3.08	3.88
15	434727	H43374	Hs.7890	Homo sapiens mRNA for KIAA1671 protein,	3.08	4.18
	435858	AF254260	Hs.283009	tuftelin 1	3.08	3.96
	430285	Al917602	Hs. 106440	ESTs	3.07	3.30
	448106	AI800470	Hs.171941	ESTs	3.07 3.07	5.19 3.85
20	432908	A1861896	11- 000004	ESTs	3.07	3.38
20	450086	AW016343	Hs.233301	ESTs	3.07	3.29
	451529	AI917901 NM_005239	Hs.208641	ESTs v-ets avian erythroblastosis virus E26 o	3.06	4.12
	418443 426848	H72531	Hs.85146 Hs.36190	ESTs	3.05	4.34
	429506	D49835	Hs.171942	ras responsive element binding protein 1	3.05	3.97
25	425955	T96509	Hs.248549	ESTs, Moderately similar to S65657 alpha	3.05	3.29
23	413822	R08950	Hs.272044	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.05	3.89
	434230	AA551569	10.2.2011	hypothetical protein PRO2822	3.04	3.63
	453655	AW960427	Hs.342874	transforming growth factor, beta recepto	3.04	8.09
	415696	AI821552	Hs.188682	ESTs	3.03	3.43
30	449618	AI076459	Hs.15978	KIAA1272 protein	3.01	3.29
-	414665	AA160873		serum armyloid A1	3.01	9.22
	446682	AW205632	Hs.211198	ESTs	3.00	3.30
	443801	AW206942	Hs.253594	intron of: trichorhinophalangeal syndro	2.99	3.74
	412446	A1768015		ESTs .	2.99	4.47
35	449271	AW338067	Hs.7869	Homo sapiens cDNA FLJ11946 fis, clone HE	2.99	4.35
	435702	A1033647	Hs.121001	Homo sapiens, clone IMAGE:3460280, mRNA	2.98	3.49
	403180			Target Exon	2.98	3.92
	434442	AA737415		ESTs	2.98	3.61
40	439593	BE073597	Hs.124863	ESTs	2.98	3.86
40	410453	AW749036		gb:RC2-BT0318-241199-011-110 BT0318 Homo	2.98	3.49
	414766	AW293452	Hs.16228	ESTs	2.97	3.63
	432566	AW439330	Hs.256889	ESTs, Weakly similar to 2109260A B cell	2.97	3.99 6.90
	451541	BE279383	Hs.26557	plakophilin 3	2.97 2.97	3.30
45	452195	AA994712	Hs.116878	ESTs	2.97 2.97	4.10
43	401747	4.4.000000	11- 445027	Homo sapiens keratin 17 (KRT17)	2.96	3.05
	431316	AA502663	Hs.145037	ESTs ESTs	2.95	7.12
	445437 421690	AI224165 AW162667	Hs.148725 Hs.106857	cathindin 2, (29kD, calretinin)	2.95	5.68
	456371	S76825	Hs.89695	insulin receptor	2.94	4.59
50	449543	AF070632	Hs.23729	Homo sapiens clone 24405 mRNA sequence	2.94	4.12
50	436664	AW197887	Hs.253353	ESTs	2.93	3.57
	406962	M13485		gb:Human metallothionein I-B gene, exon	2.93	2.66
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	2.92	7.48
	428769	AW207175	Hs.106771	ESTs	2.92	3.28
55	414629	AA345824	Hs.76688	carboxylesterase 1 (monocyle/macrophage	2.92	3.48
	444204	AI129194	Hs.143040	ESTs	2.92	3.92
	421407	T82331	Hs.182278	ESTs, Weakly similar to CGHU6C collagen	2.91	6.55
	453180	N46243	Hs.110373	ESTs, Highly similar to T42626 secreted	2.90	3.92
<b>C</b> 0	429538	BE182592	Hs.139322	small proline-rich protein 2A	2.88	4.75
60	452554	AW452434	Hs.58006	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.88 2.87	6.74 3.97
	417184	N52510	Hs.268597	Homo sapiens cDNA: FLJ21498 fis, clone C ESTs	2.86	3.48
	412093	BE242691	Hs.14947		2.86	3.32
	424135	AW994455	Hs.140978	Homo sapiens mRNA; cDNA DKFZp762H106 (fr DKFZP434B203 protein	2.86	3.87
65	437167	AL050184 BE394588	Hs.21610	ab:601311808F1 NIH_MGC_44 Homo sapiens c	2.86	3.43
0.5	454065 420230	AL034344	Hs.284186	forkhead box C1	2.85	3.67
	403108	ALUSISHI	113.204100	ENSP00000241415":Hypothetical 67.7 kDa p	2.85	2.62
	434433	AW629759		gb:hh70e05.y1 NCI_CGAP_GU1 Homo sapiens	2.84	3.35
	420544	AA677577	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	2.83	2.66
70	429429	AA829725	Hs.334437	hypothetical protein MGC4248	2.83	3.59
	451721	NM_006946		spectrin, beta, non-erythrocytic 2	2.83	3.36
	424982	U94777		phosphorylase, glycogen; muscle (McArdle	2.83	4.50
	429259	AA420450	Hs.292911	Plakophilin	2.81	4.81
	423523	AW299828	Hs.193580	ESTs	2.80	7.08
75	433637	AW024214	Hs.102307	ESTs	2.80	3.39
	452089	T97294	Hs.271492	ESTs, Weakly similar to PC4211 hepatocel	2.80	3.62
	441187	AW195237	Hs.7734	hypothetical protein FLJ22174	2.80	3.52
	421965	AA301100	Hs.345482	gh:EST14128 Testis tumor Homo sapiens cD	2.79	3.49
00	432098	AF252297	Hs.91546	cytochrome P450 retinoid metabolizing pr	2.79	2.31
80	429128	AA446869	Hs.119316	ESTs	2.78 2.77	4.17 3.65
	438913	AI380429	Hs.172445	ESTs	2.77 2.76	3.79
	445029	AF196481	U= 400040	midline 2 ESTs	2.76	3.00
	419923	AW081455	Hs.120219	Eals	2.0	4.00

	416508	R39769	Hs.56406	ESTs, Moderately similar to ALU8_HUMAN A	2.76	3.59
	412507	L36645	Hs.73964	EphA4	2.76	3.90
	446339	AL046962	Hs.14845	forkhead box O3A	2.75	3.50 3.33
5	433710	AI341867	Hs.188920	ESTs	2.75 2.74	5.77
,	432375 409213	BE536069	Hs.2962 Hs.51133	S100 calcium-binding protein P PTK6 protein tyrosine kinase 6	2.74	3.76
	426653	U61412 AA530892	Hs.171695	dual specificity phosphatase 1	2.74	8.19
	408839	AW277084	115.17 1033	gb:xp61h09.x1 NCI_CGAP_Ov39 Homo sapiens	2.73	3.93
	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	2.73	11.46
10	444026	AA205759	Hs.10119	hypothetical protein FLJ14957	2.73	6.17
• •	433713	AW976511	Hs.112592	ESTs	2.72	3.42
	453317	NM_002277	Hs.41696	keratin, hair, acidic,1	2.72	4.76
	408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle)	2.72	3.74
	432947	AA570710	Hs.270998	ESTs, Weakly similar to I38022 hypotheti	2.72	3.44
15	421428	U26726	Hs.1376	hydroxysteroid (11-beta) dehydrogenase 2	2.72	4.95
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	2.72	4.29
	435016	AI284219	Hs.130749	ESTs, Weakly similar to 138022 hypotheti	2.71	4.45
	449667	AB023227	Hs.23860	KIAA1010 protein	2.71	3.72
	407112	AA070801	Hs.51615	ESTs, Wealdy similar to ALU7_HUMAN ALU S	2.70	3.82
20	433848	AF095719	Hs.93764	carboxypeptidase A4	2.70	2.76
	430152	AB001325	Hs.234642	aquaporin 3	2.69	4.26
	456063	NM_006744	Hs.76461	retinol-binding protein 4, Interstitial	2.69	6.72
	424471	AA341329	Hs.311524	ESTs	2.68	4.57
~~	453201	AI432195	Hs.135098	ESTs	2.68	3.69
25	450912	AW939251	Hs.25647	v-fos FBJ murine osteosarcoma viral onco	2.68	4.25
	404996			Target Exon	2.67	4.28
	409453	AI885516	Hs.95612	ESTs	2.65	6.51
	430937	X53463	Hs.2704	glutathione peroxidase 2 (gastrointestin	2.65	3.78
20	452887	A1702223	Hs. 107253	hypothetical protein DKFZp761F241	264	6.38
30	444169	AV648170	Hs.58756	ESTs	2.64	3.40
	428500	AI815395	Hs.184641	fatty acid desaturase 2	2.64	3.47
	408395	BE072425	Hs.44579	hypothetical protein FLJ20199	2.64	4.01
	432093	H28383		gb:y152c03.r1 Soares breast 3NbHBst Horno	263	4.08
25	451621	AI879148	Hs.26770	fatty acid binding protein 7, brain	2.62	2.51
35	447335	BE617695	Hs.286192	hypothetical protein FLJ20940	2.61	3.62 3.68
	429343	AK000785	Hs.199480	Homo sapiens, Similar to epsin 3, clone	2.61 2.61	3.33
	431166	AW971186	Hs.293839	ESTs	2.61	3.53 3.53
	440659	AF134160	Hs.7327	claudin 1	2.61	3.33 4.48
40	413542	BE295928	Hs.75424	inhibitor of DNA binding 1, dominant neg	2.60	3.51
40	413956	AIB21351	Hs.193133	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.59	3.82
	407299	AA460205	Hs.289770	ESTs, Weakly similar to 138022 hypotheti ESTs	2.58	4.05
	449539	W80363 Al668892	Hs.58446 Hs.239758	hypothetical protein FLJ12389 similar to	2.58	4.19
	413884 445620	AI245225	Hs.17441	ESTs	2.57	3.44
45	433688	AA628467	Hs.112572	Homo sapiens cDNA FLJ14130 fis, clone MA	2.56	3.57
73	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	2.56	3.47
	407083	Z48511	115.135400	H.sapiens XG mRNA (done PEP11)	2.55	3.61
	406790	AA293303		ribosomal protein L27a	2.54	4.36
	450472	AI190071	Hs.55278	ESTs	2.54	4.30
50	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	2.54	3.82
	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member	2.54	3.44
	430821	AA487264	Hs.154974	Homo sapiens mRNA; cDNA DKFZp667N064 (fr	2.54	4.55
	402575	701107204		Rho GTPase activating protein 1	2.53	5.47
	429554	NM_012275	Hs.207224	interleukin 1, delta	2.53	2.40
55	431631	AA548906	Hs.122244	ESTs	2.52	3.79
-	408806	AW847814	Hs.75608	Homo sapiens cDNA: FLJ21532 fis, clone C	2.52	4.51
	420235	AA256756	Hs.31178	ESTs	2.51	4.21
	436314	A1983409		ESTs	2.51	3.11
	432906	BE 265489	Hs.3123	lethal giant larvae (Drosophila) homolog	2.50	5.62
60	429547	AW009166	Hs.99376	FGENESH predicted novel secreted protein	2.49	2.60
	410532	T53088	Hs.155376	hemoglobin, beta	2.49	4.73
	413475	AW021488	Hs.26981	ESTs	2.49	3.90
	429325	AW088739	Hs.243770	ESTs	2.48	3.71
15	424604	AW865388	Hs.151076	KIAA1243 protein	2.48	4.16
65	414320	U13616	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	2.48	3.80
	423929	M69136	Hs.135626	chymase 1, mast cell	2.48	3.47
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	2.47	2.09
	444935	AA262449	Hs.223569	ESTs	2.47	5.96
70	445389	NM_016831		period (Drosophila) homolog 3	2.47	3.41
70	437897	AA770561	Hs.146170	hypothetical protein FLJ22969	2.47	6.80
	446292		Hs.279682	Rh type C glycoprotein	2.46 2.46	7.37
	409178	BE393948	Hs.50915	kallikrein 5		5.59
	452865	AI924046	Hs.119567	ESTs, Weakly similar to A47582 B-cell gr	2.46 2.46	6.03 3.23
75	447179 414459		Hs.157299	ESTs	2.46 2.46	3.23 3.95
. 13	474459		Hs.76171 Hs.22	CCAAT/enhancer binding protein (C/EBP), transplutaminase 1 (K polypeptide epider	2.45	3.94
	428593			degenerative spermatocyte (homolog Droso	244	2.17
	436009		Hs.120925	ESTs	244	2.94
	412810		Hs.74615	platelet-derived growth factor receptor,	2.43	3.61
80	416749		comp Hs.79732	fibulin 1	2.43	4.46
30	444672		Hs.11669	laminin, alpha 5	2.42	6.39
	433143		Hs.294035	ESTs, Weakly similar to ALUS_HUMAN ALU S	2.42	3.45
	406997			metallothionein IV	2.42	3.92
					*	

	423184	NM_004428	Hs.1624	ephrin-A1	2.41	4.34
	421321	NM_005309	Hs.103502	glutamic-pyruvate transaminase (alanine	2.41	5.08
	456826	AJ871742	Hs.302428	wingless-type MMTV integration site fami	2.41	3.92
5	428897	AJ245719	Hs.194385	hypothetical protein FLJ20234	2.41	5.18
3	400232			NM_001895*:Homo sapiens casein kinase 2,	2.41	3.82
	421481	AW391972	Hs.104696	KIAA1324 protein	2.40	4.03
	442083	R50192	Hs.165062	EST ₈	2.39	4.21
	422287	F16365	Hs.114346	cytochrome c oxidase subunit VIIa polype	2.39	8.60
10	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	2.39	2.57
10	457008	AA410446	Hs.112011	ESTs. Wealthy similar to unknown (H.sapie	2.39	3.85
	418355	L42563	Hs.1165	ATPase, H? transporting, nongastric, alp	2.38	3.84
	431179 432563	AI338644	Hs.195432	aldehyde dehydrogenase 2 family (mitocho	2.37	7.89
	402338	NM_013261	Hs.198468	peroxisome proliterative activated recep	2.37	3.77
15	443725	AW245680	Hs.9701	Target Exon	2.37	3.46
• •	436723	AW975895	Hs.307486	growth arrest and DNA-damage-inducible, ESTs	2.37	4.57
	452669	AA216363	Hs.262958	hypothetical protein DKFZp434B044	2.37 2.37	6.39 3.92
	409212	Al082423	Hs.141892	ESTs	2.36	3.79
	451323	AJ903313	Hs.34579	ESTs, Moderately similar to ALUS_HUMAN A	2.35 2.35	3.29
20	400307	AF005081	113.04313	Homo sapiens skin-specific protein (xp32	2.35 2.35	9.96
	421993	R22497	Hs.110571	growth arrest and DNA-damage-inducible,	2.35 2.35	5.16
	451092	AI207256	Hs.13766	Homo sapiens mRNA for FLJ00074 protein.	2.34	5.24
	446948	BE409053	Hs.299629	peroxisomal long-chain acyl-coA thioeste	2.34	3.77
	424425	AB031480	Hs.146824	SPR1 protein	2.34	4.43
25	426050	AF017307	Hs.166096	E74-like factor 3 (ets domain transcript	2.34	5.64
	425180	U00115	Hs.155024	B-cell CLL/lymphoma 6 (zinc finger prote	2.33	3.51
	422106	D84239	Hs.111732	Fc fragment of IgG binding protein	2.33	6.95
	423503	M92843	Hs.343586	zinc finger protein homologous to Zfp-36	2.33	5.57
••	453999	BE328153	Hs.240087	ESTs	2.32	3.40
30	419358	T78763	Hs.90063	neurocalcin delta	2.32	6.72
	430468	NM_004673	Hs.241519	angiopoietin-like 1	2.32	3.90
	456876	AL044870	Hs.208780	ESTs, Weakly similar to T29647 hypotheti	2.32	3.27
	454947	AW846590		gb:QV0-CT0180-011099-025-d07 CT0180 Homo	2.32	4.43
26	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	2.31	7.22
35	438282	BE268268	Hs.195432	aldehyde dehydrogenase 2 family (mitocho	2.31	3.34
	420202	AL036557	Hs.95910	putative lymphocyte G0/G1 switch gene	2.31	8.47
	419245	AI732742	Hs.87440	ESTs	2.31	3.39
	444920	AW450967	Hs.235240	ESTs	2.30	3.30
40	417314	N68168		gb:za11c01.s1 Soares fetal liver spleen	2.30	3.12
40	409586	AL050214	Hs.55044	DKFZP586H2123 protein	2.30	3.52
	433662	W07162	Hs.150826	RAB25 RAB25, member RAS oncogene family	2.29	6.11
	451176	AA046457	Hs.60677	ESTs	2.29	6.59
	410531	AW752953		gb:QV0-CT0224-261099-035-g02 CT0224 Homo	2.29	3.29
45	425982	R05327	Hs.189726	ESTs	2.29	3.37
43	435684	NM_001290	Hs.4980	LIM domain binding 2	2.29	4.54
	453003	AA808466	Hs.103395	hypothetical protein FLJ14146	2.28	3.70
	434411 407394	AA632649 AF005081	Hs.201372	ESTs	2.28	4.40
	411579	AC005258	He 20020	gb:Homo sapiens skin-specific protein (x	2.28	10.57
50	401205	ACUU3238	Hs.70830	U6 snRNA-associated Sm-like protein LSm7	2.28	4.06
•	443102	AI247472	Hs.132965	Target Exon ESTs	2.27 2.27	2.71
	422109	S73265	Hs.1473	gastrin-releasing peptide	2.26	5.66 3.94
	434987	AW975114	12.1410	ESTs	2.26	3,72
	415477	NM_002228	Hs.78465	v-jun avian sarcoma virus 17 oncogene ho	2.26	3.42
55	423515	AA327017	Hs.176594	ESTs	2.25	6.21
	434903	AF161369	Hs.187763	Homo sapiens HSPC106 mRNA, partial cds	2.25	3.62
	443049	AI028613	Hs.132343	ESTs	2.25	3.13
	444637	T19101	Hs.11494	fibulin 5	2.24	6.43
	41,0026	AI912061	Hs.55016	hypothetical protein FLJ21935	2.23	3.31
60	418629	BE247550	Hs.85859	growth factor receptor-bound protein 7	2.23	4.17
	429587	AA283969	Hs.334706	Homo sapiens cDNA FLJ11801 fis, clone HE	2.23	3.79
	431986	AA536130	Hs.149018	Novel human gene mapping to chamosome 20	2.22	3.54
	409571	AA504249	Hs.187585	ESTs	2.22	3.87
<i>C</i> =	446051	BE048061	Hs.37054	ephrin-A3	2.22	4.57
65	422418	AK001383	Hs.116385	hypothetical protein FLJ10521	2.21	4.25
	453023	AW028733	Hs.31439	serine protease Inhibitor, Kunitz type,	2.21	5.07
	435748	AA699756	Hs.117335	ESTs	2.20	3.35
	420105	AW015571	Hs.32244	ESTs, Weakly similar to FMOD_HUMAN FIBRO	2.19	6.55
70	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	2.19	3.51
70	433052	AW971983	Hs.293003	ESTs, Weakly similar to PC4259 ferritin	2.19	3.32
	430310	U80115	Hs.239069	four and a half LIM domains 1	2.19	3.83
	447205	8E617015 R40978	Hs.11006	ESTs, Moderately similar to T17372 plasm	2.19	15.65
	449967		Hs.271498	ESTs, Moderately similar to ALU1_HUMAN A	2.18	3.54
75	452689	F33868 A1675944	Hs.284176 Hs.188691	transferrin	2.18	3.30
, ,	417061 432647	AI807481	Hs.278581	Homo saplens cDNA FLJ12033 fis, clone HE fibroblast growth factor receptor 2 (bac	218	3.77
	401192	A001401	13.410301	Target Exon	2.18 2.17	5.64
	421752	AK001521	Hs.107882	hypothetical protein FLJ10659	2.17 2.16	3.33 3.44
	456646	AJ243662	Hs.110196	NICE-1 protein	2.16	2.39
80	421263	AB020638	Hs.103000	KIAA0831 protein	216	3.37
	445656	W22050	Hs.21299	ESTs, Weakly similar to AF151840 1 CGI-8	2.16	5.17
	450624	AL043983	Hs.125063	Homo sapiens cDNA FLJ13825 fis, clone TH	215	3.87
	429350	AI754834	Hs.131987	ESTs	2.15	3.90

				COT- Made and the Park Control of	2.14	3.28
	448144 429002	AW169230 AW248439	Hs.2340	ESTs, Moderately similar to PC4259 ferri junction plakoglobin	2.14	5.26 5.05
	429297	XB2494	Hs.198862	fibulin 2	2.14	4.32
_	452093	AA447453	Hs.27860	Homo sapiens mRNA; cDNA DKFZp586M0723 (f	2.14	3.99
5	428848	NM_000230	Hs.194236	leptin (murine obesity homolog)	2.14	3.39
	407584	W25945	Hs.8173	hypothetical protein FLJ10803	214 214	3.38 2.51
	453155 453283	AF052126 AA694386	Hs.552 Hs.290914	steroid-5-alpha-reductase, alpha polypep ESTs	213	3.28
	456906	AF117646	Hs.156637	Cas-Br-M (murine) ectropic retroviral tr	2.13	3.76
10	414815	AW292140	Hs.130286	ESTs	2.13	4.16
	417155	T75125	Hs.299148	hypothetical protein FLJ21801	2.13	3.57
	416673	T77052	Hs.14039	ESTs	2.13 2.12	3.43 5.67
	452208 413966	AA024792 AA133935	Hs.31895 Hs.173704	hypothetical protein MGC4093 ESTs, Moderately similar to A53959 throm	2.12	4.76
15	430967	H16791	Hs.100895	ESTs	2.12	2.64
	429015	BE168484	Hs.194737	KIAA0453 protein	2.12	3.30
	439518	W76326		gb:zd60d04.r1 Soares_fetal_heart_NbHH19W	2.11	2.59
	426468	AA379306	Hs.117558	ESTs	2.10 2.10	3.56 3.66
20	407555 419336	Z48511 AA424202	Hs.83834	gb:H.sapiens XG mRNA (clone PEP11). cytochrome b-5	2.10	5.14
20	418226 423441	R68649	Hs.278359	absent in melanoma 1 like	2.10	3.64
	436961	AW375974	Hs.156704	ESTs	210	3.21
	432633	AI796390	Hs.210667	ESTs	2.10	2.58
25	426102	AF200496	Hs.166371	interleukin 1, zeta	2.09 2.09	3.77 3.85
25	445467 437124	A1239832 AA554458	Hs.15617	ESTs, Weakly similar to ALU4_HUMAN ALU S KIAA0666 protein	2.09	3.35
	407757	BE048414	Hs.165215	hypothetical protein MGC5395	2.08	4.41
	407815	AW373860	Hs.183860	hypothetical protein FLJ20277	2.08	5.01
20	443906	AA348031	Hs.7913	ESTs	2.08	3.40
30	423887	AL080207	Hs.134585	DKFZP434G232 protein	2.08 2.08	3.92 4.19
	406400 437704	AA766142	Hs.131810	kallikrein 8 (neuropsin/ovasin) (KLK8) ESTs, Moderately similar to ALU1_HUMAN A	2.07	3.30
	412533	AA679863	Hs.69606	ESTs	2.07	3.39
	426310	NM_000909	Hs.169266	neuropeptide Y receptor Y1	2.06	3.55
35	411821	BE299339	Hs.72249	three-PDZ containing protein similar to	2.06	4.98
	442599	AF078037	Hs.324051	RelA-associated inhibitor	2.06 2.04	7.23 3.52
	432212	AW137742 AB014533	Hs.33010	ESTs KIAA0633 protein ₂	2.04	4.01
	453469 443652	AI080692	Hs.134229	ESTs, Weakly similar to 154401 hypertens	2.04	3.36
40	452955	AW390282	Hs.31130	transmembrane 7 superfamily member 2	2.03	3.64
	424464	R68537	Hs.17962	ESTs	2.03	4.36
	408702	AW959893	Hs.27099	hypothetical protein FLJ23293 similar to	2.03 2.03	3.31 3.83
	439908	Al168031 AW167439	Hs.155507 Hs.190651	ESTs Homo sapiens cDNA FL113625 fis, clone PL	2.02	5.56
45	412825 406784	AI144297	Hs.169401	apolipoprotein E	2.02	3.40
	427309	NM_005714		potassium channel, subfamily K, member 7	2.02	4.58
	453195	BE241876	Hs.32352	hypothetical protein DKFZp434K1210	2.02	3.57
	404246	41/001010	11-0070	Target Exon	2.01 2.01	7.30 5.81
50	443679 410669	AK001818 AW805749	Hs.9670	hypothetical protein FLJ10948 superoxide dismutase 2, mitochondrial	2.01	3.05
50	446193	AI279390	Hs.144658	ESTs, Weakly similar to T17257 hypotheti	2.01	2.32
	449228	AJ403107	Hs.148590	protein related with psoriasis	2.00	5.10
	434346	AA630445		ESTs	2.00	3.51 4.96
55	456098 452467	AW747800 AW500815	Hs.55016	hypothetical protein FLJ21935 ESTs	2.00 2.00	4.66
55	442866	A1743317	Hs.283622	ESTs, Weakly similar to ALU5_HUMAN ALU S	1.98	3,72
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	1.98	3.11
	417553	L09190		trichohyalin	1.98	2.09
60	449142	R15913	Hs.194987	ESTs Homo sapiens brother of CDO (BOC) mRNA,	1.98 1.98	3.50 6.25
00	407597 429299	AA043925 AI620463	Hs.339352 Hs.347408	hypothetical protein MGC13102	1.97	3.77
	423031	A1278995	113.047 400	ESTs	1.97	3.62
	433495	AW373784	Hs.71	alpha-2-glycoprotein 1, zinc	1.96	4.57
66	430420	AW140027	Hs.26373	Homo sapiens cDNA: FLJ23449 fis, clone H	1.96	6.09
65	420139		7 Hs.95351 Hs.85266	lipase, hormone-sensitive integrin, beta 4	1.95 1.95	5.77 6.09
	418462 447261	BE001596 NM_006691		extraceflular link domain-containing 1	1.95	3.33
	437220		Hs.334305	GS1999full	1.94	3.45
70	407601		Hs.37129	sodium channel, nonvoltage-gated 1, beta	1.94	5.46
70	443595		Hs.9613	PPAR(gamma) angiopoietin related protein	1.94	4.67
	409007		Hs.49599 Hs.47061	Homo sapiens mRNA; cDNA DKFZp434G0827 (f unc-51 (C. elegans)-like kinase 1	1.94 1.94	3.59 4.29
	408717 420055			GCN5 (general control of amino-acid synt	1.94	3.38
	430392			latent transforming growth factor beta b	1.93	3.75
75	42507B	NM_00259	9 Hs.154437	phosphodiesterase 2A, cGMP-stimulated	1.93	4.06
	423527		Hs.105861	hypothetical protein FLJ13824	1.93	4.70
	447151		Hs.92679 Hs.111611	Homo sapiens clone CDABP0014 mRNA sequen ribosomal protein L27	1.91 1.91	3.77 3.18
_	422101 456653		Hs.104520	Homo sapiens cDNA FLJ13694 fis, clone PL	1.91	3.41
80	443444			Homo sapiens done TCCCIA00176 mRNA sequ	1.91	3.52
	420924		Hs.245321	ESTs	1.91	3.22
	426048		Hs.134478 Hs.75752	ESTs cytochrome c oxidase subunit VIIb	1.90 1.90	3.56 4.15
	414092	£14244	113.13136	ay workers a surround applicat Allia	*	٠.٠٠

	415274	AC001549	LL 70344	marin becaused with 44 and 1	4.00	c 00
	428368	AF001548 BE440042	Hs.78344 Hs.83326	myosin, heavy polypeptide 11, smooth mus	1.90 1.90	5.88 2.28
	418418	R61527	Hs.237517	matrix metalloproteinase 3 (stromelysin ESTs	1.90 1.90	3.56
	449372	AA001266	Hs.133521	ESTs	1.89	3.90
5	438752	AW238673	Hs.146038	ESTs	1.89	5.24
-	428193	NM_004235		Kruppel-like factor 4 (gut)	1.89	5.21
	433251	AB040955	Hs.322735	KIAA1522 protein	1.89	5.00
	430560	Z28942	Hs.243960	N-myc downstream-regulated gene 2	1.89	7.09
• •	427795	BE268268	Hs.180842	ribosomal protein L13	1.89	4.51
10	410209	AI583661	Hs.60548	hypothetical protein PRO1635	1.89	3.35
	449243	AW295031	Hs.198671	ESTs	1.89	4.26
	420225	AW243046	Hs.282076	Homo sapiens mRNA for KIAA1650 protein,	1.88	6.20
	443932	AW888222	Hs.9973	tensin	1.88	9.28
15	427929	BE613835	. Hs.181159	Homo sapiens mRNA; cDNA DKFZp434F0217 (f	1.87	4.25
13	400078 422639	410000377	11- 420204	Eos Control	1.87	6.73
	447374	AI929377 AF263462	Hs.173724 Hs.18376	creatine kinase, brain	1.87	5.51
	430346	AK000331	Hs.297641	KIAA1319 protein KIAA0462 protein	1.87	3.42
	428223	AA424313	Hs.98402	ESTs	1.87 1.87	4.15 3.70
20	408792	L29433	Hs.47913	coagulation factor X	1.87	4.08
	433855	AA834082	Hs.307559	ESTs	1.87	4.16
	451583	A1653797	Hs.24133	ESTs	1.87	3.81
	426377	AK001921	Hs.169575	hypothetical protein MGC2550	1.86	5.55
~~	431647	AL138578	Hs.266738	hypothetical protein dJ796i17.1	1.86	3.74
25	422055	NM_014320	Hs.111029	putative heme-binding protein	1.86	4.68
	425750	AL050276	Hs.42400	zinc finger protein 288	1.86	4.04
	422491	AA338548	Hs.117546	neuronatin	1.86	4.37
	438942	AW875398	Hs.6451	PRO0659 protein	1.85	5.06
20	400198			Eos Control	1.85	5.22
30	427136	AL117415	Hs.173716	a disintegrin and metalloproteinase doma	1.85	3.41
	427605	NM_000997	Hs.337445	ribosomal protein L37	1.85	4.73
	418253	AA215539	Hs.283643	Homo sapiens cDNA FLJ11606 fis, clone HE	1.84	5.94
	441912	AA971484	Hs.159938	ESTs	1.84	3.73
35	421632	AA825426	Hs.334689	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.83	3.62
33	440602 431882	AI743491	Hs.292692	ESTs	1.83	2.39
	420772	NM_001426 AW752656	Hs.271977 Hs.222707	engrailed homolog 1 KIAA1718 protein	1.83	3.30
	429197	H24471	Hs.26930	ESTs, Wealthy similar to T20272 hypotheti	1.83 1.82	3.73 3.41
	450796	NM 001988	Hs.25482	envoplakin	1.82	7.73
40	426928	AF037062	Hs.172914	retinol dehydrogenase 5 (11-cis and 9-ci	1.82	3.38
	415409	AW993701	119.172914	NS1-associated protein 1	1.82	3.60
	401131	7,11330101		NM_001651*:Homo sapiens aquaporin 5 (AQP	1.82	5.53·
	421324	BE257515	Hs.103503	deoxyribonuclease Hike 2	1.81	5.53
	400079	0020.0.0	113.100000	Eos Control	1.81	6.79
45	430513	AJ012008	Hs.241586	G6C protein	1.81	7.49
	426508	W23184	Hs.170171	glutamate-ammonia tigase (glutamine synt	1.81	3.55
	425883	AL137708	Hs.161031	Homo sapiens mRNA; cDNA DKFZp434K0322 (f	1.80	5.43
	429191	AF065215	Hs.198161	phospholipase A2, group IVB (cytosolic)	1.79	5.90
	432417	AL040360	Hs.162203	ESTs, Weakly similar to alternatively sp	1.79	3.63
50	406467			Target Exon	1.79	4.16
	444135	AK000374	Hs.10346	hypothetical protein FU20154	1.79	3.32
	426402	BE387327	Hs.80475	polymerase (RNA) II (DNA directed) polyp	1.78	3.51
	412524	AA417813	Hs.44208	hypothetical protein FLJ23153	1.78	3.72
55	425880	X01630	Hs.160786	argininosuccinate synthetase	1.78	3.29
55	400300	X03363		HER2 receptor tyrosine kinase (c-erb-b2,	1.78	3.44
	451304	M92642	Hs.26208	collagen, type XVI, alpha 1	1.78	3.57
	400082	NIA 01402E	11- 45540	Eos Control	1.78	3.82
	445503	NM_014835 M13903	Hs.15519	oxysterol-binding protein-related protei	1.77	3.48
60	425415 400083	M13303	Hs.157091	involucrin Eos Control	1.77 1.77	4.64
-	427620	NM_003705	Hs.179866	solute carrier family 25 (mitochondrial	1.76	6.31 3.47
	446971	AI652143	Hs.288382	hypothetical protein FU13111	1.76	4.21
	429807	AK002138	Hs.306227	Homo sapiens cDNA FLJ11276 fis, clone PL	1.76	2.63
	446560	AK001567	Hs.311002	Homo sapiens cDNA FLJ10705 fis, clone NT	1.76	3.82
65	412824	AW958075	Hs.11261	small proline-rich protein 2A	1.76	4.31
	439927	AA854650	Hs.124597	ESTs	1.75	3.63
	410223	\$73775	Hs.60708	calsequestrin 1 (fast-twitch, skeletal m	1.75	3.79
	414500	W24087	Hs.76285	DKFZP564B167 protein	1.75	3.55
~^	448182	AF244137	Hs.20597	host cell factor homolog	1.75	3.40
70	439651	AF086480	Hs.56255	ESTs	1.75	2.55
	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	1.75	3.54
	424389	AA339786		lymphocyte-specific protein 1	1.75	4.48
	450837	D58463	Hs.85969	hypothetical protein FLJ 12270	1.74	3.40
75	425920	AL049977	Hs.162209	claudin 8	1.74	3.33
75	435680	H50946	Hs.284183	Homo sapiens galectin-related inhibitor	1.74	3,47
	439639	AA370045	Hs.6607	AXIN1 up-regulated	1.73	5.22
	416950	AL049798	Hs.80552	dermatopontin	1.73	4.99
	400199	AD011530	He 66106	Ecs Control  ECS Sto demain multiple 2	1.73	6.25
80	409737 424420	AB011539 BE614743	Hs.56186	EGF-like-domain, multiple 3	1.73	4.28
50	424420 421545	AA292810	Hs.146688 Hs.90034	prostaglandin E synthase	1.72	3.42 2.12
	414323	NM_014759	Hs.334688	hypothetical protein FLJ21916 KIAA0273 gene product	1.72 1.71	4.82
	40722B	M25079	Hs.155376	hemoglobin, beta	1.70	7.02
					1.70	1.02

	100013	N77976	us 247020	homoslakia alaka 1	1.70	3.60
	406643 447299	AF043897	Hs.347939 Hs.18075	hemoglobin, alpha 2 chromosome 9 open reading frame 3	1.70	5.10
	439733	AL365412	Hs.107203	hypothetical protein from EUROIMAGE 1759	1.69	2.92
	415512	Y16270	Hs.78482	paralemmin	1.69	4.92
5	407100	R29657		gb:F1-1179D 22 week old human fetal live	1.69	3.96
	425503	W92517	Hs.158203	actin binding LIM protein 1	1.68	5.97
	433738	A1684802		ESTs	1.68	2.88
	406791	AJ220684	Hs.347939	hemoglobin, alpha 2	1.68	3.44
10	428975	NM_004672	Hs.194694	mitogen-activated protein kinase kinase	1.68 1.67	2.74 3.56
10	435661 459317	AF220263 BRCA1b	Hs.193920	MOST2 protein Eos Control	1.67	3.34
	426923	AF112977	Hs.172887	phytanoyi-CoA hydroxylase (Refsum diseas	1.67	4.53
	426682	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polype	1.67	3.36
	417029	AW952192	Hs.273385	guanine nucleotide binding protein (G pr	1.67	5.22
15	437201	F29279	Hs.171625	hypothetical protein MGC14697	1.67	5.75
	454478	AW805749		superoxide dismutase 2, mitochondrial	1.67	4.55
	406710	AI708347	Hs.184014	ribosomal protein L31	1.66	3.80
	431593	NM_002108	Hs.276590	ESTs	1.66	2.45 2.44
20	457820 441899	AA341497 Al372588	Hs.31408 Hs.8022	RAR (RAS like GTPASE) TU3A protein	1.66 1.66	4.06
20	414186	U33446	Hs.75799	protease, serine, 8 (prostasin)	1.65	6.52
	418116	AA252457	Hs.86543	ESTs, Moderately similar to T00256 hypot	1.65	3.44
	403105			Target Exon	1.64	4.12
	450014	N41322	Hs.18441	ESTs	1.64	2.90
25	436685	W28661	Hs.5288	Homo sapiens mRNA; cDNA DKFZp434M245 (fr	1.64	4.49
	401429			C14001067:gi 4126465 db  BAA36581.1  (AB	1.64	3.82
	420983	W95228	Hs.100764	cathepsin G	1.64 1.63	3.64 3.29
	433126 428150	AB021262 AW950547	Hs.99816 Hs.70312	beta-catenin-interacting protein ICAT cytochrome c oxidase subunit VIIa polype	1.63	7.05
30	412295	AW950547 AW088826	HS.70312	poly(A)-binding protein, nuclear 1	1.63	4.01
50	430831	AA703239	Hs.269804	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.63	3.60
	429348	AJ242859	Hs.199731	Langerhans cell specific c-type lectin	1.62	2.64
	407082	247055		gb:Human partial cDNA sequence, famesyl	1.62	2.13
2.5	452556	H78517	Hs.33905	ESTs	1.62	4.64
35	415688	AA166963		gb:zo86d01.s1 Stratagene ovarian cancer	1.62	3.33
	446515	AL048875	11- 724600	hypothetical protein DKFZp566l133	1.62 1.62	3.66 5.65
	445919	T53519	Hs.334692 Hs.18141	hypothetical protein MGC14141 ladinin 1	1.61	5.61
	447330 412374	BE279949 X01388	Hs.73849	apolipoprotein C-III	1.61	5.18
40	400229	A01300	115.730-5	NM_021724°:Homo sapiens nuclear receptor	1.61	3.57
	414814	D14697	Hs.77393	famesyl diphosphate synthese (farnesyl	1.61	2.08
	424397	AI950320		gb:wp08d10.x1 NCI_CGAP_Kid12 Homo sapien	1.60	3.59
	451335	AB023192	Hs.26285	imidazoline receptor candidate	1.60	5.54
4 =	426156	BE244537	Hs.167382	natriuretic peptide receptor A/guanylate	1.60	4.79
45	456267	Al127958	Hs.83393	cystatin E/M	1.60	2.50
	436950	L05779	Hs.113	epoxide hydrolase 2, cytoplasmic	1.60 1.60	3.98 3.28
	421397 419092	S67368 J05581	Hs.103998 Hs.89603	gamma-aminobutyric acid (GABA) A recepto mucin 1, transmembrane	1.60	3.69
	440160	BE560269	Hs.7010	NPD002 protein	1.59	2.49
50	417481	AA203281	Hs.6191	ESTs	1.59	3.60
	406778	H06273	Hs.101651	Homo sapiens mRNA; cDNA DKFZp434C107 (fr	1.58	3.98
	402991			Target Exon	1.58	3.36
	425169	AW292500	Hs.128514	ESTs	1.58	4.00
55	446429	AI681807	Hs.201391	ESTs	1.58 1.57	3.20 3.63
23	426445 425196	AA378739 AL037915	Hs.187711 Hs.155097	ESTs carbonic anhydrase II	1.57	3.44
	422581	NM_016339	Hs.118562	Link guanine nucleotide exchange factor	1.57	3.55
	440054	AW661947	Hs.6891	splicing factor, arginine/serine-rich 6	1.56	3.39
	415988	BE407713	Hs.78943	bleomycin hydrolase	1.56	2.43
60	441860	AW451330	Hs.348198	hypothetical protein FLJ20262	1.55	3.38
	428462	AI571486	Hs.30258	ESTs	1.55	3.65
	449518	BE395253	Hs.30861	ESTs	1.55	3.80
	420075	AF142482	Hs.203846	TEA domain family member 3	1.55 1.54	3.81 3.87
65	406799 450787	AA908548 AB006190	Hs.25475	gb:og83g12.s1 NCI_CGAP_Ov8 Homo sapiens aguaporin 7	1.54	4.06
03	419659	AB023206	Hs.92186	Leman coiled-coil protein	1.54	3.82
	408543	N78098	Hs.44289	ESTs	1.54	3.10
	410169	AI373741	Hs.59384	hypothetical protein MGC3047	1.54	4.73
=-	426068	AF02977B	Hs.166154	jagged 2	1.54	4.82
70	432191	AA043193	Hs.273186	hypothetical protein, clone Telethon(Ita	1.54	5.83
	415166	NM_003652		carboxypeptidase Z	1.54	4.58
	410048	W76467 Al123657	Hs.343874	proline oxidase homotog ESTs. Weakly similar to JC5314 CDC28/cdc	1.54 1.53	4.66 3.41
	430502 433640		Hs.127264 Hs.240443	Homo sapiens cDNA: FLJ23538 fis, clone L	1.53 1.53	4.57
75	413353		Hs.75309	eukaryotic translation elongation factor	1.53	3.59
	431021	AI869664		thiosulfate sulfurtransferase (rhodanese	1.53	3.73
	431243		Hs.252189	syndecan 4 (amphiglycan, ryudocan)	1.52	6.09
	433019		Hs.279915	translocase of inner mitochondrial membr	1.52	4.49
00	406801	AW242054	Hs.190813	ribosomal protein L9	1.51	5.56
80	427461	AA531527	Hs.332040	hypothetical protein MGC13010	1.51	3.77
	432894 415550		Hs.279772 Hs.78501	brain specific protein growth arrest-specific 6	1.51 1.50	6.72 4.02
	424707		Hs.10844	Homo sapiens cDNA FLJ14476 fis, clone MA	1.49	4.02
	747137			······································	••••	

	445624	AW140103	Hs.78880	IVB (bacterial acetolactate synthase)-l	1.48	351
	445071	AJ280246	Hs.149504	ESTs	1.40	3.61 3.39
	440763	A8028988	Hs.7407	KIAA1065 protein	1.48	4.03
5	451988 427841	AF263928	Hs.27410	papillomavirus regulatory factor PRF-1	1.47	3.58
,	426335	AW883367 AI054347	Hs.2017	hypothetical protein MGC\$306 ribosomal protein L38	1.47	3.61
	454098	W27953	Hs.292911	Plakophilin	1.47 1.46	3.76 2.95
	456766	R87310	Hs.7740	oxysterol binding protein-like 1	1.46	3,40
10	440526	AJ832243		ESTs	1.46	3.38
10	452586 433399	AW958479	Hs.289043	spindin	1.45	3.48
	430238	N46406 N72519	Hs.84700 Hs.236545	similar to phosphatidylcholine transfer	1.45	3.44
	425456	T70445	Hs.157850	hydroxyacid oxidase 2 (long chain) ribosomal protein L9	1.45 1.45	4.00 4.79
	411085	AF022991	Hs.68398	period (Drosophila) homolog 1	1.45	4.43
15	433638	AW872507	Hs.3462	cytochrome c oxidase subunit VIIc	1.44	3.89
	445156	N89367	Hs.12373	adenylate cyclase 6	1.44	3.60
	446576 440433	A1659477 AA252452	Hs.7187	dystroglycan 1 (dystrophin-associated gl	1.44	3.07
	434536	H14486	Hs.3903	hypothetical protein FLJ10707 Cdc42 effector protein 4; binder of Rho	1,43 1,42	3.67 3.35
20	423513	AF035960	Hs.129719	transglutaminase 5	1.42	3.18
	418681	AA287786	Hs.23449	insufin receptor lyrosine kinase substra	1.42	3.38
	421935	AA131632	Hs.109672	CMP-NeuAC:(beta)-N-acetylgalactosaminide	1,41	4.04
	406712 413944	M31212 AW001579	Hs.77385 Hs.9645	myosin, light polypeptide 6, alkali, smo	1.41	4.27
25	435879	AW084463	Hs.30002	Homo sapiens mRNA for KIAA1741 protein, SH3-containing protein SH3GLB2; KIAA1848	1.41 1.41	3.80 3.55
	417967	BE244373	Hs.1119	nuclear receptor subfamily 4, group A, m	1.40	4.07
	412669	AW880841	Hs.96908	p63-induced protein	1.40	3.59
	415523	AL042003	Hs.296847	cell matrix adhesion regulator	1.40	4.38
30	406713 439606	U02629 W79123	Hs.77385 Hs.58561	myosin, light polypeptide 6, afkati, smo	1.39	4.03
50	430135	NM_000035	Hs.234234	G protein-coupled receptor 87 aldolase B, fructose-bisphosphate	1.39 1.37	3.65 3.99
	422682	W05238	Hs.94316	ESTs, Weakly similar to T31613 hypotheti	1.36	3.30
	408198	AA131111		gb:zo16b06.r1 Stratagene colon (937204)	1.36	3.33
25	419600	AA448958	Hs.91481	NEU1 protein	1.35	3.49
35	437141 408250	BE304917 R92918	Hs.31097	hypothetical protein FLJ21478	1.34	3.47
	430012	NM_015373	Hs.19597 Hs.227637	KIAA1694 protein chromosome 22 open reading frame 2	1.34 1.32	3.89 4.24
	425183	W76098	Hs.19223	HCCA2 protein	1.32	4.24 3.52
40	427706	AW971225	Hs.293800	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.32	3.50
40	438303	AB028998	Hs.6147	KIAA1075 protein	1.32	3.71
	406800 442533	AA505535	11- 0270	gb:nh84h10.s1 NCI_CGAP_Br1.1 Homo sapien	1.32	3.65
	428475	AA 161224 AF 172940	Hs.8372 Hs.184542	ubiquinol-cytochrome c reductase (6.4kD) CGI-127 protein	1.32	4.14
	406742	Al468091	Hs.279860	tumor protein, translationally-controlle	1.31 1.30	3.43 3.34
45	432295	BE091049	Hs.343665	ribosomal protein S15a	1.30	3.29
	422959	AV647015		paired immunoglobulin-like receptor beta	1.28	3.53
	402956 406743	A A O 1 4 C C D	11- 970000	ENSP00000244002 :KIAA1335 protein (Fragm	1.24	3.38
	437142	AA911568 AI791617	Hs.279860 Hs.145068	tumor protein, translationally-controlla ESTs, Moderately similar to A46010 X-fin	1.24	3.70
50	424372	AW952803	Hs.21732	Homo sapiens cDNA FLJ11780 fis, clone HE	1.23 1.18	3.48 2.44
	414716	AF199598	Hs.97044	Kv channel-interacting protein 2	1.18	3.43
	431931	AB035302	Hs.272212	cadherin 9, type 2 (T1-cadherin)	1.15	2.49
	406587	A18/410000	11- 250646	C15000544*:gi 5454148 ref NP_006368.1  U	1.06	2.25
55	409574 417435	AW419080 NM_005181	Hs.250645 Hs.82129	ESTS	1.00	3.60
••	402075	000.01	113.02123	carbonic anhydrase III, muscle specific ENSP00000251056*:Plasma membrane calcium	1.00 1.00	3.44 3.37
	422330	D30783	Hs.115263	epiregulin	1.00	3.35
	418986	AJ123555	Hs.81796	ESTs .	1.00	3.28
60	404175	A A 0.274 4 F	LI- 40000C	Target Exon	1.00	3.08
00	452640 443564	AA027115 AI921685	Hs.100206 Hs.199713	ESTs, Weakly similar to A53856 anyl-acyl ESTs	1.00	2.82
	7-0001	7432 1003	115.133713	2013	1.00	2.51
	TABLE 64	<b>18</b> :				
65	Pkey:		ue Eos probeset ide	entitier number		
O)	CAT numi Accession		cluster number			
	Accession	. Gen	ank accession nun	wers		
	Pkey	CAT Number	Accession			
70	412636	1438_1	M77830 NM_004	415 AF 139065 BG681115 BG740377 BI712964 BG0006	56 AA 128470 BI438324 H2	7408 BE931630 BE167165 AW370827 AW370813
70			J05211 BG69888	i5 BG740734 BG680618 BG739778 B1765807 BM35340;	3 BM353248 AW177784 AV	V205789 AW951576 AW848592 BE182164
			BF 149266 BE94	0187 81060445 81060444 BF350983 BE720095 BE72006	9 BE715154 BE082584 BE	082576 BE004047 AA857316 BI039774 BE713818
			RE993352 RC22	0253 BE160433 B1039775 AW886475 BM462504 BE931 3489 BE819009 BF381184 BE715956 R58704 AA852213	/34 BF 149204 AAJ40/// E	BF381183 BG621737 AU12 <i>72</i> 60 AW <i>3</i> 64859 B7707 BER10046 BC010006 AA277127 BC072467
			8E819069 BE81	9048 BI036306 BG990973 BI040954 BF919911 AU14015	65 A1951766 A1434518 AWR	804674 RF752969 RFR37009 RF925826 RF149265
75			AW995615 BE81	4264 BI039782 AU140407 BE144243 BE709863 BF9856	42 BE001923 BF933510 A	W265328 BG436319 RF182166 AW365175
			AW847688 BE81	.8280 AW177933 BF873679 AW178000 BE082526 BF47	6866 BF086994 BF592276	BE082507 BE082514 BE082505 BF873693
			AW058840 AW8	47678 BF804153 AW365157 BE813930 BE002030 AW3(	55153 BE 184941 BF749421	BE 184920 BF839562 BE 184933 BF842254
			RESECTATIONS	1048 BF999889 BF368816 BE184924 BE159646 BE7146 19304 AL603116 BE149760 BE705967 BE705966 BE705	NJZ HE 184948 BG986845 A	A131126 AA099891 W39488 C04715 BF096124
80			BE696084 AW84	8371 AW376782 AW848789 AW849074 AW361413 BF9	27725 BF094211 AW99713	ATTOTOTT ATTOOST BUILDUST BE715115
			BE713297 BE71	3298 BE179915 AW799309 BF872345 BF088676 BE705	939 AW752599 BG005197	BF350086 RE715196 RE715155 RE752396
			BF093817 BF831	1190 BF752409 BE006561 BG959922 BF094833 BF0947	'48 BF094583 AW377699 A	W607238 BE082519 AW377700 BF349467
			A1150090 A15544	103 A1392926 AU158477 B1467252 AU159919 A1760816	BFU82516 AI439101 AA451	1923 A1340326 A1590975 B1791553 A1700963

5			A1142882 AA039975 AA946936 AA644381 BM314884 AA702424 Al417612 AW190555 A1220573 Al304772 AIZ70345 Al627383 AA552300 Al911702 AW166807 Al346078 W95070 AA149191 AA026864 Al830049 AW780435 Al078449 Al819984 Al858282 Bl468588 Al860584 Al025932 AA026047 AA703232 AA658154 AA515500 AW192085 AA918281 T77861 Al927207 AI205263 BF082491 AW021347 AJ568096 BE939862 AA088866 D12062 AA056527 AA782109 W19287 W02156 AW150038 AA022701 T87181 H44405 Al910434 BF082513 Al494069 AIZ70027 AI535878 AA128330 BG681425 BE706078 R20904 BG680059 BG676647 BF764409 AA026654 AV745530 BI762796 BC287391 AW799780 BE706045 BE936470 AW799118 BF087995 BE002273 AW879451 AI571075 BE067786 AV721320 Al022862 N29754 C03378 N84767 AA131077 H30146 BE714290 AI686869 AI568892 AI915596 AW105614 Al887258 AI538577 BE926474 BE067737 BG319486 AA247685 AW798833 AW103521 BF989173
10			AW660878 BE939707 BE185750 BE714064 BE713903 BE713868 BE713763 BG950164 BE713810 AW365151 BG955489 BE005272 BF915937 AW365146 AJ905927 BF992780 AW853812 BG954443 BI770853 BG679406 BG740832 BG681087 BG688430 AA455100 T87267 BE666209 BE696210 BI089483 BE006273 BE872225 AW391912 BE925515 BG677012 BG741970 AA026480 BE705999 BG677157 BE009090 BG681378 BE712291 BG961498 BG678984 BI040941 AA337270 AW384371 AW847442 BI058659 BE813656 W95048 W25458 AW177786 AA025851 BE931733 BF154837 BG9813933 BE714441 AW996245 BE711801 AJ284090 BE064323 BE719390 BE940148 BG991212 BF375714 BF349522 BG996267 T48793 BI013292 BE001925 AW365156 AW365154 AW606653 BF763109 BE931637 BE167181 BE713879 BF354008 BF678726 H90899 AW365145 W38382 A4498487
15	407328 427890 440116	534268_1 1373988_1 454673_1	AIG73735 AA978066 AA417099 AA435761 AA972917 AIG60387 R69942 BG655457 BF111453 AI149320 N23160 AI446431 AI758316 AV741781 BI791950 BM055014 AI798851 AA865357 AI417230 NG7277 T55592 T52179
	444105	649788 1	132173 AW189097 A1123917 A1123926
20	431926 424399	1237041_1 2196_1	AW972724 AA877998 AA522631 AU185388 NM_DS8173 AF414087 W72837 BF742809 AW070916 BE092421 AI905687 AA340069 BE074512 AI905623 AI905633 BG202312 W72838 AI139456 BG218084 BE326938 BE186013 AW176044 AW291950 BG185269 BG197186 BG192597 BG183176 BG207535 AI127172 BE815819 AI905624
	426101	3211_1	ALAMONT DOCTORET DOCTORA AUTOCOMO DE 150456 RE226465 AWR72412 AARR553 ANDZ689 AA442639 AAB13004 AA442040 AADOJ 100
25			AA42379 AA229448 N56349 AA460220 AW971193 AA453725 A7742087 AI860142 AW769479 A917507 AI860141 BEGGG272 AR7770057 AI877703 A229164 AW770324 AI87470 BEGG6760 AI827987 AI005467 AA8533517 AA563934 AA522837 AA812876 AW020895 AA60372 AA663178 A1187977 AA229164 AW770324 AA703066 T78981 AA632986 BE708493 R31132 AI253986 AI916737 T84795 T84294 AW961515 AI459289 BF109829 BI91853 AI084517 AW103830 BE835233 AI472712 AV741009 AA551512 N28268 AA436880 AA447794 BE835410 BE835352 BE818352 BE818350 R64648 BE646467 AA493776 AA437299 BE818343 R95914 R31089 BF576826 AU186065 BF802058 AI217018 AA247541 AI191725 BE766918
30	438962 445493	195763_1 423456_1	A)207343 BF813684 BF928775 AA828585 AV711317 A)809938 A)808768 A)240593 A)915771
30	407102	7177_2	AW945170 BF930905 F33652 BG057818 AJ368018 AJ421485 AJ300352 AJ378525 AJ264177 AJ276281 AJ245302 AJ281090 AT190096 AW451436 AW242903 AA910870 F22289 F19647 F22375 AW473816 BF445785 AA774528 F33447 C01077 AW772227 F17759 H42812 R09701 AA349096 R88772 F42892 H42537 R47898 N28263 H25721 F32386 H43971 R48205 F21390 H45809 AA007629 R47897 R83734 H45844 AW983653 H43970
35	421998	133592_1	BI757233 BG911321 BF351759 AW244016 AW026834 AW024260 AI420138 AA775354 AI033-990 AI39368 AW15127 AI37373 AIS53567 AI393760 AI401632 BE218525 AI802114 AI783721 AA845265 AW088826 AI832852 F03967 AI611148 AI720386 AW293764 N91161 R79192 W85852 AW771263 BG820263 BG012864 R74441 R85080 W04256 BE707244 BF899452 BE327552 BE669500 AI492388 AI241532 BF448184 AI209012 AA886528 N70309 AW582776 BF110563 BF448329 BE326537 AW770471 BF444926 BE674147 AI793266 AI991774 AI807726 AI218667 AA301750
40	400330	103120_1	R44328 AW469418 AA053401 AA053416
40	408239 437611	240436_1	H93045 AAR97108 AI652046 AA761626 BF882276 N68615 T88896 H93912 T84424
	456332	21353_10	BG740624 AV720262 BG198346 BG215119 AW841716 AA228357 AW841786
	458222	631332_1	AA932742 AW593558 AW139592 BF591031 AW205438 AA933791 A1434866 BF513564 A1191480 AJ972330 AJ582824 AW779392 AJ359970 Al199117 AJ910783 BF800971 AA627401
45	434206	185910_1	
,,,	400295	2196_1	AI/99/78 BF-22/33 A93/73/ AW1393/ NM_058173 AF414087 W72837 BF742809 AW070916 BE092421 AI905687 AA340069 BE074512 AI905623 AI905633 BG202312 W72838 AI139456 NM_058173 AF414087 W72837 BF742809 AW070916 BE092421 AI905687 AA340069 BE074512 AI905623 AI905633 BG202312 W72838 AI139456 NM_058173 AF414087 W72837 BF742809 AW070916 BE092421 AI905687 AA340069 BE074512 AI905623 AI905633 BG202312 W72838 AI139456 NM_058173 AF414087 W72837 BF815815 BG185269 BG197186 BG192597 BG183176 BG207535 AI127172 BE815819 AI905624 R75793 BG202313 AI905837 BE815853
50	417054	12405_2	R5733 BG32313 A1905037 BC615035 BG533564 BG618564 AW296119 A1269233 BF508328 AW364777 AW292258 AA371049 A1452471 A1092522 BG618376 AL049080 AA631068 BG564643 T53833 AV702544 BG6333452 AV705004 AA588281 T28665 BG569026 AV646874 AV647253 AV647455 AV647749 B1759444 AV652457 AV695354 AV696010 AV697248 BG617586 AV722549 A1435836 A1590676 A1245019 AW338243 AA530898 D52191 A1435352 D57473 BG566952 A1420505 AA035245 AV704972 BG564113 A1439237 A1287456 AV695686 AA349017
	423974	888155_1	A A A A A A A A A A A A A A A A A A A
55	412668	33230_1	AL 118/24 AA3322V 1-3800V AK057749 AI701055 AA115476 AI633570 AI435607 AW173392 AI092468 AI989318 AA833891 AW295964 AI804107 AI767415 AI473818 AI076758 AA278949 AA428547 N31385 H82560 AA464804 AA809073 AA832476 AW295298 BF 108690 AI492243 N22394 AA487175 AA431891 AW070941 AA278823 AA707840 AI346087 AI184307 AA336342 AI28633 AA425697 AI435960 AI301433 AA93394 AI917652 AA487234 AA40964 AA937925 AI301378 AI783840 AI093652 AA723864 BF001378 BIB18971 BI762256 AW957064 BG720359 BI821176 BI906440 AI472868 AL523506 BF962934 BF960650 BI837618 BF956256 AA487349 BF961475 AA354431 AA115452 AA491157 N75632 BF962141 AL562216 BI754640 N24091 R00062
			41000000 TECEON ALMOSEON TECHEN MOTESS DITEORA'S DIS10137 AA710796
60	444726	3503_2	BG285809 BE940673 BG432524 BE157554 BG676980 AU144284 AI745383 AU159045 AI693500 AW233668 AW371408 BE850107 AI539042 AW188320 AI698246 BE673290 AW297655 AA156532 AU017342 AI916754 AI190644 AI184302 AA857671 BE857018 AI307420 AJ318157 AW204327 AW664688 AW274339 AA582788 AI345741 AW301433 AI873468 AW137388 BF718731 BF718413 AA877495 BF001575 AI824693 AW849604
65	454404	4624 4	AW093405 AW89874 A7744241 BE717113 BE717108 BE715564 AW872527 AA029457 C00338 AW69558 BE715577 AA045413 BF843813 A991295 AW89874 A7744241 BE717113 BE717108 BE715564 AW872527 AA029457 C00338 AW69558 BE715577 AA045413 BF843813 Z993286 AV716301 BE722333 AW949687 BF732426 AW94086 AV721430 AW577332 N68315 BE672030 AW084440 AW250908 N50901 AA757364
0.5	451184	1531_4	BF515264 A188231 BE466036 AW631313 AA993514 N54411 BGG57515 AW013895 N77963 AA/08723 AZ72429 N99053 AA22606 AW6176174 AF515261 AA812266 AA553841 AW467057 W68650 A168772 AA988308 AA910057 AI888258 AA918322 AJ335847 AA621494 AA904390 AJ760007 AJ146694 AY758440 BM142562 N66507 AJ674563 AW628584 AI263902 BF223368 AJ090490 AJ452918 N71423 AA062767 T94332 AA016003
70	443072	449629_1	BG681608 AA082426 AA029451 N71873 BF437845 T54154 AV741757 AV734838 AI937532 AI032318 AW749500 AA091720
70	437596		BC022398 AV743635 AW976922 AW152652 AA910013 AA834629 BG536317 AW849807 AV713062 AI684337 BE044081 AA761490
	411962	2307710_1	AA099050 AA099526 T47733
	440469		AUGOCCO2 DEGOCCO DEGACOS DEGACOS AWGOCCO AWGOCCO A AUGOCCO A AUGOCCO ANGO 105 ANGOCCO DEGACO DEGACO A AUGOCCO AWGOCCO ANGO 110/
75	450860	40397_1	BE162152 R77997 BG059091 AV722360 AA370451 AA033785 AV729790 AW953851 AW953855 BE504303 A1765853 BF 059302 AA410685 A1976745 AA399236 BG14945 BE670366 A1694777 BE503109 AA633474 A1700568 A1432181 A1637714 AW302164 AA196790 A1928519 BE673464 BF437523 A1281974 A1306156 AW418884 AA523952 AA683187 AW075563 AA67270 AW204404 AW771341 AJ913892 AW770312 AW242851 AU154858 AA021007 A1521932 AA034044 A1760631 R34679 AJ915923 AJ911609 AW242360 AA059025 AA370450 BF432186 AW862279 AW859976 BE159936
80	418481	17381_1	BF514075 BI057841 R34781 R77900 AA011413 S53911 NM_001773 AL572644 AL550179 A1688653 AW025002 AW614285 AU158779 AI017002 AA434387 AI252665 AI262206 AU147582 A1144193 AW952860 A1128776 AI017793 A1160509 AA906021 A1149563 AU154950 A128488 W77409 AI970362 A1141453 AU158772 W58493 BM148338 R73091 AW020496 B1491517 AA022917 AI432610 AI879448 R69099 A1708954 AW014274 AA483672 AA528783 AA912271 AI926942 BE677587 AI874217 AA152376 AA640408 AI287334 BF830285 AA311473 C18678 AA922603 C00910 A1124073 R38730 AA043439 W94644 W58646 AA664247

			TOTAL DESCRIPTION OF THE PROPERTY OF THE PROPE
			BE061934 H01096 R59613 AI383162 AU133723 AA311526 R67942 H01097 H72113 R72430 R39494 AV744074 AA535925 BI759288 BI052385
	412477	8669_2	BF854687 AW608286 AA043438 R72478 AL513811 R69214 AA188435 AA054965 AI220117 AI857837 AI218371 BM091400 AI304964 AI188508 AI400738 AW571549 AW950042 AI089943 AA437280 AU150878 BF197070 AI267984
	412477		RESDA 181 RE1966RR AIA33152 AI33R921 AI62036A AI280197 AA652531 AI674938 AI342447 AI620350 AI281295 AI148621 N54787 AI338121
5			AIRN 153 NG 1899 AIRN 73 AA 954788 AWNG 9054 AIRAG 309 RG 529629 AIRAG 135 BFO83036 AI 167365 AWB 19657 AA 935468 AI 467868 AW 14870 1
			A1383720 BE047685 AW015498 AA937149 AA708346 AW771478 AW802508 H53334 AW389204 AW798230 A1553922 A1560688 AW950043 A1961682
			AVT06506 R01853 AA126514 N62757 AI536893 AI926052 AI418720 N99964 AI568933 AI915737 AI080691 AI185358 N48996 N68575 H82824 H60037 AI247247 T95664 BF593863 AI749637 AW088541 AA991294 AA887452 AID73726 AA633132 AA629674 AA629664 AA629656 AA578595 AI168758
			AAB04572 A1085786 AA994396 AA991209 AA948663 AA929054 AA927952 T87001 AA928210 AA629296 AW802267 AW384129 BF744400 AA194110
10			AJ382839 AA194837 AA406284 AJ250750 R37035 AJ525586 W01244
	412947	1568055_1	AA122277 BE183957 BE183956
	432908	452541_1	AF150424 AI861896 AA570057 AV738855 AF119900 NM_018539 AA702388 N53043 BF351064 N70103 AI207469 AA551569 AW383189 W00906 W00935 N54252
	434230 414665	41110_1 23751_3	BG567713 AW665841 AB14924 AW978339 AW264036 AJ373950 AW183157 AW082249 AJ201658 AJ364196 AA150743 AA160873 AA453757
15	717000	20101_0	RER71646 RER71640 AA565311 AA989511 R10152 AA807154 T77900 AV751591
	412446	63467_1	BC021735 Al669212 AL 120184 AJ769949 BE701002 BE184363 BE819031 BG702238 BF090049 BF963318 BF961912 BF943013 AA934514 AA151245
			BF960659 AA987907 Z41449 BF908059 BF908053 BF908049 BE699424 BF908060 BF962832 BF952020 BF963134 BI035538 BF908057 BF909026 BF943159 AI632924 BF512340 BF952021 BF960776 BF943437 BF942847 AI768015 F09778 F04816 F02721 AA102645 AI633838
			AA617929 BF947001 BI035448 BE935876 AW890837 AW898604 BF957405 BF963433 BG704815
20	434442	111738_1	AA662701 AA633929 AA737415
	410453	1027545_1	BE065904 AW749036 BE175748 BE175746 BE175747 BE175745 T64217
	454065	517162_1	BE394588 AW024754 BE183167 BE183166 BE378353
	434433	111338_1	AA633408 AW749955 AW629759 AI651005 AK057547 BG181248 AA883756 F25670 AA778128 F27657 F18914 F25171 AA178844 F21556 F25872 F20457 F27617 F36059 F34817 F26967
25	424982	25362_1	F25922 F31278 F34666 F01176 F36333 F01226 F27406 F27130 F26742 F24126 F29891 AA195955 AA086351 W69291 F25880 F32791 F31311
23			F32380 F25216 F19679 F18656 F29700 F24954 F32741 F30404 F35470 F33989 F33141 F36382 F34118 F17714 AA176345 F24700 AA550940
			F18617 F16859 F15633 F34675 F16528 F17281 AA086388 F30859 F21852 C02644 F29425 F25286 C03553 F35259 W80691 F16457 F24094 F16783
			AA 1803 19 F28443 F17763 F17448 F00542 AA 197179 AA 1930 12
20	445029	82093_1	BG566720 AA010276 W92098 BE837833 BF541660 AW889587 AI651246 AI339033 AI078183 AI686504 AA813616 BF056955 RA3664 BF509917
30	400000	224000 4	AW663717 W95054 A1382907 A1399929 F10511 AA427819 AW269408 BE825398 BG654856 AA037082 A1203007 AW593522 H65211 AA010218 A1355222 BF378422 AA366587 BF874552 AW277084 R26970 D79194 R27662
	408839 432093	234669_1 1237011_1	AUSSICZE BPS 10422 AUSGOSOF BPS 1432 AWZ 17604 RZ 0310 DTS 154 RZ 1002 AW972670 AA525808 H28359 H28383
	406790	0.0	AA293303 AA492458 AA948195 AI341912 AI436673
	436314	142774_1	AA708982 Al095911 Al983409
35	406997	29867_1	NA
	400232	928_1	AL581381 BEZ20341 AI695121 BG149299 AI205526 AI968389 BI752979 AI291204 AI954763 AA344460 AA344581 BF082319 AU125758 BE825566 AA954549 AI286069 AA948280 BG149854 BI862122 AI024440 AI090013 NM_001895 M55265 BC002615 BC011668 BM452475 AL560958 AU125134
			BE408670 AL 134963 AIS89577 AIS52244 AW972197 AW403214 AW069872 AI804464 AU123365 AI342226 H50982 AV738572 R94284 BG536938
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40			AARASOS AH13219R AH130091 AH375624 AW183031 AH129003 AH373257 H92896 BE244655 AW028253 AW571546 BH258630 AH807134 AW672915
			AW893438 BF036080 AW054815 AW963200 AI797895 AA604241 AI014611 BE092080 BE092076 AA639870 AA714906 N39594 AA173857 AW951102
	400000	~~	AW951101 BG823603 AI478558 R32009 AW149282 BG818283 R69507 T29481 BE766560 AI693579 H06201
	400307 454947	27110_2 1083824_1	AF005081 BG193848 AW846590 AW846615 AW846584 AW846592 AW846621 AW846610
45	417314	2097082_1	N58158 N59188 N90450
	410531	1030559_1	H88044 BE156092 AW752953
	407394	27110_2	AF005081 BG193848
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50	437124	59408_1	ALDSDOL3 RC339500 AWG69191 AA769925 AL377973 AL625545 AA811365 AA521114 N24705 AL379579 AA424899 AL684671 AA829715 AL453010
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55			A1218758 H25588 N36282 AA024987 N36687 B1919187 N49471 AA889970 AW166152 AA468546 A1262504 A1452782 AA554458 AA807080 AA724542 AW102730 AA909978 AW118134 AW827241 W56431 BM127381 BF436987 A1016509 AW663972 BM127686 C15552 N63435 N51744 T98800 N56980
23			AW102/30 AAS993/6 AW 118/38 AW32/421 W3034/1 BM12/30 1 DF40393 AW1003/2 BW12/30 AV3993/6 AW318 18/4886 D612/78 B1756612 AA508234 R49885 BF8504/22
	432212	629625_1	AW972351 AW182936 AI478370 AA528309 BG997292 AW137742 AI632006 AA775020 AA961625 W85628 BF112014 A1275423 AI680786
	410669	4273_16	AW796921 AW798102 AW805749 AW806872 RE985060 AW794380 BE380449 AW794466 AW794538
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	452467 417553	90115_1 258857_1	AL545411 AI096369 BF431750 AI130946 W60065 W80663 AA258580 W73279 W76156 W80662 AW058658 AI204699 W60115 N56751 N30878
	417555	230007_1	AI769345 R71350 AI363766 R22777 R17009 R27985 R28243
	423031	14129_4	A1278995 AW964552 A1885189 A1571775 A1660803 A1299327 A1719401 Z39652 H25636 BF091855 A1218354 A1928704 A1817774 A1885495 A1695453
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			AW874084 BE720622 A1127241 AA236239 A1679709 A1679135 A1572470 AA573434 A1568487 BE049325 AA687950 BG925989 A1338031 A1365073
			AIG24576 AA208805 HG4601 H45668 RG682146 AI 552388 RI462361 RG547513 RG896863 HIZ56661
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75	400300	1507_2	AWRGGGG AL149552 AAD1088D AA627121 AA778233 RE936663 RG998842 AA652426 AL240816 N80859 T29383 M11730 NM_004448 X03363
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			BF923905 BG283493 AA299475 R80150 BG387145 BF837559 BG469759 AA496412 BF758339 BG957192 AW373869 BG952345 BF229957
			BE697472 BE697475 AA011005 BG005000 T56558 AA908196 AA716585

				W961118 W77994 AA339877 AW845121 AW845129 BG181820 BE716719 AI125483 AI161017 W73951 AI250771 AA912611 AA339786
	424389	1059_4	OC029286 DE	:818282 RE716636 AA777148 WQ4063 RE716628 BE716625 BE8383/1 BF3/1044 BE/10031 BE/10442
	433738	593682_1	ALCGREE AV	V607643 A1280025 A1 037665 AW291619 A1280142 AA765506 A1684802 AW085941 A1088002
	454478	4273_16	414F0000014 AT	M700403 MM00E740 MM06E773 DE09E0E0 MW70479A RF7RD449 AW7944bb AW7945JB
5	412295	133592_1	BI757233 BG	911321 BF351759 AW244016 AW026834 AW024260 AI420138 AA779354 AI093360 AI934858 AW151292 AI373133 AI335587 AI969728
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			R44328	1000 A 1100 E 110
10	415688	1235745_1	A14074740 A	A493942 AA166963
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15			A A 722230 A	MONOCONO ANDROGAN AACORGOT ALGENERO AAGNAOTT AIRETEOT REARTEDE AABORESS ALTRA144 ALGREGIS AV/5255/ AV/5250/ AAV/5250/
			AA764744 A	W149075 N30700 H92303 W79523 A1762795 AA282784 H78923 AA252879 H98107 R23754 AA005152 N39239 N74632 H80133 H24710
		400.0	R38907 R66	368 R42466 R52648 H11010 R98493 M24898 X72631 BE550221 BF436030 F18898 AL567477 BG033127 BG747927 BF823716 AA371902 AL137978 AL577786 BI490529
	400229	462_3	MM_UZ1724 AA021622 A	M24036 X / 2031 DE300221 DF 40000 F 10030 X 2001 47 F 00000 21 DO 1000 1 DE
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30	440526 446576	629517_1		89902 BI518252 AI659477 T89628 H22349
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	406800	0_0	AA505535	N954159 AL041618 Al028269 AA769325 AW780241 AW129462 AIZ71476 BF798303 AA836991 AW273346 Al436321 AI375545 AL040967
	422959	MH905_3	A A DOG 4DE	A102252A AA509567 AAA2380A A1 0A0Q10 NRO2Q2 A1954063 A1923968 A1400578 AA748499 BEb//845 AWUZU/88 AABUUZU AYYJ13ZUJ
35			A A 707204	A10COA4D AAA7CD2C ANAAC2280 AIM47CQC AARDCQAD RIAG7DD5 ANDSSSS ANDSSS AND AAA0U3D03 ANG 3 130 OF 43U340 AA4432U
33			A 100 1000 A	1704400 01404762 A1006000 DEC71706 A1421067 A1197038 A1678429 A1273421 AA897667 AAS86499 BEZ41923 AF 101001 NM V13940
			BE073169	1/34/22 B149/173 A1CASSO 1610/1739 A2 1610/1
			A1964200 Y	Y09408 AA132432 N33100 M343270 AW 100313 F20000 AA300003 1 37 107 51002 7 2
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45 50 55 60 65	Pkey: Ref: Strand: Nt_positis 401781 401783 401785 402294 402845 403740 401760 403593 400945 401905 403180 401905 401905 4011912 406407 401191 404246 401131 406467 403148 401429	Uni Sec s	que number co quence source. quence of huma icates DNA stra icates nucleotic Strand Minus Minus Minus Minus Minus Minus Plus Plus Plus Plus Plus Plus Minus Minus Plus Plus Minus Minus Plus Plus Plus Minus Plus Plus Minus Plus Minus Plus Minus Plus Minus Minus Plus Minus	rresponding to an Eos probeset The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA in chromosome 22" Dunham, et al. (1999) Nature 402:489-495.  and from which exons were predicted.  be positions of predicted exons.  Nt. position 8211-83435,83531-83656,83740-83901,8423 23397-28617,28920-29045,29135-29296,2941 172961-173056,173868-173928 165776-165996,166189-166314,166408-16656 2575-3000 160451-160617,160788-161009 27413-29978 83126-83250,85320-85540,94719-95287 62534-62712,69449-69602 169845-170272 89366-89622 153965-154441,156599-156819 63803-63759 118596-118816,19119-119244,119609-11976 93253-938667 37999-38145,38652-38999,39727-39872,4055 109742-109883 38915-37250 167373-167433,167936-168031 69559-70101 1553-1712,1878-2140,4252-4385,5922-6077 82477-82628,82727-82817,82910-83071,8314 94802-94897,55804-95887,96323-96487,9759 18298-161579 18298-161579 18298-161579 182991-136035 142967-165035
45 50 55 60 65 70	Pkey: Ref: Strand: Nt_positive Volume	Uni Sec s	que number co quence source. quence of huma icates DNA stra icates nucleoix  Strand Minus Minus Minus Minus Minus Plus Plus Plus Plus Plus Plus Plus Pl	rresponding to an Eos probeset The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA and from which exons were predicted.  the positions of predicted exons.  Nt_position 82115-83435, 83531-83656,83740-83901,8423 23937-28617, 28920-29045,29135-29296,2941 172961-173056,173868-173928 155776-166596,166183-166314,166408-16656 2575-3000 160451-160617,160788-161009 27413-28978 31326-83250,85320-85540,94719-95287 62554-62712,69449-69602 169845-170272 83936-809622 153965-154441,136659-156819 63603-63753-9118366-118816,119119-119244,119609-11976 93253-93367 37999-38145,38652-38998,39727-39872,4055 109742-109883 36915-37250 167373-167433,167936-168031 69559-70101 1553-1712,1878-2140,4252-4385,5922-6077 82477-82628,82721-82817,82910-83071,8314 94802-94987,95304-95887,96322-96487,9759 18294-161579 135901-136035

TABLE 65A: ABOUT 838 GENES DOWNREGULATED IN BENIGN NEVI RELATIVE TO NORMAL SKIN
Table 65A lists about 838 genes downregulated in benign nevi relative to normal skin. Genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene
expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

80

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Pkey: ExAcon: UnigenetD: Unigene Tite: R1: R2:

Unique Eos probeset identifier number
Exemplar Accession number, Genbank accession number
Unigene number
Unigene gene title
90th percentile of normal skin Als divided by the average of benign nevi Als
90th percentile of normal skin Als divided by the average of benign nevi Als, where the 15th percentile of normal tissue Als was subtracted from both the numerator and denominator

	Pkey	ExAcon	UnigenelD	Unigene Title	RI	R2
10	420813	X51501	Hs.99949	prolactin-induced protein	27.72	28.59
	408591	AF015224	Hs.46452	mammaglobin 1	26.40	28.34
	422166	W72424	Hs.112405	S100 calcium-binding protein A9 (calgran	21.33	21.57
	418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	18.06	18.96
	429441	AJ224172	Hs.204096	lipophilin 8 (uteroglobin family member)	16.61	18.06
15	428087	AA100573	Hs.182421	troponin C2, fast	14.70	14.60
	407245	X90568	Hs.172004	titio	13.08	13.84
	428824	W23624	Hs.173059	ESTa	12.89	13.36
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	12.78	13.98
••	444816	Z48633	Hs.283742	H.sapiens mRNA for retrotransposon	12.26	9.86
20	453309	AJ791809	Hs.32949	defensin, beta 1	12.02	10.62
	423024	AA593731	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	11.90	10.86
	445227	AJ281459	Hs.270114	ESTs	11.79	12.32
	413902	AU076743	Hs.75613	CD36 antigen (collagen type I receptor,	11.19	10.82
0.5	432877	AW974111	Hs.292477	ESTs	11.18	11.30
25	426752	X69490	Hs.172004	titin	10.97	12.63
	427899	AA829286	Hs.332053	serum amyloid A1	10.85	13.85
	407230	AA157857	Hs.182265	keratin 19	10.79	11.40
	451029	AA852097	Hs.25829	ras-related protein	10.78	10.35
20	421296	NM_002666	Hs.103253	perilipin	10.73	11.25
30	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	10.66	7.24
	422633	X56832	Hs.118804	enolase 3, (beta, muscle)	10.57	9.92
	405121			mitogen-activated protein kinase 8 inter	10.41	10.54
	450912	AW939251	Hs.25647	v-fos FBJ murine osteosarcoma viral onco	10.26	23.20
	420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	10.25	9.45
35	410850	AW362867	Hs.302738	Homo sapiens cDNA: FLJ21425 fis, clone C	10.15	9.88
	416931	D45371	Hs.80485	adipose most abundant gene transcript 1	10.13	11.58
	447966	AA340605	Hs.105887	ESTs, Wealthy similar to Homolog of rat Z	10.09	5.51
	401203			Target Exon	9.95	10.74
	425545	N98529	Hs.158295	Homo sapiens, clone MGC:12401, mRNA, com	9.94	11.47
40	425580	L11144	Hs.1907	galanin	9.66	6.60
	414092	Z14244	Hs.75752	cytochrome c oxidase subunit VIIb	9.45	6.44
	420919	M57892	Hs.100322	carbonic anhydrase VI	9.41	10.49
	443162	T49951	Hs.9029	DKFZP434G032 protein	9.36	10.58
	430154	AW583058	Hs.234726	serine (or cysteine) proteinase inhibito	8.91	10.27
45	452322	BE566343	Hs.28988	glutaredoxin (thioltransferase)	8.90	7.26
	430071	AA355986	Hs.232068	transcription factor 8 (represses interl	8.86	8.94
	417240	N57568	Hs.48028	EST	8.81	18.90
	415477	NM_002228	Hs.78465	v-jun avian sarcoma virus 17 oncogene ho	8.72	6.86
	430130	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (	8.39	10.26
50	408491	AI088063	Hs.7882	ESTs	8.00	8.20
	414657	AA424074	Hs.76780	protein phosphatase 1, regulatory (inhib	7.99	8.14
	409738	BE222975	Hs.56205	insulin induced gene 1	7.95	7.75
	428221	U96781	Hs.183075	ATPase, Ca transporting, cardiac muscle,	7.89	8.86
	451831	NM_001674	Hs.460	activating transcription factor 3	7.79	7.51
55	410867	X63556	Hs.750	fibrillin 1 (Marfan syndrome)	7.76	7.55
	444984	H15474	Hs.132898	fatty acid desaturase 1	7.75	5.64
	413076	U10564	Hs.75188	wee1 (S. pombe) homolog	7.68	5.65
	410532	T53088	Hs.155376	hemoglobin, beta	7.64	4.73
<b>~</b> ^	442757	AJ739528	Hs.28345	ESTS	7.62	7.66
60	412047	AA934589	Hs.49696	ESTs	7.61	7.48
	410052	AA525225	Hs.334630	Homo sapiens cDNA FLJ14462 fis, clone MA	7.52	7.28
	439394	AA149250	Hs.56105	EST8	7.52	6.72
	442941	AU076728	Hs.8867	cysteine-rich, anglogenic inducer, 61	7.51	6.27
	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	7.51	4.10
65	456525	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	7.49	8.08
	407334	AA494411	Hs.296031	ESTs	7.48	6.78
	414449	AA557660	Hs.76152	decorin	7.39	8.30
	432305	M62402	Hs.274313	insufin-like growth factor binding prote	7.38	8.79
	407328	AA508857		ESTs, Wealdy similar to ALU1_HUMAN ALU S	7.35	7.20
70	431842	NM_005764	Hs.271473	epithelial protein up-regulated in carci	7.06	6.93
	426488	X03350	Hs.4	alcohol dehydrogenase 1B (class I), beta	7.03	7.85
	445502	AW379160	Hs.12813	DKFZP434J214 protein	7.01	6.63
	419285	D31887	Hs.89868	KIAA0062 protein	7.01	5.82
76	409024	AW883529	Hs.173830	ESTs, Weakly similar to ALU7_HUMAN ALU S	6.99	4.58
75	422963	M79141	Hs.13234	ESTs	6.99	4.08
	447918	AI129320	Hs.115175	ESTs, Highly similar to JC5818 gamma-act	6.98	6.49
	410530	M25809	Hs.64173	ATPase, H transporting, lysosomal (vacuo	6.96	7.04
	444381	BE387335	Hs.283713	ESTs, Wealthy similar to \$64054 hypotheti	6.95	8.08
00	417993	AW963705	Hs.301183	molecule possessing ankyrin repeats indu	6.94	7.12
80	443060	D78874	Hs.8944	procollagen C-endopeptidase enhancer 2	6.94	6.79
	427890	AA435761		ESTs	6.94	6.68
	444207	AI565004		cathepsin D (lysosomal aspartyl protease	6.93	4.66
	442083	R50192	Hs.165062	ESTs	6.92	6.92

	441633	AW958544	Hs.112242	normal mucosa of esophagus specific 1	6.87	5.07
	407722	BE252241	Hs.38041	pyridoxal (pyridoxine, vitamin B6) kinas	6.87	4.99
	444051	N48373	Hs.10247	activated leucocyte cell adhesion molecu	6.84 6.84	5.33 3.47
5	414841	H55601	Hs.77490	glutathione S-transferase theta 1	6.79	7.14
,	430314 427704	AA369601 AW971063	Hs.239138 Hs.292882	pre-B-cell colony-enhancing factor ESTs	6.72	7.30
	431713	AK000388	Hs.267997	EHM2 gene	6.72	7.10
	451253	H48299	Hs.26126	claudin 10	6.71	7.20
	453187	Al161383	Hs.34549	ESTs, Highly similar to S94541 1 clone 4	6.68	3.02
10	400304	AF005082	Hs.113261	Homo sepiens skin-specific protein (xp33	6.64	6.08
	434625	W01370	Hs.46824	ESTs	6.61	6.92
	408063	BE086548	Hs.42346	calcineurin-binding protein calsarcin-1	6.60	7.29
	425280	U31519	Hs.1872	phosphoenolpyruvate carboxytkinase 1 (sol	6.55	6.79
	411388	X72925	Hs.69752	desmocotlin 1	6.55	3.44
15	413731	BE243845	Hs.75511	connective tissue growth factor	6.52	4.86
	455863	AA907305	Hs.36475	ESTs	6.50	4.24
	412247	AF022375	Hs.73793	vascular endothelial growth factor	6.49	4.56
	407102	AA007629		glycerol-3-phosphate dehydrogenase 1 (so	6.47	7.23
00	421407	T82331	Hs.182278	ESTs, Wealdy similar to CGHU6C collagen	6.47	6.55
20	406867	AA157857	Hs.182265	keratin 19	6.44	6.23
	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3) (NGAL)	6.43	6.79
	446945	Al193115	Hs.16611	tumor protein 052-like 1	6.43	5.66
	413172	M38180	Hs.38586	hydroxy-delta-5-steroid dehydrogenase, 3	6.39	7.09
25	407395	AF005082	11. 4000	gb:Homo sapiens skin-specific protein (x	6.39	4.76
25	450626	AW190989	Hs.1508	insulin-degrading enzyme	6.37 6.37	6.22
	450713	AL133611	Hs.25362	Homo sapiens mRNA; cDNA DKFZp43401317 (f	6.35	4.91
	437596	AA761490	14- 100000	ESTs, Moderately similar to S65657 alpha	6.34	5.31 6.15
	430191	Al149880	Hs.188809	ESTs	6.34	5.67
30	433713	AW976511	Hs.112592 Hs.7886	ESTs	6.33	6.39
30	420107	AL043980	Hs.343603	pellino (Drosophila) homolog 1 titin-cap (telethonin)	6.33	5.77
	422069 437176	AJ010063 AW176909	Hs.42346	calcineurin-binding protein calsarcin-1	6.30	5.45
	433412	AV653729	Hs.8185	CGI-44 protein; suffide dehydrogenase ii	6.29	6.68
	447335	BE617695	Hs.286192	hypothetical protein FLJ20940	6.28	10.35
35	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	6.21	5.98
. 55	440116	AI798851	113.10101	hemoglobin, gamma G	6.18	6.86
•	454229	AW957744	Hs.278469	lacrimal proline rich protein	6.17	6.54
	441188	AW292830	Hs.255609	ESTs	6.12	6.68
	451144	AW956103	Hs.61712	pyruvate dehydrogenase kinase, isoenzyme	6.12	5.79
40	431319	AA873350	Hs.302232	ESTs	6.11	7.91
	442498	U54617	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	6.10	5.63
	414555	N98569	Hs.76422	phospholipase A2, group IIA (platelets,	6.08	6.96
	418321	D63477	Hs.84087	KIAA0143 protein	6.08	4.71
	443072	A1937532		gb:wp78d02.x1 NCI_CGAP_Bm25 Homo sapien	6.07	5.48
45	423712	W46802	Hs.81988	disabled (Drosophila) homolog 2 (mitogen	6.04	5.81
	442679	R53718		hypothetical protein FLJ10659	6.03	5.67
	424824	AJ217440	Hs.143873	ESTs	6.02	5.46
	413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	6.01	7.05
50	428358	AA993222	Hs.101915	Stargardt disease 3 (autosomal dominant)	5.94	7.17
50	430821	AA487264	Hs.154974	Homo sapiens mRNA; cDNA DKF2p667N064 (fr	5.92	5.79
	424670	W61215	Hs.116651	epithelial V-like antigen 1	5.92	5.63
	424673	AA345051	Hs.294092	ESTs, Weakly similar to 138022 hypotheti	5.91	6.81 6.95
	418205	L21715	Hs.83760	troponin I, skeletal, fast	5.91 5.89	7.01
55	400440	X83957	Hs.83870 Hs.10706	nebulin epithelial protein lost in neoplasm beta	5.89	5.49
23	444239 419517	R57988	Hs.90797	Homo sapiens clone 23620 mRNA sequence	5.86	5.88
	432626	AF052107 AA471098	Hs.278544	acetyl-Coenzyme A acetyltransferase 2 (a	5.86	5.58
	407584	W25945	Hs.8173	hypothetical protein FLJ10803	5.81	5.09
	449335	AW150717	Hs.345728	STAT induced STAT inhibitor 3	5.79	6.33
60	445607	AA488107	Hs.30156	ESTs, Weakly similar to unnamed protein	5.78	5.91
	424571	BE379766		polymerase (RNA) II (DNA directed) polyp	5.78	3.74
	412630	AA738437	Hs.26226	Homo sapiens cDNA: FLJ21286 fis, clone C	5.76	4.21
	408819	AW163483	Hs.48320	double ring-finger protein, Dorfin	5.71	4.59
	433027	AF191018	Hs.279923	putative nucleotide binding protein, est	5.70	4,71
65	406704	M21665	Hs.929	myosin, heavy polypeptide 7, cardiac mus	5.68	6.12
	408515	Al289507	Hs.299883	hypothetical protein FLJ23399	5.67	4.81
	443827	AI087867	Hs.134667	ESTs	5.67	5.54
	429693	BE254962	Hs.211612	SEC24 (S. cerevisiae) related gene famil	5.67	4.12
70	427373		Hs.130760	myosin phosphatase, target subunit 2	5.66	4.27
70	428666	AL080190	Hs.189242	Homo sapiens mRNA; cDNA DKFZp434A202 (fr	5.65	5.16
	421834	BE543205	Hs.288771	DKFZP586A0522 protein	5.65	4.52
	427081	AJ474533	Hs.170528	ESTs, Moderately similar to ALUC_HUMAN !	5.65	4.81
	419731	S47242	Hs.92909	SON DNA binding protein	5.64 5.64	3.77
75	420787		Un gorna	ESTs, Weakly similar to 138022 hypotheti	5.64 5.63	3.27
13	420682		Hs.88602	ESTs	5.63	4.13
	410541		Hs.64179	syntenin-2 protein	5.62 5.61	5.84
	431350			loricrin membrane cofactor protein (CD46, trophob	5.61 5.61	5.14 4.28
	418127 430332		Hs.83532 Hs.239483	Human clone 23933 mRNA sequence	5.60	4.26 5.76
80	430332		Hs.161051	ESTs, Moderately similar to ALU6_HUMAN A	5.51	16.04
50	427630			tumor necrosis factor, alpha-induced pro	5.49	5.28
	422082		Hs.111244	hypothetical protein	5.49	5.23
	419461		Hs.288869	nuclear receptor subfamily 2, group F, m	5.49	4.40

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	430714 407744	AA484757 AB020629	Hs.287601 Hs.38095	Homo sapiens cONA FLJ13830 fis, clone TH ATP-binding cassette, sub-family A (ABC1	5.48 5.46	5.38 5.11
	400494	1145400	LIS 40757	ENSP0000238970":CIG30 (Fragment).	5.45 5.43	3.63 4.25
5	415062 449291	H45100 BE176893	Hs.49753 Hs.23440	uveal autoantigen with coiled coil domai KIAA1105 protein	5.41	3.82
,	435538	AB011540	Hs.4930	low density Epoprotein receptor-related	5.41	2.62
	417035	AA192455	Hs.22968	Homo sapiens clone IMAGE:451939, mRNA se	5.40	5.40
	434535	AI611729	Hs.167619	ESTs, Moderately similar to ALUC_HUMAN I	5.40 5.39	5.20 4.59
10	408085	N25929 AA090235	Hs.342849 Hs.75535	ADP-ribosylation factor-like 5 myosin, light polypeptide 2, regulatory.	5.37	14.96
10	413778 436090	A1640635	Hs.332879	EST	5.37	5.33
	406805	AI686003	Hs.296031	ESTs	5.35	5.49
	426510	AW861225	Hs.251928	BANP homolog, SMAR1 homolog	5.35	6.83
15	406706	X03740	Hs.231581	myosin, heavy polypeptide 1, skeletal mu	5.34 5.34	7.50 4.88
15	456332 421999	AA228357 U50535	Hs.110630	gb:nc39d05.r1 NCI_CGAP_Pr2 Homo sapiens Human BRCA2 region, mRNA sequence CG006	5.34	4.75
	418479	AA829976	113.110000	mannosidase, alpha, class 1A, member 2	5.34	3.59
	417059	AL037672	Hs.81071	extracellular matrix protein 1	5.34	4.71
20	424008	R02740	Hs.137555	putative chemokine receptor, GTP-binding	5.34	4.75
20	415694	AW194301	Hs.339283	Human DNA sequence from clone RP1-187J11	5.34 5.31	8.69 5.81
	452747 449271	BE153855 AW338067	Hs.61460 Hs.7869	lg superfamily receptor LNIR Homo sapiens cONA FLJ11946 fis, clone HE	5.30	4.35
	437135	AL038624	Hs.208752	ESTs, Wealdy similar to ALUS_HUMAN ALU S	5.29	4.92
	419925	AA159850	Hs.93765	liporna HMGIC fusion partner	5.29	5.02
25	415192	D17793	Hs.78183	eldo-keto reductase family 1, member C3	5.28	5.33
	453999	BE328153	Hs.240087	ESTs	5.28 5.28	3.40 2.84
	408958 452496	T99607 AA114926	Hs.49346 Hs.169531	signal recognition particle 54kD ESTs	5.28	5.48
	424058	AL121516	Hs.138617	thyroid hormone receptor interactor 12	5.27	3.72
30	443265	Af916207	Hs.9167	SH3 domain binding glutamic acid-rich pr	5.26	4.62
	407013	U35637	Hs.83870	gb:Human nebulin mRNA, partial cds	5.26	6.21
	414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f armyloid beta precursor protein-binding p	5.26 5.26	4.21 4.43
	410284 445107	U50939 Al208121	Hs.61828 Hs.147313	ESTs, Wealdy similar to I38022 hypotheti	5.25	5.61
35	446267	AW450103	Hs.151124	ESTs	5.24	4.44
-	422278	AF072873	Hs.114218	frizzfed (Drosophila) homolog 6	5.23	3.14
	448585	AB020676	Hs.21543	KIAA0869 protein	5.23	6.21
	421993	R22497	Hs.110571	growth arrest and DNA-damage-inducible,	5.22 5.22	6.84 5.29
40	414407 423720	AA147026 AL044191	Hs.76704 Hs.23388	ESTs hypothetical protein DKFZp434F0318	5.22	5.85
70	415997	NM_003590	Hs.78946	cultin 3	5.21	3.66
	411531	AB014511	Hs.70604	ATPase, Class II, type 9A	5.21	3.95
	441619	NM_014056	Hs.7917	DKFZP564K247 protein	5.20	4.38
A.E	435232	NM_001262	Hs.4854	cyclin-dependent kinase inhibitor 2C (p1	5.19 5.10	4.52 3.13
45	415167	AA160784	Hs.26410	ESTs ESTs	5.19 5.18	5.38
	431416 439995	AA532718 AL137480	Hs.178604 Hs.6834	KIAA1014 protein	5.17	3.14
	416784	AA334592	Hs.79914	tumican	5.17	6.18
	446082	AI274139	Hs.156452	ESTs	5.16	5.14
50	400196			Eos Control	5.16	5.05 4.31
	414525	C14904	Hs.45184	Homo sapiens cDNA FLJ12284 fis, clone MA dolichyl-phosphate (UDP-N-acetylgtucosam	5.16 5.15	4.89
	414242 430699	AA749230 AW969847	Hs.26433 Hs.292718	ESTs, Weakly similar to RET2_HUMAN RETIN	5.14	5.22
	440383	AA884208	Hs.30484	ESTs	5.13	5.09
55	431628	AF146277		CD2-associated protein	5.13	5.03
	407047	X65965		gb:H.sapiens SOD-2 gene for manganese su	5.13	4.31 3.57
	433688	AA628467	Hs.112572	Homo sapiens cDNA FLJ14130 fis, clone MA	5.12 5.12	3.30
	437704 426101	AA766142 AL049987	Hs.131810	ESTs, Moderately similar to ALU1_HUMAN A Homo sapiens mRNA; cDNA DKFZp564F112 (fr	5.11	6.08
60	428297	AA236291	Hs.183583	serine (or cysteine) proteinase inhibito	5.10	4.31
• •	416382	D86985	Hs.79276	KIAA0232 gene product	5.10	3.79
	437150	R51407	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	5.10	6.58 4.82
	454947	AW846590	11- 102100	gb:QV0-CT0180-011099-025-d07 CT0180 Homo	5.09 5.09	4.90
65	434647 418730	W74158 AA091027	Hs.103189 Hs.325625	lipopolysaccharide specific response-68 Homo sapiens clone 23938 mRNA sequence	5.09	3.46
05	449338	H73444	Hs.394	adrenomedullin	5.09	6.26
	438962	BE045594		gb:hn41c11.x1 NCI_CGAP_RDF2 Homo sapiens	5.08	5.60
	431693	AJ459519		serine (or cysteine) proteinase inhibito	5.07	2.83
70	420583	H77859	Hs.65450	reticulon 4	5.06 5.06	6.71 6.06
70	431048 432125	R50253 AW972667	Hs.249129 Hs.183006	cell death-inducing DFFA-like effector a Homo sapiens cDNA FLJ12300 fis, clone MA	5.05	6.32
	447945	A1922838	Hs.9670	ESTs. Weakly similar to ALU1_HUMAN ALU S	5.05	3.72
	442547	AA306997	Hs.217484	ESTs, Wealdy similar to ALU1_HUMAN ALU S	5.05	2.86
~~	414176	BE140638	Hs.75794	EDG-2 (endothelial differentiation, lys	5.03	4.43
75	445263	H57646	Hs.42586	KIAA1560 protein	5.03 5.03	6.67 4.88
	448490	AI523897	Hs.271692	ESTs, Wealdy similar to 138022 hypotheti biphenyl hydrolase-like (serine hydrolas	5.03 5.03	4.36
	450515 440624	AW304226 AF017987	Hs.7306	secreted trizzted-related protein 1	5.01	5.48
_	417165		Hs.302738	Homo sapiens cDNA: FLJ21425 fis, clone C	5.01	5.61
80	417640		Hs.82353	protein C receptor, endothelial (EPCR)	5.01	5.32
	413475	AW021488	Hs.26981	ESTs	5.01 5.00	3.90
	414792		Hs.87128	hypothetical protein FLJ23309 ESTs, Wealdy similar to I38022 hypotheti	5.00 5.00	4.54 3.19
	424074	A1902456	Hs.210761		3.00	
				606		

					4.00	6.25
	424620		Hs.151254	kallikrein 7 (chymotryptic, stratum com	4.99 4.99	6.60
	439039	AI656707	Hs.48713	ESTs	4.98	9.59
	422305	A1928242	Hs.293438	ESTs, Highly similar to AF198488 1 trans	4.98	4.52
	410579	AK001628	Hs.64691	KIAA0483 protein	4.98	3.84
5	449710	AA002207	Hs.17385	Homo sapiens clone IMAGE:119716, mRNA se	4.98	3.63
	434230	AA551569		hypothetical protein PRO2822	4.98	3.56
	426468	AA379306	Hs.117558	ESTS	4.96	6.41
	421690	AW162667	Hs.106857	calbindin 2, (29kD, calretinin)	4.96	3.28
• •	448144	AW169230		ESTs, Moderately similar to PC4259 femi	4.96	5.75
10	412129	M21984	Hs.73454	troponin T3, skeletal, fast	4.96	3.21
	450071	AA018283	Hs.24359	Homo sapiens cDNA FLJ11174 fis, clone PL	4.95	4.39
	433934	AW273261	Hs.216292	ESTs	4.95	4.01
	446320	AF126245	Hs.14791	acyl-Coenzyme A dehydrogenase family, me	4.94	4.54
	446161	AA628206	Hs.14125	p53 regulated PA26 nuclear protein	4.94	4.49
15	453225	BE258769		acetyl-Coenzyme A acytransferase 2 (mit	4.94	4.19
	444476	AF020038	Hs.11223	isocitrate dehydrogenase 1 (NADP), solub	4.93	5.68
	445493	AI915771		metallothionein 1E (functional)	4.93	5.47
	422292	AI815733	Hs.114360	transforming growth factor beta-stimulat	4.93	4.51
	417054	AF017060		aldehyde oxidase 1	4.93	3.34
20	425917	W28517	Hs.117167	Homo sapiens cDNA: FLJ23067 fis, clone L	4.93	5.61
	408681	AW953853	Hs.281462	ESTs, Weakly similar to 138022 hypotheti	4,92	3.27
	451267	AI033894	Hs.117865	solute carrier family 17 (anion/sugar tr	4.91	4.26
	447137	AW970192	Hs.171942	ras responsive element binding protein 1	4.90	6.00
	427451	A1690916	Hs.178137	transducer of ER8B2, 1	4.90	3.79
25	432314	AA533447	Hs.312989	ESTs	4.89	3.71
	440692	AL031591	Hs.7370	phosphotidylinositol transfer protein, b	4.89	3.27
	428594	BE387236	Hs.75415	beta-2-microglobufin	4.87	4.06
	437802	AJ475995	Hs.122910	ESTs	4.86	6.54
	437974	T74445	Hs.5957	Homo sapiens clone 24416 mRNA sequence	4.86	5.15
30	427156	BE621719	Hs.173802	KIAA0603 gene product	4.86	5.50
	433179	AW362945	Hs.162459	ESTs	4.85	5.29
	428957	NM_003881	Hs.194679	WNT1 inducible signaling pathway protein	4.85	3.59
	453855	AA039576	Hs.37858	ESTs, Weakly similar to ALUB_HUMAN !!!!	4.85	3.45
	433143	BE552155	Hs.294035	ESTs, Weakly similar to ALU5_HUMAN ALU S	4.83	3.80
35	429279	AB018271	Hs.198689	KIAA0728 protein	4.82	4.20
	445773	H73456	Hs.13299	Homo sapiens mRNA; cDNA DKFZp761MD111 (f		4.01
	416349	X69089	Hs.79227	myomesin (M-protein) 2 (165kD)	4.82	4.19
	408138	AA535740		tumor protein p53-binding protein, 1	4.81	3.99
	432566	AW439330	Hs.256889	ESTs, Weakly similar to 2109260A B cell	4.80	3.50
40 ⁻	444677	AL110212	Hs.301005	purine-rich element binding protein B	4.80	3.50 10.20
	42265B	AF231981	Hs.250175	homolog of yeast long chain polyunsatura	4.80	
	431926	AW972724		gb:EST384816 MAGE resequences, MAGL Homo	4.79	4.39 2.98
	407839	AA045144	Hs.161566	ESTs	4.79	4.78
	421998	R74441		poly(A)-binding protein, nuclear 1	4.77	3.99
45	416987	D86957	Hs.80712	KIAA0202 protein	4.76	7.59
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	4.76	4.38
	440494	BE618768	Hs.7232	acetyl-Coenzyme A carboxylase alpha	4.75	3.92
	453180	N46243	Hs.110373	ESTs, Highly similar to T42626 secreted	4.75	5.68
	413276	Z24725	Hs.75260	mitogen inducible 2	4.75	5.57
50	437239	AW503395	Hs.5541	ATPase, Ca transporting, ubiquitous	4.74	11.58
	414622	A1752666	Hs.76669	nicotinamide N-methyltransferase	4.74	3.79
	429587	AA283969	Hs.334706	Homo sapiens cDNA FLJ11801 fis, clone HE	4.74	4.88
	407242	M18728		gb:Human nonspecific crossreacting antig	4.73	4.79
	445229	BE276013	Hs.172364	Homo sapiens mRNA for FLJ00086 protein,	4.73	2.38
55	447429		Hs.18586	KIAA0451 gene product	4.72	
	444930		Hs.301183	molecule possessing ankyrin repeats indu	4.71	5.10
	414848	AI803447	Hs.77496	small nuclear ribonucleoprotein polypept	4.71	2.51
	439652	W67826	Hs.55412	ESTs, Wealty similar to K1CJ_HUMAN KERAT	4.70	6.13
	453145	R63438	Hs.183454	Homo sapiens cDNA FLJ14883 fis, clone PL	4.70	3.06
60	421302		Hs.103291	neuritin	4.69	4.96 5.01
	425118	AU076611	Hs.154672	methylene tetrahydrofolate dehydrogenase	4.68	3.97
	448079	R76981		thyroid hormone receptor-associated prot	4.68	
	434558	AW264102	Hs.39168	ESTs	4.67	3.42 6.17
	408239	AA053401		ESTs, Moderately similar to ALU7_HUMAN A	4.67	
65	454416	Al912097	Hs.163208	ESTs	4.66	3.97
	427215	AW246148	Hs.268371	hypothetical protein FLJ20274	4.66	3.37
	451583		Hs.24133	ESTs	4.65	3.81
	446525	AW967069	Hs.211556	hypothetical protein MGCS487	4.65	6.14
	436178	5 AL121422	Hs.54900	serologically defined colon cancer antig	4.65	3.65
70	450528	8 NM_01407	72 Hs.25063	PRO0461 protein	4.64	2.99 4.72
	417259		8 Hs.81800	chondroitin sulfate proteoglycan 2 (vers	4.64	
	40874		Hs.646	carboxypeptidase A3 (mast cell)	4.63	5.55
	41773		Hs.82503	H.sapiens mRNA for 3UTR of unknown prot	4.63	5.04
	43628			Homo sapiens cDNA: FLJ22562 fis, clone H	4.63	3.55
75	42874		Hs.192853	ubiquitin-conjugating enzyme E2G 2 (homo	4.63	2.85
. •	42700			transforming, acidic coiled-coil contain	4.63	3.00
	45376			extracellular matrix protein 2, female o	4.62	5.14
	44997			Homo sapiens cDNA FLJ14296 fis, clone PL	4.62	4.49
	40959	8 NM_0140	18 Hs.55097	mitochondrial ribosomal protein S28	4.62	3.56
80	41330			Homo sapiens cDNA: FLJ23176 fis, clone L	4.62	4.24
	41257	7 Z22968	Hs.74076	CD163 antigen	4.61	8.03
	42404	6 AF02786		serine (or cysteine) proteinase inhibito	4.61	6.86
	45228		5 Hs.28827	mitogen-activated protein kinase kinase	4.61	4.33

	458971	AL119206	Hs.101874	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.61	4.16
	433256	AW604447	Hs.339408	ESTs, Weakly similar to \$26689 hypotheti	4.61	3.58
	440596	H13032	Hs.103378	hypothetical protein MGC11034	4.61	3.22
_	427919	AA173942	Hs.326416	Homo sapiens mRNA; cDNA DKFZp564H1916 (I	4.60	4.74
5	424651	AI493206	Hs.32425	ESTs	4.60 4.60	4.11 2.34
	436701 413691	AW959032 AB023173	Hs.75478	ESTs, Moderately similar to 178885 serin ATPase, Class VI, type 118	4.59	4.36
	448625	AW970786	Hs.178470	hypothetical protein FLJ22662	4.59	4.00
	436283	Al480319	Hs.120058	ESTs	4.59	3.76
10	451710	AW867467	Hs.278712	eukaryotic translation initiation factor	4.59	3.51
	436086	Z43133	Hs.9961	Homo sapiens cDNA: FLJ21954 fis, clone H	4.59 4.58	3.64 5.10
	434697 402294	AL133033	Hs.4084	KIAA1025 protein Target Exon	4.57	5.47
	424098	AF077374	Hs.139322	small profine-rich protein 3	4.57	5.12
15	406648	AA563730	Hs.277477	major histocompatibility complex, class	4.57	4.66
	428423	AU076517	Hs.184276	solute carrier family 9 (sodium/hydrogen	4.57	4.15
	441566	AA604110	Hs.151725	ESTs	4.57 4.56	3.21 4.76
	400109 419740	AB037835	Hs.92991	Eos Control KIAA1414 protein	4.56	3.63
20	421481	AW391972	Hs.104696	KIAA1324 protein	4.55	7.16
	440266	AA088809	Hs.19525	hypothetical protein FLJ22794	4.55	4.44
	421979	AW062518	Hs.233150	hypothetical protein MGC5560	4.55	4.36
	408702	AW959893	Hs.27099	hypothetical protein FLJ23293 similar to	4.54 4.54	5.78 4.61
25	418021 422068	M15881 Al807519	Hs.1137 Hs.104520	uromodulin (uromucoid, Tamm-Horsfall gly Homo sapiens cDNA FLJ13694 fis, clone PL	4.54	4.32
23	421986	AL137438	Hs.110454	SEC15 (S. cerevisiae)-like	4.54	2.59
	414798	AI286323	Hs.97411	hypothetical protein MGC12335	4.53	6.18
	410132	NM_003480	Hs.300946	Microfibril-associated glycoprotein-2	4.53 4.53	5.87 4.87
30	449843	R85337	Hs.24030	solute carrier family 31 (copper transpo Al905687:IL-BT095-190199-019 BT095 Homo	4.53 4.53	10.61
30	424399 452924	AI905687 AW580939	Hs.97199	complement component C1q receptor	4.51	6.07
	454000	AA040620	Hs.5672	hypothetical protein AF140225	4.51	4.59
	404730			Target Exon	4.51	4.30
25	449943	AF104266	Hs.24212	latrophilin	4.51 4.50	3.40 2.97
35	414217	AJ309298 AJ033259	Hs.279898 Hs.118317	Homo sapiens cDNA: FLJ23165 fis, clone L Homo sapiens cDNA FLJ12088 fis, clone HE	4.50 4.50	4.77
	435992 421311	N71848	Hs.283609	hypothetical protein PRO2032	4,50	3.30
	449785	AI225235	Hs.288300	hypothetical protein FLJ23231	4.49	5.06
	437611	AA897108		gb:am08a06.s1 Soares_NFL_T_GBC_S1 Homo s	4.49	4.24
40	419612	AI498267	Hs.110613	KIAA0421 protein	4.49 4.49	4.16 3.15
	414496 450306	W73853 AL080080	Hs.24766	ESTs thioredoxin domain-containing	4.48	3.38
	444895	A1674383	Hs.22891	solute carrier family 7 (cationic amino	4.47	4.45
	432559	AW452948	Hs.257631	ESTs	4.47	5.39
45	442554	AW467376	Hs.129640	ESTs	4.47	4.00
	421429	NM_014922	Hs.104305	death effector filament-forming Ced-4-fi	4.46 4.45	4.47 5.07
	422313 435748	AF045941 AA699756	Hs.115166 Hs.117335	sciellin ESTs	4.45	3.35
	453283	AA694386	Hs.290914	ESTs	4.45	3.28
50	441925	R83113		protein kinase C substrate 80K-H	4.45	3.28
	440030	AA932693		EST	4.45 4.44	3.20 3.66
	446515	AL048875 S73840	Hs.931	hypothetical protein DKFZp5661133 myosin, heavy polypeptide 2, skeletal mu	4.44	5.90
	406707 432341	AL137662	Hs.274401	Homo sapiens mRNA; cONA DKFZp434P086 (fr	4.44	3.99
55	410453	AW749036		gb:RC2-BT0318-241199-011-f10 BT0318 Homo	4.44	3.49
	450196	AW956868	Hs.24608	DKFZP564D177 protein	4.43	4.13
	444147	AB002306	Hs.10351	KIAA0308 protein	4.43 4.42	3.95 3.88
	427809 428157	M26380 A1738719	Hs.180878 Hs.198427	lipoprotein tipase hexokinase 2	4.42	5.46
60	413299	AA857487	Hs.75275	ubiquitination factor E4A (homologous to	4.42	3.77
	440245	AK001913	Hs.7100	hypothetical protein	4.42	3.51
	442379	NM_004613		transglutaminase 2 (C polypeptide, prote	4.42 4.42	1.79 3.35
	408569	BE066047 AI033965	Hs.86412 Hs.239926	chromosome 9 open reading frame 5 sterol-C4-methyl oxidase-like	4.41	5.78
65	430361 414489	A1620677	Hs.73105	ESTs	4.41	5.43
•	447731	AA373527	Hs.19385	CGI-58 protein	4.41	5.28
	443195	BE148235	Hs.193063	Homo sapiens cDNA FLJ14201 fis, clone NT	4,41	4.41
	448503	BE243146	Hs.21332	BTB (POZ) domain containing 1	4,41 4,41	3.68 3.55
70	432546 445620	8E618778 AI245225	Hs.180638 Hs.17441	hypothetical protein FLJ13081 ESTs	4.41	3.44
, 0	454065	BE394588	113.77	gb:601311808F1 NIH_MGC_44 Homo sapiens c	4,41	3.43
	418802	AB028989	Hs.88500	mitogen-activated protein kinase 8 inter	4.40	2.04
	431816	T87431	Hs.190738	ESTs	4.39	4.26
75	429138	AB020657	Hs.197298	NS1-binding protein HIV TAT specific factor 1	4.39 4.39	4.47 3.09
13	426643 448943	AA857131 AI608810	Hs.171595 Hs.193288	ESTs	4.39	2.63
	414002			FBJ murine osteosarcoma viral oncogene h	4.37	19.16
	403593			Target Exon	4.37	6.35
80	408104		Hs.293968	ESTs ESTs Marchy similar to 13131848 atchal	4.31 4.31	5.82 4.14
90	429624 429538		Hs.99476 Hs.139322	ESTs, Wealdy similar to 13131848 alpha 1 small proline-rich protein 2A	4.25	6.61
	414505		Hs.23558	ESTs, Weakly similar to A48042 lysosomal	4.18	5.28
	438533		Hs.170673	ESTs, Wealthy similar to T24832 hypotheti	4.18	5.81

					4.15	5.12
	426143	BE379836	41- 70000	proteasome (prosome, macropain) subunit,	4.13 4.14	5.12
	414527	BE241739	Hs.76359	catalase cytochrome c oxidase subunit VIIa polype	4.13	8.60
	422287	F16365 AA132637	Hs.114346 Hs.15396	Homo sapiens, clone IMAGE:3948909, mRNA,	4.12	5.94
5	408199 412477	AA150864	rs.13330	microsomal glutathione S-transferase 1	4.10	10.00
•	411558	AA102670	Hs.70725	gamma-aminobutyric acid (GABA) A recepto	4.09	5.39
	444252	R21135	Hs.54985	ESTs	4.07	6.01
	400295	W72838		Al905687:IL-BT095-190199-019 BT095 Homo	4.06	13.32
4.5	438746	AJ885815	Hs.184727	Human melanoma-associated antigen p97 (m	4.06	7.57
10	429856	AA971576	Hs.225951	topoisomerase-related function protein 4	4.05 4.01	6.24 4.61
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	4.00	4.06
	403710		11- 247020	C4000160:gi]12735793[ref]XP_011928.1] pr	3.97	7.22
	406643	N77976	Hs.347939 Hs.310286	hemoglobin, alpha 2 ESTs	3.96	5.41
15	436372 428340	AW972301 AF261088	Hs.154721	aconitase 1, sotuble	3.94	5.33
13	424604	AW865388	Hs.151076	KIAA1243 protein	3.91	7.59
	426653	AA530892	Hs.171695	dual specificity phosphatase 1	3.91	14.81
	410204	AJ243425	Hs.326035	early growth response 1	3.87	9.96
	448520	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	3.87	5.09
20	443021	AA368546	Hs.8904	lg superfamily protein	3.86	7.65
	430418	R98852	Hs.36029	heart and neural crest derivatives expre	3.81	6.19
	447796	AW953622	Hs.223025	RAB31, member RAS oncogene family	3.76 3.76	5.10 5.12
	419407	AW410377	Hs.41502	hypothetical protein FLJ21276	3.75	5.46
25	443725	AW245680	Hs.9701	growth arrest and DNA-damage-inducible, oxidation resistance 1	3.74	5.14
25	426281	AK000987	Hs.169111 Hs.136574	arachidonate 12-lipoxygenase, 12R type	3.74	6.30
	423973	AF038461 AW137636	Hs.146059	ESTs	3.72	5.59
	445234 457411	AW085961	Hs.130093	iraqueis-class homeobox protein IRX2	3.71	4.85
	456063	NM_006744	Hs.76461	retinal-binding protein 4, interstitial	3.71	6.72 .
30	413880	AI660842	Hs.110915	interleukin 22 receptor	3.71	4.01
-	422640	M37984	Hs.118845	troponin C, slow,	3.71	9.10
	452241	AL050204	Hs.28540	Homo sapiens mRNA; cDNA DKFZp586F1223 (1	3.70	3.21
	453560	AA348626	Hs.5890	hypothetical protein FLJ23306	3.69	5.13
	410197	NM_005518	Hs.59889	3-hydroxy-3-methylgtutaryl-Coenzyme A sy	3.69	7.69 4.80
35	413922	AI535895	Hs.221024	ESTs	3.68 3.64	5.22
	428698	AA852773	Hs.334838	KIAA1866 protein	3.64	3.69
	451951	AW082870	Hs.210954	ESTs ESTs	3.64	4.35
	452308	AI167560	Hs.61297	ESTs, Weakly similar to T23273 hypotheti	3.63	2.91
40	441128	AA570256 AJ243662	Hs.110196	NICE-1 protein	3.61	6.05
40	421978 418533	NM_004533	Hs.85937	myosin-binding protein C, fast-type	3.61	6.22
	452413	AW082633	Hs.215030	ESTs	3.58	3.03
	453003	AA808466	Hs.103395	hypothetical protein FLJ14146	<b>3</b> .55	6.39
	408522	AI541214	Hs.46320	Small proline-rich protein SPRK [human,	3.54	10.68
45	423503	M92843	Hs.343586	zinc finger protein homologous to Zfp-36	3.53	15.11
	419879	Z17805	Hs.93564	Homer, neuronal immediate early gene, 2	3.53	5.29
	428382	AF007132	Hs.184019	Homo sapiens clone 23551 mRNA sequence	3.51 3.51	4.46 3.67
	447165	AL042400	Hs.75668	Homo sapiens, Similar to RIKEN cDNA 1700	3.51	3.74
50	418067	Al127958	Hs.83393	cystatin E/M	3.50	14.64
50	420202	AL036557	Hs.95910 Hs.152423	putative lymphocyte G0/G1 switch gene Homo sapiens cDNA: FLJ21274 fis, clone C	3.50	2.79
	432543 442321	AA552690 AF207664	Hs.8230	a disintegrin-like and metalloprotease (	3.48	7.91
	450860	AA021007	113.02.00	integrin, beta 8	3.47	5.89
	414665	AA160873		serum armyloid A1	3.46	9.22
55	413663	BE247585	Hs.75462	BTG family, member 2	3,46	5.63
	427408	AA583206	Hs.2156	RAR-related orphan receptor A	3.45	3.08
	430171	AF086289	Hs.234766	skin-specific protein	3.45	4.77
	453655	AW960427	Hs.342874	transforming growth factor, beta recepto	3.42	8.09 6.43
60	450607	AL050373	Hs.25213	hypothetical protein	3,41 3,41	6.10
60	412596	AA161219	Hs.799	diphtheria toxin receptor (heparin-bindi tumor necrosis factor receptor superfami	3.39	6.59
	427681	AB018263	Hs.180338	mosaic serine protease	3.34	3.09
	440590		Hs.266308 Hs.262958	hypothetical protein DKFZp4348044	3.31	10.06
	452669 422101	AW404176	Hs.111611	ribosomal protein L27	3.30	3.93
65	431985		Hs.149018	Novel human gene mapping to chomosome 20	3.30	3.54
05	412649			integrin, alpha 7	3.28	6.89
	423017			serine (or cysteine) proteinase inhibito	3.28	5.44
	425163		Hs.154890	fatty-acid-Coenzyme A ligase, long-chain	3.28	5.93
	412061		Hs.330211	ESTs	3.27	5.75
70	437592			cellular repressor of E1A-stimulated gen	3.27	5.83 5.66
	452849		Hs.30792	hook2 protein	3.26 3.25	5.00 4.98
	421462		Hs.104624	aquaporin 9 arachidonate 15-lipoxygenase, second typ	3.25 3.24	6.56
	422083		1 Hs.111256 Hs.223569	ESTs	3.24	5.96
75	444935 422057		Hs.30348	ESTs	3.22	5.72
13	4/2007			Homo sapiens clone 24775 mRNA sequence	3.21	5.26
	407948			ICEBERG caspase-1 inhibitor	3.21	4.61
	452089		Hs.271492	ESTs, Wealdy similar to PC4211 hepatocel	3.19	4.42
	448249			ESTs	3.18	2.97
80	430869	D10511	Hs.37	acetyl-Coenzyme A acetyltransferase 1 (a	3.17	5.66
	443623	AA345519		complement component 1, q subcomponent,	3.16	12.00
	452865		Hs.119567	ESTs, Weakly similar to A47582 B-cell gr	3.16	6.03 5.70
	452392	2 L20815	Hs.507	comeodesmosin	3.15	5.70

					245	5.87
	410231	AA314163	Hs.61153	proteasome (prosome, macropain) 26S subu	3,15	
	420309	AW043637	Hs.21766	ESTs. Weakly similar to ALU5_HUMAN ALU S	3.15	4.98
	406791	AI220684	Hs.347939	hemoglobin, alpha 2	3.13	17.37
	419648	T73661	Hs.91877	thyroid hormone responsive SPOT14 (rat)	3.12	4.63
5	421485	AA243499	Hs.104800	hypothetical protein FLJ10134	3.12	3.02
-	432375	BE536069	Hs.2962	S100 catcium-binding protein P	3.12	8.51
	417713	D42047	Hs.82432	KIAA0089 protein	3.12	5.82
				peroxisomal long-chain acyl-coA thioeste	3.11	6.51
	446948	BE409053	Hs.299629		3.11	5.44
10	444195	AB002351	Hs.10587	KIAA0353 protein		6.61
10	415704	NM_001677	Hs.78629	ATPase, Na? transporting, beta 1 polypep	3.11	
	401905			ENSP00000252232*:Sterol regulatory eleme	3.10	3.52
	443071	AL080021	Hs.8986	complement component 1, q subcomponent,	3.10	5.10
	427095	AA316080	Hs.173554	ubiquinol-cytochrome c reductase core pr	3.10	5.39
	413835	AJ272727	Hs.249163	fatty acid hydroxylase	3.08	5.56
15	448106	AI800470	Hs.171941	ESTs	3.07	5.19
13	432908	AI861896		ESTs	3.07	3.47
			Hs.112341	protease inhibitor 3, skin-derived (SKAL	3.07	7.48
	422158	L10343			3.05	3.97
	429506	D49835	Hs.171942	ras responsive element binding protein 1	3.02	6.75
00	424998	US8515	Hs.154138	chitinase 3-like 2		
20	419358	T78763	Hs.90063	neurocalcin delta	3.00	7.68
	414541	BE293116	Hs.76392	aldehyde dehydrogenase 1 family, member	2.99	5.44
	426402	BE387327	Hs.80475	polymerase (RNA) II (DNA directed) polyp	2.99	6.84
	450472	AJ190071	Hs.55278	ESTs	2.98	5.06
	421335	X99977	Hs.103505	ARS component B	2.97	9.31
25	431316	AA502663	Hs.145037	ESTs	2.96	4.30
23			Hs.100895	hypothetical protein FLJ10462	2.96	2.97
	420996	AK001927			2.95	6.59
	451176	AA046457	Hs.60677	EST6	2.93	3.92
	444204	Al129194	Hs.143040	ESTs		
	436723	AW975895	Hs.307486	ESTs	2.93	6.64
30	436664	AW197887	Hs.253353	ESTs	2.93	3.82
	406962	M13485		gb:Human metallothionein I-B gene, exon	2.93	3.10
	453092	X64838	Hs.31638	restin (Reed-Steinberg cell-expressed in	2.93	5.35
	444734	NM_001360	Hs.11806	7-dehydrocholesterol reductase	2.91	9.84
	430310	U60115	Hs.239069	four and a half LIM domains 1	2.91	7.02
35		AA918425	Hs.177744	ESTs	291	5.41
33	420876			E74-like factor 3 (ets domain transcript	2.91	5.64
	426050	AF017307	Hs.166096		2.90	9.54
	428232	BE272452	Hs.183109	monoamine oxidase A	2.89	5.37
	413796	AW408094	Hs.75545	interleukin 4 receptor		
	413884	AI668892	Hs.239758	hypothetical protein FLJ12389 similar to	2.88	5.34
40	411372	AJ147861	Hs.213289	low density lipoprotein receptor (famili	2.86	6.31
	428500	AJ815395	Hs.184641	fatty acid desaturase 2	2.86	3.93
	444135	AK000374	Hs.10346	hypothetical protein FLJ20154	2.86	6.05
	452689	F33868	Hs.284176	transferrin	2.85	6.11
	403108	1 30000	110.201110	ENSP00000241415*:Hypothetical 67.7 kDa p	2.85	3.17
45		414/00750		gb:hh70e05.y1 NCI_CGAP_GU1 Homo sapiens	2.84	3.35
43	434433	AW629759	11- 1000		2.83	4.05
	434952	T10269	Hs.4285	Homo sapiens cDNA: FLJ22505 fis, clone H	2.83	3.57
	420544	AA677577	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT		
	406922	S70284	Hs.119597	gb:stearoyl-CoA desaturase [human, adipo	2.82	3.80
	437470	AL390147	Hs.134742	hypothetical protein DKFZp547D065	2.82	6.40
50	429807	AK002138	Hs.306227	Homo sapiens cDNA FLJ11276 fis, clone PL	2.82	2.97
	425180	U00115	Hs.155024	B-cell CLL/lymphoma 6 (zinc finger prote	2.81	5.15
	415409	AW993701		NS1-associated protein 1	2.80	6.16
		AF095719	Hs.93764	carboxypeptidase A4	2.80	2.88
	433848			zinc finger protein 288	2.79	5.99
55	425750	AL050276	Hs.42400		2.78	5.25
23	433638	AW872507	Hs.3462	cytochrome c oxidase subunit VIIc	2.78	4.17
	429128	AA446869	Hs.119316	ESTs		7.37
	446292	AF081497	Hs.279682	Rh type C glycoprotein	2.77	
	430420	AW140027	Hs.26373	Homo sapiens cDNA: FLJ23449 fis, clone H	2.76	6.09
	419923	AW081455	Hs.120219	ESTs	2.76	4.31
60	407555	Z48511		gb:H.sapiens XG mRNA (clone PEP11).	2.76	4.12
	425240	AA306495	Hs.1869	phosphoglucomutase 1	2.74	5.92
	459317	BRCA1b		Eas Control	2.74	19.85
	425819	N92165	Hs.93231	ESTs	2.74	5.72
		AW277084	113.50201	gb:xp61h09.x1 NCI_CGAP_Ov39 Homo sapiens	2.73	3.93
65	408839		11- 202642	Homo sapiens cDNA FLJ11606 fis, clone HE	2.72	5.94
05	418253	AA215539	Hs.283643		2.72	6.51
	409453	AJ885516	Hs.95612	ESTs	2.72	3.80
	406625	Y13647	Hs.119597	stearoyl-CoA desaturase (delta-9-desatur		4.04
	420074	AA253425	Hs.190074	ESTs	2.71	
	429547	AW009166	Hs.99376	FGENESH predicted novel secreted protein	2.71	2.84
70	444026	AA205759	Hs.10119	hypothetical protein FLJ14957	2.71	6.17
	407112	AA070801	Hs.51615	ESTs, Weatly similar to ALU7_HUMAN ALU S	2.70	5.23
	429615	AF258627	Hs.211562	ATP-binding cassette, sub-family A (ABC1	2.69	5.33
	419098	AA234041	Hs.87271	ESTs	2.69	3.22
				arnine oxidase, copper containing 3 (vasc	2.69	6.64
76	424206	NM_003734			2.68	5.85
75	443102	A1247472	Hs.132965	ESTs	2.68	5.38
	411939	AI365585	Hs.146246	ESTs		3.69
	453201	AI432195	Hs.135098	ESTs	2.68	
	420231	R06866	Hs.19813	ESTs	2.67	4.70
	404996			Target Exon	2.67	4.97
80	452955	AW390282	Hs.31130	transmembrane 7 superfamily member 2	2.66	6.36
	447205		Hs.11006	ESTs, Moderately similar to T17372 plasm	2.65	15.65
	417365		Hs.82028	transforming growth factor, beta recepto	2.65	7.74
	444169		Hs.58756	ESTs	2.64	3.40
	444 103	M1040110	1 13.30/30			

	431247	AL021578	Hs.278489	matrilin 4	2.64	3.35
	423960	AA164516	Hs.136309	SH3-containing protein SH3GLB1	2.63	5.12
	432093	H28383		gb:yl52c03.r1 Soares breast 3NbHBst Homo	2.63	4.08
_	408669	AI493591	Hs.78146	platelet/endothelial cell adhesion molec	2.61	6.44
5	440924	AF151872	Hs.7527	small fragment nuclease	2.59	6.37
	416232	AW502678	Hs.79090	exportin 1 (CRM1, yeast, homolog)	2.59	6.46
	425320	U29344	Hs.83190	fatty acid synthase	2.59	3.93
	402315	1400000	Un EDA46	NM_003430:Homo sapiens zinc finger prote	2.58 2.58	6.09 4.05
10	449539	W80363	Hs.58446	ESTs	2.58 2.58	5.61
10	418271	NM_000919	Hs.83920	peptidylglycine alpha-amidating monooxyg	2.58 2.58	3.54
	449967	R40978	Hs.271498	ESTs, Moderately similar to ALU1_HUMAN A	2.58 2.58	5.24
	438752	AW238673	Hs.146038	ESTs	2.57	5.16
	424675	NM_005512	Hs.151641	glycoprotein A repetitions predominant	2.57	6.45
15	438763	A1583207	Hs.99029	CCAAT/enhancer binding protein (C/EBP), delta steep inducing peptide, immunoreac	2.56	6.38
I J	413630	AL036883	Hs.75450		2.56	2.90
	424834	AK001432 Al791495	Hs.153408 Hs.180142	Homo sapiens cDNA FLJ10570 fis, clone NT calmodulin-like skin protein (CLSP)	2.56	2.67
	427666 426403	NM_000361	Hs.2030	thrombomodulin	2.56	5.19
	432906	BE265489	Hs.3123	, lethal giant larvae (Drosophila) homolog	2.55	5.62
20	420924	R01026	Hs.245321	ESTs	2.55	3.22
20	427527	AI809057	Hs.153261	immunoglobulin heavy constant mu	2.55	5.45
	407083	Z48511	1.0.100201	H.sapiens XG mRNA (clone PEP11)	2.55	4.50
	445437	AI224165	Hs.148725	ESTs	2.54	4.72
	425097	NM_014247	144.740.60	PDZ domain containing guanine nucleotide	2.54	5.28
25	420105	AW015571	Hs.32244	ESTs, Weakly similar to FMOD_HUMAN FIBRO	2.53	6.55
~~	429554	NM_012275	Hs.207224	interleukin 1, delta	2.53	2.84
	408896	AI610447	Hs.48778	niban protein	2.53	7.08
	409169	F00991	Hs.50889	(clone PWHLC2-24) myosin light chain 2	2.52	8.68
	420235	AA256756	Hs.31178	ESTs	2.51	4.21
30	436314	AI983409	1.2.2.1110	ESTs	2.51	3.11
-	440602	AI743491	Hs.292692	ESTs	2.50	2.71
	444946	AW139205	Hs.156457	hypothetical protein FLJ22408	2.48	2.86
	430235	BE268048	Hs.236494	RAB10, member RAS oncogene family	2.48	5.37
	423929	M69136	Hs.135626	chymase 1, mast cell	2.48	3.21
35	426689	BE245550	Hs.171825	basic helix-loop-helix domain containing	2.48	7.88
	421811	AA022550	Hs.108548	PABP-interacting protein 2	2.48	5.28
	414420	AA043424	Hs.76095	immediate early response 3	2.47	8.33
	420693	NM_001972	Hs.99863	elastase 2, neutrophil	2.47	2.78
	420139	NM_005357	Hs.95351	lipase, hormone-sensitive	2.46	10.12
40	447179	AW015633	Hs.157299	ESTS	2.46	3.45
	451687	AL041260	Hs.26837	Homo sapiens mRNA; cDNA DKFZp586K1123 (f	2.46	5.47
	420322	AB014555	Hs.96731	huntingtin interacting protein-1-related	2.45	6.18
	421064	AI245432	Hs.101382	turnor necrosis factor, alpha-induced pro	2.45	5.75
	421818	AW992976	Hs.50098	NM_002489:Homo sapiens NADH dehydrogenas	2.45	6.73
45	412524	AA417813	Hs.44208	hypothetical protein FLJ23153	2.44	10.55
	439639	AA370045	Hs.6607	AXIN1 up-regulated	2.44	5.22
	436009	H57130	Hs.120925	ESTs	2.44	2.94
	414814	D14697	Hs.77393	famesyl diphosphate synthase (famesyl	2.43	5.17
	434060	AA744902	Hs.197922	hypothetical protein PRO1489	2.43	5.56
50	425335	BE394327	Hs.296267	follistatin-like 1	2.43	10.52
	406997	U07807		metallothionein IV	2.42	4.35
	431545	AF095703	Hs.8110	L-3-hydroxyacyl-Coenzyme A dehydrogenase	2.42	6.72
	417029	AW952192	Hs.273385	guanine nucleotide binding protein (G pr	2.41	5.22
	412825	AW167439	Hs.190651	Homo sapiens cDNA FLJ13625 fis, clone PL	2.41	5.56
55	445462	AA378776	Hs.288649	hypothetical protein MGC3077	2.41	5.24
	448954	AB014564	Hs.22616	KIAA0664 protein	2.40	5.31
	447218	BE617762	Hs.10748	hypothetical protein DKFZp434B195	2.40	5.24
	423810	AL132665	Hs.132955	BCL2/adenovirus E1B 19kD interacting pro	2.39	5.55
60	450440	AB024334	Hs.25001	tyrosine 3-monooxygenase/tryptophan 5-mo	2.39	7.63
60	430356	N87990	Hs.239870	Homo sapiens mRNA; cDNA DKFZp564H0764 (f	2.38	5.99
	418355	L42563	Hs.1165	ATPase, H? transporting, nongastric, alp	2.38	3.84
	416273	AW575691	Hs.79123	KIAA0084 protein	2.38	5.22
	427272	NM_001096		ATP citrate lyase	2.38	5.41
65	437186	AA338305	Hs.5472	hypothetical protein FLJ20173	2.35 2.33	5.13 5.81
05	443679	AK001810	Hs.9670	hypothetical protein FLJ10948	2.33	
	431179	AI338644	Hs.195432	aldehyde dehydrogenase 2 family (mitocho		7.89
	418400	BE243026 AL044870	Hs.301989	KIAA0246 protein	2.33 2.32	5.36 3. <i>2</i> 7
	456876		Hs.208780	ESTs, Weakly similar to T29647 hypotheti	2.31	4.65
70	407082	Z47055 W23184	Me 170171	gb:Human partial cDNA sequence, famesyl glutamate-ammonia ligase (glutamine synt	2.31	9.37
70	426508 408536	AW381532	Hs.170171 Hs.135188	giotamate-ammonia igase (giotamine synt ESTs	2.31	2.60
	410552	X66945	Hs.748	fibroblast growth factor receptor 1 (fms	2.30	5.94
	437201	F29279	Hs.171625	hypothetical protein MGC14697	2.30	5.75
	417314	N68168	13.111023	gb:za11c01.s1 Soares fetal liver spteen	2.30	3.12
75	433738	AJ684802		ESTs	2.30	3.91
, ,	410531	AW752953		gb:QV0-CT0224-261099-035-g02 CT0224 Homo	2.29	3.61
	422491	AA338548	Hs.117546	neuronatin	2.29	5.66
	434411	AA632649	Hs.201372	ESTs	2.28	4.40
	451926	AW134519	Hs.96125	Homo sapiens, Similar to clone FLB3816,	2.28	5.14
80	401131			NM_001651*:Homo sapiens aquaporin 5 (AQP	2.27	5.62
	401205			Target Exon	2.27	2.98
	422109		Hs.1473	gastrin-releasing peptide	2.26	3.94
	456646		Hs.110196	NICE-1 protein	2.26	2.52
		· · · · -		•		

	443049	AJ028613	Hs.132343	ESTs	2.25	3.13
	440160	BE560269	Hs.7010	NPD002 protein	2.25	4.93
	438367	N79688	Hs.204354	ras homolog gene family, member 8	2.25	9.58
5	442987	AA075975		Homo sapiens clone TCCCIA00427 mRNA sequ	2.24	6.19
5	421545	AA292810	Hs.90034	hypothetical protein FLJ21916	2.24 2.23	2.58 9.03
	447150 450014	AI439011 N41322	Hs.86386 Hs.18441	myeloid cell leukemia sequence 1 (BCL2-r ESTs	2.23	4.50
	426611	BE178050	Hs.171271	catenin (cadherin-associated protein), b	2.22	5.64
	434039	L32977	Hs.3712	ubiquinal-cytochrome c reductase, Rieske	2.22	5.57
10	427569	BE299197	Hs.179665	cyclin-dependent kinase inhibitor 1A (p2	2.22	5.10
	444637	T19101	Hs.11494	libulin 5	2.22	6.43
	406710	AJ708347	Hs.184014	ribosomal protein L31	2.21	9.10
	424909	S78187	Hs.153752	cell division cycle 258	2.20 2.20	6.13 11.34
15	407228 450612	M25079 AL359946	Hs.155376 Hs.14779	hemoglobin, beta acetyl-CoA synthetase	2.20	7.03
13	458568	AI769067	Hs.127824	ESTs, Weakly similar to T28770 hypotheti	2.20	5.68
	407370	AA682384	Hs.182084	ESTs	2.20	7.00
	438942	AW875398	Hs.6451	PRO0659 protein	2.19	6.09
	400228			NM_021724*:Horno sapiens nuclear receptor	2.19	6.95
20	410185	BE294068	Hs.737	immediate early protein	2.18	11.72
	428150	AW950547	Hs.70312	cytochrome c oxidase subunit VIIa polype	2.17 2.17	7.05 6.41
	400307	AF005081	Hs.146824	Homo sapiens skin-specific protein (xp32	217 217	3.68
	424425 414459	AB031480 Y11525	Hs.76171	SPR1 protein CCAAT/enhancer binding protein (C/EBP),	2.17	3.11
25	400082	111025	18.7077	Eos Control	2.16	8.40
	434702	AL039734	Hs.4099	nardilysin (N-arginine dibasic convertas	2.16	6.83
	439651	AF086480	Hs.56255	ESTs	2.16	3.72
	431838	AI097229	Hs.217484	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.15	3.34
20	420225	AW243046	Hs.282076	Homo sapiens mRNA for KIAA1650 protein,	2.14	6.20
30	428848	NM_000230	Hs.194236	leptin (murine obesity homolog)	2.14 2.14	3.42 9.81
	415213	NM_002933 . AF217798	Hs.78224 Hs.3850	ribonuclease, RNase A family, 1 (pancrea US1-interacting protein NUDEL; endoolig	2.14	6.75
	434454 452467	AW500815	NS.3030	ESTs	2.13	4.66
	418226	AA424202	Hs.83834	cytochrome b-5	2.13	5.41
35	414815	AW292140	Hs.130286	ESTs	2.12	4.14
	430967	H16791	Hs.100895	ESTs	2.12	4.14
	426102	AF200496	Hs.166371	interleukin 1, zeta	2.12	3.77
	410223	S73775	Hs.60708	catsequestrin 1 (fast-twitch, skeletal m	211	5.30 4.01
40	439518	W76326	U= 1740E1	gb:zd60d04.r1 Soares_fetal_heart_NbHH19W	2.11 2.10	5.13
40,	427228 436961	AA115770 AW375974	Hs.174051 Hs.156704	small nuclear ribonucleoprotein 70kD pol ESTs	2.10	3.33
	417139	M69043	Hs.81328	nuclear factor of kappa light polypeptid	2.10	8.13
	445831	NM_006055	Hs.13351	LanC (bacterial lantibiotic synthetase c	2.08	5.42
	431593	NM_002108	Hs.276590	ESTs	2.08	4.43
45	423887	AL080207	Hs.134585	DKFZP434G232 protein	2.08	3.92
	424389	AA339786		lymphocyte-specific protein 1	2.07	5.52
	407394	AF005081		gb:Homo sapiens skin-specific protein (x	2.06 2.05	5.93 10.48
	400198	A IOE 4247	Hs.2017	Eos Control ribosomal protein L38	204	5.57
50	426335 443652	AI054347 AI080692	Hs.134229	ESTs, Weakly similar to I54401 hypertens	2.04	3.36
50	448804	AW512213	Hs.342849	ADP-ribosylation factor-like 5	2.02	3.32
	443932	AW888222	Hs.9973	tensin	2.02	9.28
	421324	BE257515	Hs.103503	deoxyribonuclease Hike 2	2.02	5.71
	426406	AJ742501	Hs.169756	complement component 1, s subcomponent	2.01	5.49
55	410669	AW805749		superoxide dismutase 2, mitochondrial	2.01 2.01	3.05 2.77
	446193	AI279390	Hs.144658	ESTs, Weakly similar to T17257 hypotheti Eos Control	2.00	11.41
	400078 456267	Al127958	Hs.83393	cystatin E/M	1.99	3.59
	413125	BE244589	Hs.75207	glyoxalase I	1.98	6.70
60	415433	W70067	Hs.58066	ËSTs	1.98	5.59
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	1.98	3.52
	417553	L09190		trichohyalin	1.98	3.39
	403105			Target Exon	1.98 1.97	5.05 8.74
65	414081	AW969976	Hs.173724	matrix Gla protein creatine kinase, brain	1.97	5.51
05	422639 452208	A1929377 AA024792	Hs.31895	hypothetical protein MGC4093	1.97	5.67
	436106	AI050715	Hs.2331	E2F transcription factor 5, p130-binding	1.97	5.75
	439265	AL134430	Hs.6906	Homo sapiens cDNA: FLJ23197 fis, clone R	1.96	5.09
	430037	BE409649	Hs.227789	mitogen-activated protein kinase-actival	1.96	5.49
70	440054	AW661947	Hs.6891	splicing factor, arginine/serine-rich 6	1.95	5.95
	417088	M54915	Hs.81170	pim-1 oncogene	1.95	8.19
	429451	BE409861	Hs.202833	heme oxygenase (decycling) 1	1.95 1.95	5.19 6.78
	415274 452472	AF001548 AW957300	Hs.78344 Hs.294142	myosin, heavy polypeptide 11, smooth mus ESTs, Weakly similar to C55663 oligodend	1.50 1.94	5.98
75	414860	BE255593	Hs.77502	methionine adenosytransferase II, alpha	1.94	5.13
	437220	AL117542	Hs.334305	GS1999hdl	1.94	3.42
	450461	BE408081	Hs.46736	hypothetical protein FLJ23476	1.94	5.66
	424924	AL039103	Hs.153834	pumilio (Drosophila) homolog 1	1.93	5.28
0/	413945	NM_000591		CD14 antigen	1.93	5.38 5.75
80	428193			Kruppel-like factor 4 (gut) blaomycin hydrolase	1.93 1.92	4.65
	415988 425783		Hs.78943 Hs.1948	nbosomal protein S21	1.92	9.79
	431476		Hs.256697	histidine triad nucleotide-binding prote	1.91	7.00
				<b>▼ •</b> · · ·		

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			11. 40.4500	Name agains aDNA EL 112004 fie close Pl	1.91	3,41
	456653 401846	AI807519	Hs.104520	Homo sapiens cDNA FL113694 fis, clone PL NM_000988*:Homo sapiens ribosomal protei	1.91	5.62
	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (strometysin Eos Control	1.90 1.89	4.00 15.74
5	400199 429367	AB007867	Hs.278311	plexin B1	1.88	5.58
	400083	AL/CC77770	Un 2214	Eos Control selenoprotein P, plasma, 1	1.88 1.88	9.07 5.16
	433465 400079	AV657778	Hs.3314	Eos Control	1.87	8.57
10	411807	AK000290	Hs.44033	dipeptidyl peptidase 8 kaltikrein 5	1.86 1.85	5.19 2.75
10	409178 422624	BE393948 BE616678	Hs.50915 Hs.76152	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	1.85	5.33
	443121	219267	Hs.9006	VAMP (vesicle-associated membrane protei	1.85 1.84	6.01 2.82
	451092 430572	A1207256 U33114	Hs.13766 Hs.245188	Homo sapiens mRNA for FLJ00074 protein, tissue inhibitor of metalloproteinase 3	1.83	5.10
15	426812	AF105365	Hs.172613	solute carrier family 12 (potassium/chlo	1.83	6.48 3.63
	439927	AA854650 N25117	Hs.124597 Hs.299465	ESTs ribosomal protein S26	1.82 1.82	6.69
	415089 406400	MZ3117	115.235403	kallikrein 8 (neuropsin/ovasin) (KLK8)	1.82	2.95
20	406467	*********		Target Exon	1.79 1.79	2.65 5.24
20	426672 414088	AW270555 AW797956	Hs.171774 Hs.75748	hypothetical protein proteasome (prosome, macropain) subunit,	1.78	6.02
	433271	BE621697	Hs.14317	nucleolar protein family A, member 3 (H/	1.78 1.77	5.92 5.44
	429307 433640	AU076592 AW390125	Hs.198951 Hs.240443	jun B proto-oncogene Homo sapiens cDNA: FLJ23538 fis, clone L	1.77	5.79
25	425503	W92517	Hs.158203	actin binding LIM protein 1	1.77	9.27 5.44
	429191	AF065215	Hs.198161 Hs.160483	phospholipase A2, group IVB (cytosofic) erythrocyte membrane protein band 7.2 (s	1.77 1.77	6.97
	425875 431021	AU077333 AI869664	rs.160463	thiosulfate sulfurtransferase (modanese	1.77	5.23
20	432891	AF161483	Hs.279761	HSPC134 protein	1.75 1.75	5.73 5.72
30	432872 451335	Al908984 AB023192	Hs.279623 Hs.26285	selenoprotein X, 1 imidazoline receptor candidate	1.75	6.87
	428975	NM_004672	Hs.194694	mitogen-activated protein kinase kinase	1,74 1,74	3.01 5.75
	417824 439908	AA084798 AI168031	Hs.82646 Hs.155507	Dnaj (Hsp40) homolog, subfamily B, membe ESTs	1.74	2.63
35	433308	AA360154	Hs.177415	Finkel-Biskis-Reilly murine sarcoma viru	1.74	6.80
_	445919	T53519	Hs.334692	hypothetical protein MGC14141 hypothetical protein FLJ10350	1.74 1.73	5.65 6.13
	427391 425299	W60675 AW505214	Hs.155560	catnexin	1.73	5.88
40	430449	AA352723	Hs.241471	RNB6	1.72 1.71	5.14 4.35
40	456766 407694	R87310 U77594	Hs.7740 Hs.37682	oxysterol binding protein-like 1 retinoic acid receptor responder (tazaro	1.71	6.16
	412374	X01388	Hs.73849	apolipoprotein C-III	1.70	5.18
	417483	BE549343	Hs.82208	acyl-Coenzyme A dehydrogenase, very long KIAA0540 protein	1.70 1.69	7.46 6.19
45	410584 431882	AB011112 NM_001426	Hs.64742 Hs.271977	engrailed homolog 1	1.68	2.63
	441379	AW175787	Hs.334841	setenium binding protein 1	1.67 1.67	7.42 6.93
	422115 406742	A1878953 A1468091	Hs.111811 Hs.279860	microsomal glutathione S-transferase 3 tumor protein, translationally-controlle	1.66	6.26
	432191	AA043193	Hs.273186	hypothetical protein, clone Telethon(Ita	1.65	5.83 7.54
50	452363	A1582743 AF279865	Hs.94953 Hs.15711	Homo sapiens, Similar to complement comp kinesin family member 13B	1.65 1.65	5.36
	446623 406712	M31212	Hs.77385	myosin, light polypeptide 6, alkali, smo	1.65	12.30
	400202			NM_002795":Homo sapiens proteasome (pros C14001067:gi 4126465 dbj BAA36581.1  (AB	1.64 1.64	5.70 3.82
55	401429 415166	NM_003652	2 Hs.78068	carboxypeptidase Z	1.62	5.95
	410169	AJ373741	Hs.59384	hypothetical protein MGC3047	1.61 1.60	6.60 11.13
	406713 453027	U02629 AI879341	Hs.77385 Hs.539	myosin, light polypeptide 6, alkalii, smo ribosomal protein S29	1.60	10.97
	416955	AW889150	Hs.80595	NM_004552*:Homo sapiens NADH dehydrogena	1.60	5.90 5.60
60	439053 400201		Hs.6456	chaperonin containing TCP1, subunit 2 (b NM 006156*:Homo sapiens neural precursor	1.57 1.57	5.32
	407049			NM_021724*:Homo sapiens nuclear receptor	1.57	5.42
	430775		Hs.250895	ribosomal protein L34 interferon gamma receptor 2 (interferon	1.57 1.56	7.09 5.37
65	427380 407143		4 Hs.177559 Hs.332329	EST	1.56	6.54
	436127	W94824	Hs.11565	RIKEN cDNA 2010100012 gene	1.56 1.55	6.35 5.96
	413659 445624			gb:PM2-HT0353-130100-002-e09 HT0353 Homo llvB (bacterial acetolactate synthase)-l	1.55	4.09
	435044		2 Hs.4745	proteasome (prosome, macropain) 26S subu	1.55	5.71 5.14
70	410397		Hs.63042 Hs.195453	DKFZp564J157 protein ribosomal protein S27 (metallopanstimuli	1.54 1.54	8.70
	429071 412915			NM_004541:Homo sapiens NAOH dehydrogenas	1.54	6.57
	446429	A1681807	Hs.201391	ESTs encyl Coenzyme A hydratase, short chain,	1.53 1.53	2.87 6.07
75	414551 406801		Hs.76394 4 Hs.190813	ribosomal protein L9	1.52	5.63
, ,	43789	5 AB014568	Hs.5898	KIAA0668 protein	1.51	5.74 6.40
	413925		Hs.75617 Hs.157850	collagen, type IV, alpha 2 ribosomal protein L9	1.51 1.51	7.08
<u>.</u> .	425456 40963		Hs.55296	HLA-B associated transcript-1	1.50	5.26
80	40446	7		Target Exon	1.50 1.50	5.82 5.25
	40674 45409		Hs.279860 Hs.292911	tumor protein, translationally-controlle Plakophilin	1.48	3.14
	42920			UDP-Gal:betaGlcNAc beta 1,4- galactosylt	1.48	6.24

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	413825	8E299181	Hs.75564	CD151 antigen	1.47	5.64
	421143	AB024536	Hs.102171	immunoglobulin superfamily containing to	1.45	6.19
	440254	AI879332	Hs.7101	anaphase-promoting complex subunit 5	1.45	5.50
5	406711 423513	N25514 AF035960	Hs.77385 Hs.129719	myosin, light polypeptide 6, alkali, smo transplutaminase 5	1.42 1.42	11.24 3.18
5	406896	D00159	ns.129/13	gb:Horno sapiens gene for pancreatic elas	1.41	6.92
	433453	BE548307	Hs.3297	ribosomal protein \$27a	1.40	5.38
	406800	AA505535		gb:nh84h10.s1 NCI_CGAP_Br1.1 Homo sapien	1.37	5.51
10	421748	NM_014718	Hs.107809	KIAA0726 gene product Homo sapiens cDNA FLJ11780 fis, clone HE	1.37 1.36	5.46 4.06
10	424372 408250	AW952803 R92918	Hs.21732 Hs.19597	KIAA1694 protein	1.27	2.74
	431931	AB035302	Hs.272212	cadherin 9, type 2 (T1-cadherin)	1.15	2.65
	406587			C15000544*:gij5454148 ref]NP_006368.1  U	1.06	3.11
15	409574	AW419080	Hs.250645	ESTs	1.00 1.00	3.60 3.08
15	404175 452640	AA027115	Hs.100206	Target Exon ESTs, Weakly similar to A53856 aryl-acyl	1.00	2.82
	443564	AJ921685	Hs.199713	ESTs	1.00	2.51
		_				
20	TABLE 65 Pkey:		ue Eos probeset iden	ntifier number		
	CAT numb	per: Gene	duster number			
	Accession	: Gent	oank accession numb	Den'S		
•	Pkey	CAT Number	Accession			
25	407328	534268_1	A1673735 AA9780	66		
	427890	1373988_1	AA417099 AA435	761 AA972917 A1660387 221 AA865491 A1828293 AA470456 A1276739 AA169357 BE93	2464 446148	80 AWR19079 AWR19083 RERAZOAR AIA32496 AIA70335
	444207	9172_3	A1247243 RG5339	94 AA5137R3 AIRR7309 AA528036 AW972006 AW873028 AI9	24914 AI8188	10 AW152378 AW084946 AI521413 AI669583 BE932521
			AISR1370 RE1802	38 AW089750 AW771461 AW089714 AI590949 AI819148 AA7	/31056 BF815	234 BF911506 AA235803 AA485373 AI735658
30			AW393133 AW07	3080 AI707637 BF353320 BE843111 AW819036 AW393135 B	G697291 AV6	48670 AV654332 AV687530 BG566964 AI807430
			AI676072 AA8370	110 A1452482 A1625817 AW241750 BE048616 A1290928 A1680 208 AA948166 BE175650 AA524664 AA490345 A1244948 AA6	KRBAA RZPCN	492 AA918178 AW802049 BG675859 AV658871
			RCG78060 AISSSC	104 AWR19026 RERA1092 AV6R6437 AV723049 BG616948 AIS	911647 AI7434	ISD A1091096 BE85/251 A19620/4 AAU4002/ A74/0331/
			AA343477 AA64N	112 RFR76213 RR2948 H26425 H82876 RE843095 BE843140	BG536641 BC	3617830 AA235802 BE774985 BE006682 BF342375
35			AA903144 BF338	083 BF984258 AV657998 AI749532 BE768614 BE857252 BE9	132516 BE768	373 AV657993 AV657777 AV752631 BE774974 155641
	407102	7177_2	BF095761 BF911	511 BE710793 BE180119 BG617338 H45942 T55897 AV6577 0905 F33652 BG057818 AJ368018 AJ421485 AJ300352 AJ3785;	16 BG565437 25 Al264177 A	J276281 AJ245302 AJ281050 AJ190036 AW451438
	407102	1111_2	AWZAZONI AAGII	1971 F22280 F19647 F22375 AWAZ3816 RF445785 AAZZ4528	1 F33447 C010	)77 AW772227 F17759 H42812 R09701 AA349096
			R48772 H42892 H	+42537 R47898 N28263 H25721 F32386 H43971 R48205 F21:	390 H45809 A	A007629 R47897 R83734 H45844 AW983653 H43970
40		2075 4	H42536 H24495 F	R48875 H42961 H22079 R86018 1635 AW976922 AW152652 AA910013 AAB34629 BG536317 A	WRADROT AV	713062 AIGRA337 REGAAGR1 AA761490
	437596 440116	2875_1 454673_1	BCU22398 AV743	57 BF111453 AI149320 N23160 AI446431 AI758316 AV741781	B1791950 BM	055014 AI798851 AA865357 AI417230 N67277 T55592
	440110	434073_1	T52179	71 DI 111433 PA 143320 1123100 PA 441310 PA 141332 PA 141332		
	443072	449629_1	AV734838 AI937	532 AI032318 AW749500 AA091720		D
45	442679	31783_3	BG621493 BI056	706 BG496376 R53718 W65356 R79357 BG434247 AA357769 6754 BG434311 AW978683 AW273417 BM054662 AJ799886 A	3 AW9/8686 5	(55/3200 BF 132113 BF 066709 AA300930 D7 9234 0708 A1433742 RF056186 A1281606 AW015046 A1439585
			A1245530 A10782	67 AARO7170 AAR37395 W61252 AAR31885 AA287371 AW76	8354 AA8906(	36 A1302539 A1708575 A1673031 A124ZZ60 AW514U69
			AA293058 AA926	iaso aistiosa aaaoskok aaassaoo aarotkot Roskss D2024	40 AA772517 I	H13802 R66972 R79360 R27351 F03379 AAU31952
			N69504 R33143	R79358 R39136 R38800 R15089 R52937 R37502 H01021 R33	3634 R46551 Z	40404 BG291052 BG570357 AW391046 BG496872
50	404574	0759 4	H23558	2643 AI803450 AI564343 AI092711 AI140525 AW152156 AI62	0740 AI55468	9 A1161209 A1290242 A1339745 A1374611 A1347388
	424571	9758_1	A1858296 A11405	39 AIRE 124 AA493912 AA406235 AA493889 AI057160 AW02	22264 AJ09727	7 AI144126 AI080051 AA983529 AA860507 N53469
			AAR43767 NR116	53 N70628 AAA24577 AA983537 RF003004 AA626688 AA2359	977 AIO571 <b>52</b> .	A1095366 A1095356 AA458646 AW194479 AA15U439
55			AI375272 AW571	1777 A1359198 AA993793 BE614394 BE738239 AA127883 AI0 5 BE244980 AA548596 AW449675 A1191008 BF223749 N7075	134344 159504 62 N22266 A11	, D81508 AA908/04 AW051665 AA382765 AA307206 (01012 AA028001 AIA19106 RF215661 RF591548
23			N24639 AI3/U/ 1 RGQA2356 AI474	5 BE244980 AAS48598 AW449673 ATT91006 BF223749 M7013 1968 BE858217 BF793358 AV756758 BG483603 A1093724 BF0	693395 BG545	345 AI744294 T59549 AA811773 BG499757
	420787	55832_7	BE674920 AA56	4248 AA280309		
	456332	21353_10	BG740624 AV72	0262 BG198346 BG215119 AW841716 AA228357 AW841786 4455 BE672212 AI151416 AI566231 AI417585 AI378391 AA23	COCA A122757	A A1246166 AA406600 AA748618 AW771957 AA478626
60	418479	175360_1	AUAPSSONTS ALOOF	NAAA AIDANSAE DEENSEES DICSSABBE AIBBBSSN AISBBANS BESI	Q463R AW/07£	N94 AW517456 AAR3ZZZ9 AID56108 ARZSS868 AIZ456U0
00			D61957 AI093R4	1 AJ721013 AJ597594 AA993022 AJ128620 AJ285106 W37459	W35410 N900	)37 AA890323 K39943 AI468741 AA829976 AA4792V1
			AI539018 AA875	875 AA448827 AW779493 Z39056 H84925 AAZZ3923 AW517	592 AI804400	AA911882 BM353143 D62885 Al457883 Al880626
		*****	R31694 R42772	R68804 R44147 R71463 AV742540 BF966987 )12120 AF164377 AW976054 AW662923 AW770101 AL59718	A A A 713050 A	ARDRO21 AWA44F4D AID18159 AL050105 AW958324
65	431628	30288_1	RIRS8773 RM313	2584 RE594436 A1629024 AA311487 BG617872 AW629675 AA	4384810 AW9	53668 BF171208 BE768429 BF326254 AW181992
05			AW118462 AW5	72001 RC5331R4 AA768779 AA825697 AA808149 BF036424 .	AJ420469 AW	175925 AA 173981 AA557142 AW302163 AW000600
			AA847195 AJ418	3480 BM353163 Al015673 Al357621 Al374592 Al245029 Al580 71202 BE138896 R80586 BM090998 D25882 M85322 Al5413	)659 Al370154	. AA767503 AA643885 BM091307 BG496655 AVV364502 DC696656 AA697866 RER79221 RE504796 RE675714
			AW377222 AW3	71702 BE138896 R80586 BM090998 D25882 M85322 A15913 0411 BG217933 BG219447 BF886143 BG403278	03 670/3114	3G32G323 MA021000 DC013221 G1 334130 G1 0751 14
70	426101	3211_1	ALCA0097 RC62	NGG7 RG5710R4 AW362R42 RE150456 RE326465 AW872412	AA868553 AK	)24689 AA442638 AA813604 AA442648 AA663108
. •	.20101		AAAA2370 AA22	IOAAR NEERAG AAAENOON AWIGT 193 AAAERTOS AITAORRT AIRE	50142 AW7694	179 A1917507 A1860141 BE045272 AW277065 A1921333
			AI354470 BE466	6760 A1827987 A1005467 AA833517 AA563934 AA522837 AA8 81 AA632986 BE708493 R31132 A1253986 A1916737 T84796	112676 AWUZU	1515 AA6UUJ/2 AA6031/8 A118/9/7 AA229104 A42/0024
			BE835233 AIA7	81 AA632986 BE708493 K31132 A1253986 A1918737 184796 2712 AV741009 AA551512 N28268 AA436880 AA447794 BE8	35410 BE8353	85 BE818352 BE818350 R64648 BE646467 AA493776
75			AA437299 BE81	18343 R95914 R31089 BF576826 AU186065 BF802058 AI2170	018 AA247541	Al191725 BE766918
-	454947		AW846590 AW8	346615 AW846584 AW846592 AW846621 AW846610		
	438962		AR075855 AI70	3684 BF928775 AA828585 9883 AI952039 BM313847 AW167132 AW264027 AI394192 BI	M272158 BM2	72359 BG057287 BE464852 AI620722 BE046016
	431693	1414_4	A1758979 AWA7	MATAS AWATASTA AWAAASSA AIZSSASSA AWAATTO AIASSI 69 A	U634183 AJ12	5609 AI951377 AI631154 AI453490 AI857358 AI469756
80			RGERISOI AIAI	4048 F09546 AW518770 RF855622 AI659151 AA985193 AI81	4412 AW2981	84 H09775 AI869379 AW207026 AI659678 AI826075
			BF940660 AA74	14971 C00469 A1672560 AL045697 BF847489 BF842860 T654 8346 B1038045 W94876 AA093121 B1523346 AW470130 N927	IUU AI863491 I ??? &&?588??	129843 134772 BEUSUSUB BEUSUS17 BEUSU877 AA132265 R62397 RIS23168
			BE244501 BIO3	ODER DELIGIOUS PRODUCTION DE DISTA CHOOMIS SECO		***************************************

			100 100 100 100 100 100 100 100 100 100
	450515	13638_2	BE299605 AI589870 AA847598 AI470122 BF939896 AI304356 BE223045 BF435800 AI394207 AI708171 AW025415 AI079409 AW008420 AW304226 N34543 AW603578 AA526961 AA983631 N99134 AA626645 R45023 AA902417 AW672925 AA449985 AA953982 AW675471 AA010062 N80194 H14620 H28475 H26247 BF333581 AW842369 H06848 H05608 H81745 H15016 R51905 AA860423 AI880904 AA876023
_	434230	41110_1	H1622 H2647 17224 B 17
5	448144	48653_1	
	453225	12287_1	
10			
			BG59898 AAU31803 APUG147 AA12919 BG74300 (1930) Al935538 Al689743 AW966083 BE326704 AU147054 AW129250 BE463425 AU149980 Al242161 AW615658 AU145096 BE465120 AU159062 Al659438 AW473145 BG236394 Al292110 Al985496 AA995857 BE551066 Al632625 AW511387 A080003 AW243240 Al640340 Al075293 AW205957
15			
13			
			BF198432 AW341091 AL517119 BG608247 F2224 AN00673 AN00673 BGC007 AA781222 AA100912 BE886334 AL534518 H02114 BG740469 BI760879 BG545253 BE7313692 A1339338 BF195296 AA3527395 BE253769 AA160087 AA781222 AA100912 BE886334 AL534518 H02114 BG740469 BA76079 BG545253 BE7313956 AA183736 BF211944 BG6489143 AA330736 H933354 BE622370 BG426627 AA352143 BG743030 BG695884 W42513 BG674719 AW802577 BF313256 AA183356 BF211944 BG6489143 AA330736 H93354 BE622370 BG426627 AA352143 BG743030 BG695884 W42513 BG674719 AW802577 BF313256 AA18336 BF211944 BG6489143 AA330736 H93354 BE622370 BG426627 AA352143 BG743030 BG695884 W42513 BG674719 AW802577 BF313256 AA183736 BF211944 BG489143 AA330736 H93354 BG74308 BF211944 BG748078 AA33078 AA34078 AA
20			158371 AA773564 AA470563 W42415 161646 AA173565 A053225 A05432518 BE622820 AA587251 AW149318 H07926 R40908 AA011079 A1766899 AA031697 AA129593 D25761 AA100913 AW134585 AA129330 BF434518 BE622820 AA587251 AW149318 H07926 R40908 AA011079
20			RES67287 BE253428 AI681438
	445493	423456_1	
	417054	12405_2	AV711317 AIBU9938 AIBU8768 AIZ4U933 AI915771 BGS33564 BG618564 AW296119 AIZ69233 BF508328 AW364777 AW292258 AA371049 AIX62471 AI092522 BG618376 AL049080 AA631068
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30			AAAGONSA AIDONOGO WOAGAA AAAAAAA WGAGAA WGGAGA WGGAGAA WGGAGA WGGAGA WGGAGA WGGAGAA AAAAAAA AAAAAAA AAAAAAAA
			AA973639 W68358 BE170126 T81345 N50135 AI567418 W67220 BF437728
	431926	1237041_1 133592_1	AW972724 AA877998 AA522631 AU185388 BI757233 BG911321 BF351759 AW244016 AW026834 AW024260 AH20138 AA779354 AI093360 AI934858 AW151292 AI373133 AI335587 AI969728
	421998	133592_1	
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55			AW771253 BG820253 BG012854 R74441 R86060 W04256 BC107244 67635-354 BE674147 AI793266 AI991774 AI807726 AI218667 AA301750 AA886528 N70309 AW582776 BF110563 BF448329 BE326537 AW770471 BF444926 BE674147 AI793266 AI991774 AI807726 AI218667 AA301750
			R44328 AK054894 AW978550 AI984051 AW205843 AW205839 AI379941 AI383948 AW129532 BF197455 AI954133 AI668869 AI360826 AW614392 AI619505
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40			DEDECES AMPASSA AIRCAADS DEGEST C17731 744731 AB 344194 HIRLS / / / / / / / / / / / / DESCRIPTION CONSTRUCTION OF THE CONTROL
70			BE808333 AWX43724 AUG1467 A00031 G17171 261731 BG426009 BG611801 BE090425 BF672863 BF132610 BF184312
	408239	103120_1	
	436280	36296_1	AW459418 AA05-3401 AA05-34 16 AK026215 AI201248 BE671206 AA660436 AA730787 AA834507 D79304 D79806 AW961628 AI017068 BE044373 AA322458 AA987927 AA385869 BI492783 AW021853 R79299 N73208 AI016622 N24609 AW192569 AA707819 AI690734 R79189 AI535900 AW589301 AI128434 BE838011 BE837891
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			P75793 RG202313 AI905837 RE815853
	437611	240436_1	H93046 AA897108 AI652046 AA761626 BF882276 N68615 T88896 H93912 T84424 AK058006 BF724822 W65303 AW887764 AW023806 Z25353 AW022095 AA730973 W00417 W73819 BF982096 AI927669 AW188021 AW770478 AK058006 BF724822 W65303 AW887764 AW023806 Z25353 AW022095 AA730973 W00417 W73819 BF982096 AI927669 AW188021 AW770478
55	414496	1526_1	
60			A772384 AW104985 A1724324 AW10494 ANDS-3004 ANDS-3004 ANDS-301 ANDS-31734 ANDS-31735 AW175228 AW275204 AW20247 AA975336 AI697042 AI091778 W65401 AI687374 A1218085 A1765158 AI018002 AI653068 AI3335704 AI520850 AW275228 AW275204 AI420247 AA975336 AI698930 AI193399 AW182235 AA736386 AI281682 AW169698 AW263325 BE645834 AI377438 AI146706 AA613808 AA716538 BW56247 AA032248 AI658930 AI193399 AW182235 AA736386 AI281682 AW169698 AW263325 BE645834 AI377438 AI146706 AA613808 AA716538 BW56247 AA032248 AI658930 AI193399
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			BF445607 AA699324 AA025643 AW573103 A1167444 AA580002 AW103144 AI640654 AA857115 AA923021 A1066439 A1358865 AA843287 AI824604 AA732370 AW002202 A1219540 AA621697 A1950639 AA904277 AI867527 BF437695 AA808593 A1784144 AI648539 AV752557 AV752603 AA025642 AA764744 AW149075 N30700 H92303 W79523 A1762795 AA282784 H78923 AA252879 H98107 R23754 AA005152 N99239 N74632 H80133 H24710
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	454065 426143	517162_1 3806_1	BE394588 AW024754 BE183167 BE183166 BE378353 BC005265 BG176720 AW006077 BM352064 AW026316 AIG33822 AI880584 AIG93769 AI092211 BI492387 AI400449 AW166297 BF939910 AA232282 AW072473 AIG3980 AA64378 AA854789 AM55795 AW059756 AA587373 AI097748 AA993184 AI125077 AI081758 AI240886 AI251863 AI378423
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15	412477	8669_2	AIZ20117 AIS57837 AIZ18371 BM091400 AI30496A AI198508 AI400738 AW571549 AW950042 AI089943 AAA37280 AU150878 BF197070 AI267884 BF594181 BF196688 AI433152 AI338921 AI662036A AI280197 AA652531 AI674938 AI342447 AI620350 AIZ81295 AI148621 N54787 AI338121 AIZ81153 N51899 AI087072 AA954788 AW069064 AI346309 9IGS29629 AI340135 BF083036 AI167365 AW819657 AA935468 AI467868 AW148701 AI383720 BE047685 AW015498 AA937149 AA708346 AW771478 AW802508 H53334 AW389204 AW798230 AI553922 AI560688 AW950043 AI951682 AV706506 R01853 AA126514 N62757 AI538893 AI926052 AI418720 N99954 AI568033 AI915737 AI080691 AI185389 AI9969 N68575 H82824 H60037 AI247274 TRISS6A BF5037867 AI7496747 AW789541 AA991294 AA887452 AI073776 AA633132 AA629574 AA6226549 AA629556 AA578595 AI168758
20	400295	2196_1	AA804572 AJ085786 AA994396 AA991209 AA948663 AA922954 AA927952 T87001 AA928210 AA629296 AW802267 AW384129 BF744400 AA194110 AJ382839 AA194837 AA406284 AJ250750 R37035 AJ525586 W01244 NM_058173 AF414087 W72837 BF742809 AW070916 BE092421 AJ905687 AA340069 BE074512 AJ905623 AJ905633 BG202312 W72838 AJ139456
25		_	BG218084 BE926938 BE186013 AW176044 AW291950 BG185269 BG197185 BG192597 BG183176 BG207535 A1127172 BE815819 AI905624
25	441128	20932_1	BC014072 BE328850 AJ356567 AJ148171 AJ022165 BG149661 BF000671 AA233101 AA573721 AA447991 AW016855 AJ005068 AA554071 BF478215 AA906902 AW014761 BE905651 BE512923 BM047129 AA243852 AA232991 AA127550 AA127551 AA570256 AJ473237 BF033706 N90525 AW973623 AJ359627 BG674574 BE903322
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35	414665	23751_3	BGS67713 AW665841 AIB14924 AW978339 AW264036 AI373950 AW1B3157 AW082249 AI201658 AI364196 AA150743 AA160873 AA453757 BF871646 BF871640 AA565311 AA989511 R10152 AA807154 T77900 AV751591
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	434433 415409	111338_1 34886_1	AVISS188 BM455117 BC527027 AA480032 AW993701 AA164703 AL537682 AA836491 AA515961 AL537681 BF437856 AA683484 AW152367
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	408839	234669_1	AJ355222 BF378422 AA366587 BF874552 AW277084 R26970 D79194 R27662
45	432093 425097	1237011_1 23175_2	AW972670 AA525808 128359 128383 AF070570 BF439282 BF109960 A1480268 A1038060 AW082339 BF516290 BE218214 A1469956 AA039955 BE644674 A1861871 AA766231 AA845840 W85716 AA676253 A1087188 AA022908 AW953178 T33195 BF594711 AA488969 R55652 D81245 D80778 D81560 AW960933 BF930897 BE688103 AA040024 BF515960 BE168475 AA453247 A1267601 R60894 R44223 T33194 AA114936 W31640 W38829 W39109 AA004849 H41952 W88634 BF031932 BM423354 AL041825 H29654 A1908178 W85754 A1905762 AA309860 CD4540 AA340246 H84669
	436314	142774_1	AA708982 AI095911 AI983409
50	406997	29867_1	NA NA
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55	442987	66995_1	BC016329 BC530458 AW811919 AW811918 BG777252 NZ8284 AA280517 NZ6361 BG612488 BI491654 BE042557 NJ921004 AW665869 AA845400 BF057417 AJ735558 BM146017 AJ538936 AJ439915 AJ745155 AA993066 AA935277 AJ161350 AA884866 AJ692463 AA938040 AV717682 AJ439961 AJ439956 AJ885932 AJ538058 H60829 AA513966 AJ249944 Z39473 AJ832915 AA565386 AA074079 BM145279 BF791544 AW811909 BF964902
	400228	462_3	BG113250 N99606 AA312166 BF696463 D61610 AV757976 AA092342 BE972583 BG776159 NM_021724 M24898 X72631 BE550221 BF436030 F18898 AL567477 BG033127 BG747927 BF823716 AA371902 AL137978 AL577786 BI490529
60	400307	27110_2	AA021622 AA151679 AA745053 AA454168 R85506 AA016015 AF005081 BG193848
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65	407394	27110_2	AF005081 BG193848
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70	414081	19335_1	BI754027 BF696071 A351939 BG151298 AI919334 AI401620 BI770165 W72057 T96158 T29478 AA181252 BG927793 AA714431 AA500749 AA181247 AA614756 AA081092 H52207 BG926934 BF222579 BG899001 N64245 AA953040 AI832405 AA102441 BG928081 AA993445 AA916041 AA987847 AA983329 AA737219 AA916443 AW128994 AI492560 AI761847 BC005572 NM_000900 X53331 M58549 BI758956 AL598829 BI754530 BG699770 BE439699 BE440148 AV704355 AV733652 BG212015 BG184149 BG201080 BG212690 BI761222 BG182079 AW338822 AI925631 AA23741 AW074181 AIR89876 AW172112 RG395379 AI017633 AA568964 BF725590 AI004210 AI809799 BC083097 BG896220 AW997681 BF668788
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10	427391	9048_3	H79704 AI984 AA053459 AA AY007099 AU	1704 A1984483 BG952614 BF345358 AW083336 AA643660 A1476232 AA603071 BE7 F4413 KHIVT0000 KHIV THE THE THE THE TOTAL ASSESSED A145748 BG954446 BF760569 107099 AU150467 A1177583 BE753800 A1125772 A1373009 A1215670 A1769136 AA586848 AW451158 N50799 AA936337 A1355427 BE677905 107099 AU150467 A1177583 BE753800 A1125772 A1373009 A1215670 A1769136 AA586848 AW451158 N50799 AA936337 A1355427 BE677905							
15			A1494204 AA9 T03896 BF93	94204 AA953319 AA155753 AU052675 AA044804 AI282678 BG741226 F.5799 AA16220 FA05020 AA054804 AI753954 BE908511 AW628731 AA034958 896 BF939430 AA974325 AW072996 AW005963 BG252471 AI192002 AI918080 AA776144 BI834864 AI753954 BE908511 AW628731 AA034958							
13			BG575588 BII	054960 H51485 AW799491 AI370437 H26413 AA	85334 AU151276 AAU14274 AASSOCIOS ATTISTOTO FALL TOO						
20	400202	11771_2	BE873890 BF BF972860 BG BE904726 BI BG472870 BB	28335 BI035010 F22360 BF849322 E873890 BF745945 AA156007 AA573157 AW874610 AA916387 N75963 BM083306 AW044671 BC013008 NM_002795 D26598 BG118716 BI910891 E873890 BF745945 AA156007 AA573157 AW874610 AA916387 N75963 BM083306 AW044671 BC013008 NM_002795 D26598 BG118716 BI910891 E972860 BG119842 BI094093 AL538757 BE271653 BI856538 BE909573 BG109826 BE784430 BE899255 BI833973 BM010809 BE621321 BG684956 E904726 BI871370 AV708990 BF971483 BE298241 BI197007 BE272092 BG120374 AW963509 BE540572 AV744947 BG943041 AW327463 E904726 BI871370 AV708990 BF971483 BE298241 BI197007 BE272092 BG120374 AW963509 BE540572 AV744947 BG943041 AW327463 E904726 BI871370 AV708990 BF971483 BE298241 BI197007 BE272092 BG120374 AW963509 BE540572 AV744947 BG943041 AW327463 E904726 BI871370 AV708990 BF971483 BE29824 AA360459 AA72870 BE393597 N28533 AA316042 N42043 AW404246 AW892094 AA379896 AW801110 AW406977 AA379791 BG943890 BG202360 AA379385 AA320056 BG942618 D31230 AA308300 AA360371 AA371733 AA732937 AAA94241 BG34207 BE343707 BE175930 BF037316 BG942671 AI752472							
25	400201	24179_2	NM_0061561 AW009362 B	023662 BF038671 BI670321 BI603145 BI666956 B E379126 BI198555 BF126026 N28289 BE388301	163/16526 BG/10/4/5 BG/08616 GEJ7207 B BG327102 A1571450 BF038400 A1884649 A1718962 A1742314 AA977058 BG327102 A1571450 BF038400 A1884649 A1718962 A1742314 AA977058	Al150699 20 F30164					
23	413659 406800	1526081_1 0_0	AA133181 BI BE155647 BI AA505535	F768974 H30334 AA034968 AA384232 AA353297	AW407023 AA337516 F38177 AA374444 AA402758 A1141545 B1021470	A010014					
30	TABLE 6	EC.									
30	Pkey: Ref:	Un Se se	quence source.	chromosome 22" Dunnam, et al. (1999) <u>Nature</u> 40	entifier (GI) numbers. "Dunham, et al." refers to the publication entitled "Th 2:489-495.	e DNA					
35	Strand: Ni_positi	Inc	ticates DNA strar	d from which exons were predicted. spositions of predicted exons.							
33	мсрови										
	Pkey	Ref	Strand Minus	Nt_position 35816-36004,36587-36684							
	405121 401203	8102330 9743387	Minus	172961-173056,173868-173928							
40	400494	9714719	Plus	169845-170272							
70	402294	2282012	Minus	2575-3000							
	404730	8389582	Plus	119832-120016,124110-124275							
	403593	6862650	Minus	62554-62712,69449-69602							
	403710	6437516	Plus	27413-28978							
45	401905	8671966	Plus	153965-154441,156599-156819							
	403108	8980955	Plus	93253-93667							
	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,4055							
	402315	7381741	Minus	30728-32065							
	401131	8699812	Minus	94802-94987,95804-95887,96323-96487,9759							
50	401205		Plus	167373-167433,167936-168031							
	403105		Minus	145287-145744							
	401846		Minus	82775-82823,82912-83022							
	406400		Plus	1553-1712,1878-2140,4252-4385,5922-6077							
	406467		Plus	182212-182958							
55	401429	8217890	Minus	86946-87579							
	404467	8077630	Minus	24951-25853							
	406587	8189273	Minus	120577-120718							
	404175	9931117	Minus	107420-107547,109625-109796							
۲0											
60	=	*** 5.55*	C INDICATIONS	AND PREFERRED UTILITIES FOR SELECTED C	ENES						
	Table ( Primek	56A provides d :ey: Unique	isease indications Eos probeset ide	s and preferred utilities for about 439 selected gene entifier number	s. These genes were identified using Eos/Affymetrix Genechip arrays.						
65	ExAcc		lar Accession nur e ID number	noer							
05	UgID:					re- re-const bub					
	UgTitle Oiseas			elected gene as described in table 1 and abbreviate	d as follows: AWPC (androgen independent prostate diseases), arth (arth	Autoc diseases Y nhu					
	Uiscas	fhenin	n prostatic hypern	lasia), blad (bladder diseases), angio (blood vesse	diseases), EWS (bone diseases), glio (brain diseases), breast (breast	casta), USI V ma diseasee\ loute					
		lannia	al diseases), colo	n (colorectal diseases), esoph (esophageal diseas	ossesses), leto (fibrotic diseases), head & neck diseases), leto (letomyoss), fibro (fibrotic diseases), head (head & neck diseases), leto (letomyoss), fibro (fibrotic), neck diseases), neck diseases,	ind (IISEdSCS), ICUA					
70		fleuko	nte diseases), he	enC (liver diseases), lung (lung diseases), ovar (ova	is), into (into useases), incoming into interest diseases), omuc (ovarian muc viran diseases), endo (ovarian endometrioid diseases), omuc (ovarian muc ovarian diseases), styru (styruach diseases), lest (lesticular diseases	inous diseases),					
70		none f	nancreatic diseas	es), pros (prostate diseases), renal (renal diseases	), mela (skin diseases), stom (stomach diseases), test (lesticular diseases	), vier (vienne					
	Utility:	orefen	ed utilities for sel	ected gene as described in the text and abbreviate	d as follows: CTL (DNA vaccine target), diag (diagnostic or prognostic target)	jey, mao					
	Outly:	/moss	clonal antihody to	arget), s.m. (small molecule target)	•						
75		fuelte	and a move y	Badi and farmer mere and an A.		I nere.					
,,	Drimo	key Ex Acon	UgID	Ug Title	Disease	Utility					
		9 X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	angio, btad, lung, cerv, ovar, headnk, esoph	mAb+diag+s.m.					
	40029			hypothetical protein DKFZp564O1278	breast, blad, colon, pros	mAb					
	4002			LIV-1 protein, estrogen regulated	breast, ovar, pros, storn, uter, blad, lung, headnk	mAb					
80	40034		- 1.5.75166	NM 003105* Homo saniens sortifin-related	blad	S.M.					
50	4020			ENSP00000251056*:Plasma membrane calciu	n blad, lung, headnk, cerv, mela, esoph	mAb+diag					
	4029			NM_025206":Homo sapiens hypothetical pro	blad	CTL					
	4042			FGENESH predicted novel CUB-domain conta	panc, tung, colon, uter, esoph	mAb+s.m.					
	4442	٠.									

						_
	404682			ortholog of mouse polydomain protein	panc	diag CTL+s.m.
	404875				blad	mAb+diag
	404977			Insulin-like growth factor 2 (somalomedi	blad, over	S.M.
5	405033			Greenes Sterres Milanus 1	blad	mAb+s.m.
5	405547			NM_018833*:Homo sapiens transporter 2, A ltallikrein 8 (neuropsin/ovasin) (KLK8)	cerv, mela ovar, uter	diag
	406400 406964	M21305		FGENES predicted novel secreted protein	angio, blad, fibro	diag
			Hs.62604	Homo sepiens, clone IMAGE:4299322, mRNA,	glio, blad	CTĽ
			Hs.39384	putative secreted ligand homologous to f	ovar, uter, cerv, panc	mAb+diag
10			Hs.40098	cysteine knot superfamily 1, BMP antagon	blad, panc, stom, uter, lung, esoph	diag
	407836	T79340	Hs.22575	B-cell CLLAymphorna 6, member B, zinc 6	angio	ÇΠL
		X89426	Hs.41716	endothelial cell-specific molecule 1	angio, renal	diag
		Y00787	Hs.624	interleukin 8	blad, stom, headrik, cerv, lung, angio, esoph, panc	diag mAb+s.m.
1.6			Hs.44424	Homo sapiens orphan neurotransmitter tra	meia	mAb
15		R38438	Hs.118747	SLC15A2 Solute carrier family 15 (H+/pep	pros, tung, fibro, uter, glio, cerv, ovar tung, blad, headrik, panc, storn, fibro, esoph, mela	CTL
		AF123050	Hs.44532	diubiquitin	tung, esoph, headnik, pane, suxii, noro, esoph, mesa tung, esoph, headnik	mAb+s.m.
	408482 408562	NM_000676		adenosine A2b receptor roundabout (axon guidance receptor, Dros	uter, fibro	mAb+s.m.
		AI436323 AW580227	Hs.31141 Hs.47860	neurotrophic tyrosine kinase, receptor,	tung	mAb+s.m.
20	408908	BE296227	Hs.250822	serine/threonine kinase 15	blad, lung, headnk, stom	s.m.
20	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	uter, ovar, lung, colon, stom, headnk, breast, panc	CTL+diag
	409079	W87707	Hs.82065	interleutiin 6 signal transducer (gp130,	breast, pros	mAb+s.m.
	409103	AF251237	Hs.112208	XAGE-1 protein	tung	CTL
	409178	BE393948	Hs.50915	kallikrein 5	ovar, breast, mela	diag
25	409220		Hs.51233	tumor necrosis factor receptor superfami	angio, renal, colon, stom	mAb+s.m. mAb+s.m.+CTL
	409348		Hs.146090	ESTs	renal, glio	mAb+diag
	409389	AB007979	Hs.301281	Homo sapiens mRNA, chromosoma 1 specific	glio lung, headnik, panc, storn, cerv, esoph, blad	diag
	409420		Hs.54451	taminin, gamma 2 (nicein (100kD), kalini	lung, blad, headnk	diag
30	409632		Hs.55279	serine (or cysteine) proteinase inhibito Homo sapiens mRNA; cDNA DKFZp434K0621 (		mAb+s.m.+CTL
30	409637 409663	AA323940 AI743750	Hs.55407 Hs.98306	KIAA1862 protein	renal	CTL
	409745	AA077391	113.50500	gb:7B14E12 Chromosome 7 Fetal Brain cDNA	ovar, renal	mAb+s.m.+CTL
	409757	NM 001898	Hs 123114	cystatin SN	panc, stom, lung, blad,	diag
	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	tung, cerv, blad, test, esoph	CTL+s.m.
35		AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	breast, panc, ovar, colon, headnk, lung, blad, esoph	diag
	410001	AB041036	Hs.57771	kallikrein 11	ovar, pros, uter, cerv, lung	diag
	410055	AJ250839	Hs.58241	gene for serine/threonine protein kinase	renal	s.m. CTL
	410153	BE311926	Hs.15830	hypothetical protein FLJ12691	renal, blad	CTL
40	410274	AA381807	Hs.61762	hypoxia-inducible protein 2	lung, renal	s.m.
40	410309	BE043077	Hs.278153	alpha-2,8-siatyttransferase III	panc	mAb+s.m.
	410407	X66839	Hs.63287	carbonic anhydrase IX	renal, hung, colon, stom, ovar, uter, blad colon, blad, lung, ovar, panc, headnk	mAb+diag+s.m.
	410418	D31382	Hs.63325	transmembrane protease, serine 4	colon, ovar, uter, cerv, headk, panc	diag
	411274	NM_002776 AA345241	Hs.55950	kaltikrein 10 ESTs, Weakly similar to KIAA1330 protein	renal	mAb+s.m.
45	411411 411773	NM_006799		protease, serine, 21 (testisin)	ovar	diag
73	412078	X69699	Hs.73149	paired box gene 8	ovar	CTL
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	lung, blad, headnk, breast, ovar, panc, angio, test, mela	s.m.
	412580	AA113262	Hs.17901	similar to CABLES [Homo sapiens]	mela	mAb+s.m.+CTL
	412609	Z48804	Hs.74124	ocutar albinism 1 (Nettleship-Falls)	mela	s.m.
50	412628	AI972402	Hs.306051	hypothetical protein MGC2648	pros	diag
	412709	AL022327	Hs.74518	KIAA0027 protein	glio	mAb+s.m.
	412719	AW016610	Hs.816	ESTs	lung, headrik, blad, glio, cerv	s.m. CTL+s.m.
	412959	D87458	Hs.75090	KIAA0282 protein	glio	mAb+s.m.
55	412986	X81120	Hs.75110	cannabinoid receptor 1 (brain)	glio	mAb
55	413048	M93221	Hs.75182	mannose receptor, C type 1	fibro, panc glio, ovar, blad, lung	diag
	413063	AL035737 BE563085	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	panc, fung, blad, breast, cerv, ovar, headnik, esoph, meia, stom	CTL+s.m.
	413278 413324		Hs.833 Hs.75294	interferon-stimulated protein, 15 kDa corticotropin releasing hormone	blad	diag
	413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	blad, lung, mela, fibro, uter	s.m.
60	413554		Hs.75426	secretogranin II (chromogranin C)	panc, glio	diag
00	413719		Hs.75498	small inducible cytokine subfamily A (Cy	panc, lung, headrik, cerv, colon, uter, stom, esoph	diag
	414577		Hs.72116	hypothetical protein FLJ20992 similar to	angio	CTL+diag
	414774		Hs.77274	plasminogen activator, urokinase	lung, blad, headnk, panc, stom, ovar, esoph	diag
	414812	X72755	Hs.77367	monokine induced by gamma interferon	breast, blad, lung, fibro, panc, colon, headnk,	dian
65					cerv, storn, renal, ovar, test, mela, esoph	diag mAb+s.m.+CTL
	414825		Hs.77432	epidermal growth factor receptor (avian	glio, tung, renal, esoph, panc, headnk, arth	s.m.
	414883		Hs.348669	CDC28 protein kinase 1	tung, ovar, storn, colon, cerv, headnk, test	s.m.
	414907		Hs.77597	polo (Drosophia)-like kinase	blad, tung, ovar, test mela	mAb+s.m.
70	414945		Hs.77667	lymphocyte antigen 6 complex, locus E tissue factor pathway inhibitor 2	angio, panc, stom, lung, uter	CTL+diag
70	415138		Hs.295944 Hs.182362	ESTs	blad, ovar, renal	mAb+s.m.+CTL
	415511 415539		Hs.72472	BMP-R1B	breast, uter, pros	mAb÷s.m.
	415668			Homo sapiens lysyl oxidase-like 4 (LOXL4	mela	diag
	415669		5 Hs.78589	serine (or cysteine) proteinase inhibito	tung	mAb+diag+s.m.
75	415817		Hs.78867	protein tyrosine phosphatase, receptor-t	tung, gilo, headnk, cerv, mela, esoph, fibro	mAb+s.m.
	415910		Hs.78913	chemokine (C-X3-C) receptor 1	gtio	mAb+s.m.
	415929		Hs.304950	Homo sapiens mucolipin-3 (MCOLN3)	mela	mAb
	415989	AI267700	Hs.351201	ESTs	pros, ovar, blad, lung, headnk, panc, colon, stom	mAb+s.m.+CTL
00	416091			defensin, beta 3	headnik, esoph, mela	CTL+diag CTL+s.m.
80	416209			MAD2 (mitotic arrest deficient, yeast, h	lung, headrik, colon, uter, stom	mAb+s.m.
	416250			Kremen 2	esoph, lung, cerv, over	CTL
	416350			phospholipase A2, group IID kallikrein 6 (neurosin, zymė)	test, mela, fibro ovar, uter	diag
	416530	U62801	Hs.79361	SCHOOL A SUCCESSION STATES	(10)	-

						ıAb+s.m.
	416636	N32536	Hs.42645	2000 Catter terral to humanage and an	reast, panc, uter, meta	iag
	416658	U03272	Hs.79432	Military E (condomina announce -	ing, ovar, usar, usar, angua, usar inos FWS alio	iag
	416836	D54745 AA188775	Hs.80247 Hs.292453		dia '	nAb+s.m.
5		NM_006183		noumtoncin (	ung, meatrik, cerv	liag Siag
,		U65590	Hs.81134	and desired the second	180, jung, neauna, corr, coopii	CTL
		AA431323	Hs.42146	to the Common and D	nio meia	nAb+s.m.
	417355	D13168 BE260964	Hs.82002 Hs.82045	enconican receptor type o	nuar lung Mari inter cery, panc, stom, meta, test, colon	mAb+diag
10	417389 417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	panc, breast, blad, lung, headrik, cerv, uter, ovar, storn, renar	mAb mAb+diag
10	417542	J04129	Hs.82269	progestagen-associated endometrial prote		mAb
	417771	AA804698	Hs.82547	ICUION BOID ICOOPER TOOP TOOP	hino nanc breast, ovar, headnk, storn	CTL
	417866 417931	AW067903 W95642	Hs.82772 Hs.82961	trafail factor 3 (intestinal)	ovar, panc, stom, colon, uter, pros	diag s.m.
15	417933		Hs.82962	thymidylate synthetase		mAb+diag+s.m.
1.5	418007	M13509	Hs.83169	THE REAL PROPERTY OF THE PERTY	lung, biao, libro, libabilik, paise, statit, obtait, event event event	diag
	418030	BE207573	Hs.83321	neuromedin B S100 calcium-binding protein, beta (neur	glio, panc mela	diag
	418064 418281	BE387287 U09550	Hs.83384 Hs.1154	oviductal glycoprotein 1, 120kD (mucin 9	uter, ovar	CTL+diag s.m.
20	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	tung, blad, ovar, headnk, panc, cerv, mela	mAb+diag
20	418506	AA084248		Unknown protein for MGC:29643 (formerly	angio, ovar, glio, uter, lung, blad, panc, mela lung, blad, renal, panc, stom, colon, ovar	mAb+s.m.
	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic Fas (TNFRSF6)-associated via death domai	esoph, headnik	s.m.
	418558	AW082266	Hs.86131 7 Hs.167379	cancer/lestis antigen (NY-ESO-1)	lung, blad, stom, ovar, panc, esoph, cerv, mela	CTL
25	418678 418830	BE513731		hypothetical protein MGC4816	lung	CTL s.m.
23	418867	D31771	Hs.89404	msh (Drosophila) homeo box homolog 2	blad	mAb+s.m.
	418870	AF147204		chemokine (C-X-C motif), receptor 4 (fus	leuk, ovar, breast, blad, renal renal, uter, lung	CTL
	419080		Hs.18878	hypothetical protein FLJ21620 parathyroid hormone-like hormone	lung, esoph, headnk, blad	diag
20	419121	AA374372	Hs.89626 16 Hs.89655	omtein tyrosine phosphatase, receptor t	tung	mAb+s.m.
30	419171 419172		5 Hs.22026	ESTS: Similar to TRANSMEMBRANE 4 SUPER	Fangio, renal	mAb+s.m. CTL+s.m.
	419183		Hs.89663	cytochrome P450, subfamily XXIV (vitamin	blad, tung, headnk, panc panc, tung, stom, cerv, pros, headnk, esoph	diag
	419216	AU076718		small inducible cytokine subfamily B (Cy	panc, fibro, headnik, lung	mAb+diag
25	419235		1 Hs.288433	neurotrimin PTK7 protein tyrosine kinase 7	ovar, pros, lung, breast, uter, lest, panc, storn	mAb+s.m.
35	419452 419508		Hs.90572 8 Hs.90786	ATP-binding cassette, sub-family C (CFTR	glio, omuc, stom, lung, panc, colon, renal, uter	mAb+s.m. mAb+diag
	419556		Hs.91093	chitinase 1 (chitotriosidase)	lung, fibro, test	CTL+s.m.
	419704			ESTs	gio	mAb+diag
40	41972			longevity assurance (LAG1, S. cerevisiae	glio blad, lung, colon, ovar, test, esoph, mela	CTL+s.m.
40	41974		19 Hs.93002 Hs.99785	ubiquitin carrier protein E2-C Homo sapiens cDNA: FLJ21245 fis, clone C	blad, stom	mAb
	42015	9 Al572490 2 BE37843		cyclin-dependent kinase 4	lung, mela	s.m. CTL
	42020			silver (mouse homolog) like	mela	mAb
		0 Y13645	Hs.97234	uroplakin 2	blad ovar, uter, cerv	diag
45	42044		107 Hs.97644	mammaglobin 2 regulator of G-protein signalling 20	headnk, glio, cerv, mela	CTL+s.m.
	42060	2 AF06087 0 Al68318:		distal-less homeo box 5	uter, endo, lung	CTL mAb+s.m.
	42073		Hs.99899	CD70; tumor necrosis factor (ligand) s	renal	mAb+s.m.+CTL
		9 AI67005			renal pano, blad	s.m.
50	42087				blad, lung	CTL+s.m.
		6 AU07673 0 AJ25071		cathepsin E	blad, panc, storn, lung, fibro, ovar, esoph	sm+diag
		0 F07783	Hs.1369	decay accelerating factor for complement	ongio page stom	diag ph diag
		9 Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	breast, panc, headnk, lung, storn, blad, cerv, colon, fibro, test, mela, eso	mAb+s.m.
55	4214				renal lung	mAb+s.m.
	4214				blad, esoph, lung, mela	mAb+s.m.+CTL
	4215 4215		1833 Hs.105115 82 Hs.105445		breast	mAb+s.m. diag
	4215	52 AF0266			breast, ovar, panc, cerv, uter, pros, tung, storn, headnk	CTL+diag
60	4215	74 AJ0001	52 Hs.10592		headnk, lung	diag
		82 AI9102		trefoil factor 1 (breast cancer, estroge endothelin 3	breast, panc, rung, ornuc mela	mAb+diag
		66 AL0352 53 BE3148			lung	mAb+s.m. mAb+s.m.
		17 AF1460		<ul> <li>ATP-binding cassette, sub-family C (CFTR)</li> </ul>	lung, cerv, headnk, blad	mAb+s.m.
65	4220	33 AW245	805 Hs.11090	3 claudin 5 (transmembrane protein deleted	gio	diag
	4220		2445 Hs.28812	6 spondin 2, extracellular matrix protein .	panc, pros panc, lung, colon, fibro	diag
		09 \$73265		gastrin-releasing peptide protease inhibitor 3, skin-derived (SKAL	headnik, blad, lung, cerv, stom, esoph	diag
		158 L10343 163 AF027			colon, breast, fibro	mAb+s.m. s.m.
70	422	192 AA305		19 fts485	mela	mAb+diag
. •	422	260 AA315	993 Hs.10548		colon, omuc, storn, panc blad, lung, headnk, renal	diag
		282 AF019			tung, blad, test, cerv, headnk, esoph	S.M.
		283 AW41 ⁻ 309 U7974			mela	mAb+s.m.+CTL mAb+diag
75	422	309 07974 330 D3078		63 epiregulin	pane, colon, blad	CTL+s.m.
, .	422	397 AJ223	366 Hs.1160	51 MYEOV Myeloma overexpressed gene (in a	s panc, stom, colon, esoph, renal, blad blad, panc, pros, angio, colon, stom, tung, mela	diag
	422	424 Al186			colon, renal	mAb+diag
	422	627 BE338	5857 Hs.1187 9701 Hs.1578		tung, blad	s.m.
80	) 422	765 AW40 809 AK00	1379 Hs.1210	28 hypothetical protein FLJ 10549	blad, cer, lung, uter, angio, storn, test	ş.m. diag
3(		867 L3213	7 Hs.1584	cartilage ofigomeric matrix protein (pse	breast, ovar, pros, panc, lung, colon, uter ovar, blad, panc, lung, headnik, colon, stom	CTL+s.m.
	. 422	956 BE54			renal, ovar, blad	mAb+s.m.
	423	3161 AL049	3227 Hs.1247	10 COMISSINGLE CAGNESIS (by 3.540)	440	

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	400404	LUL 004430	LL 4004	ankin Al	noe none rend	mAb+s.m.
		NM_004428 AL039402			pros, panc, renal breast, renal, ovar, pros, colon	CTL
					dio	mAb
					renal, colon	mAb
5			Hs.129836		pros	s.m.
•					lung, blad, headnk, panc	diag
			Hs.1695		blad, lung, headnk, ovar, panc, colon, storn, uter, cerv, esoph, test	mAb+diag+s.m.
			Hs.135639		colon, stom, ovar	CTL mAb+diag
10			Hs.136348		breast, colon, blad, lung, fibro, panc, headrik, ovar, mela	mAb+s.m.
10			Hs.137555		blad, headrik, stom, cerv, esoph headrik, lung, cerv	diag
			Hs.138202 Hs.143811		colon, stom	mAb+s.m.+CTL
			Hs.1765		mela, fibro	s.m.
			Hs.146329		tung, colon, test	s.m.
15		NM_005209			panc	s.m.
			Hs.149585		fung	8.m.
		NM_002205			panc, pros, angio, blad, lung	m.a+dAm
	424620		Hs.151254		OVAF	diag diag
20	424687 424735	J05070 U31875	Hs.151738 Hs.272499	matrix metalloproteinase 9 (gelatinase B short-chain alcohol dehydrogenase family	headnik, panc, lung, blad, uter, cerv, colon, stom, test, meta blad, breast	CTL+s.m.
20	424735		Hs.153357	procollagen-lysine, 2-oxoglutarate 5-dio	mela	CTL+s.m.
	424905	NM_002497		NIMA (never in mitosis gene a)-related k	ovar, blad, fung, headnk, panc, stom	8.m.
	425009	X58288	Hs.154151	protein tyrosine phosphatase, receptor t	renal, fibro	mAb+s.m.
	425071	NM_013989		deiodinase, iodothyronine, type fl	pros, colon, stom, uter, cerv, headnik, esoph, panc	diag
25	425088	AA663372	Hs.169395	hypothetical protein FLJ 12015	glio, mela	mAb+s.m.+CTL
	425115	R44664	Hs.123956	downstream of: G protein-coupled recept	glio	mAb+s.m. mAb+diag+s.m.
	425247	NM_005940		matrix metalloproteinase 11 (stromelysin	breast, ovar, tung, colon, panc, headnk, stom, uter, cerv, blad, esoph	S.M.
	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	tung, headnk	mAb+s.m.
30	425535	AB007937 NM 001944	Hs.158287	syndecan 3 desmoglein 3 (pemphigus vulgaris antigen	mela, glio tuno, headnik, cerv, escoth, blad	mAb
30	425650 425721	AC002115	Hs.159309	uroplakin 1A	blad	mAb
	425723	NM_014420		dickkopf (Xenopus laevis) homolog 4	endo, uter, colon	CTL+diag
	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg	tung	s.m.
	425776	U25128	Hs.159499	parathyroid hormone receptor 2	ovar, uter, lung	mAb+diag
35	425842	A1587490	Hs.159623	NK-2 (Drosophila) homolog B	panc, glio	s.m. mAb+s.m.
	425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member	blad, lung, headnk	mAb
	425883	AL137708	Hs.161031	Homo sapiens mRNA; cDNA DKFZp434K0322 (		mAb+s.m.
	425921	NM_007231 AU076629	Hs.162211 Hs.165950	solute carrier family 6 (neurotransmitte fibroblast growth factor receptor 4	stom, panc renal	mAb+s.m.
40	425998 426028	NM_001110		a disintegrin and metalloproteinase doma	blad	mAb+diag
70	426215	AW963419	Hs.155223	stanniocalcin 2	breast, lung, renal, colon, ovar, uter	mAb+diag
	426227		Hs.154299	Human proteinase activated receptor-2 mR	panc, lung, colon, esoph, stom	mAb+s.m.
	426322	J05068	Hs.2012	transcobatamin I (vitamin 812 binding pr	panc, blad, stom	diag
	426344	H41821	Hs.322469	transcriptional activator of the c-fos p	glio	CTL+s.m.
45	426427	M86699	Hs.169840	TTK protein kinase	ovar, tung, headnk, cerv, colon, uter, storn, test	CTL+s.m. s.m.
	426451		Hs.169946	GATA-binding protein 3 (T-cell receptor	blad, breast	mAb+diag
	426514		Hs.170195	bone morphogenetic protein 7 (osteogenic	ovar, coton, blad, lung, cerv mela	diag
	426600 426761	AI015709	Hs.171014 Hs.172089	VGF nerve growth factor inducible PORIMIN Pro-oncosis receptor inducing me	tung, esoph, pros, uter, panc, colon, ovar, headnk	mAb+s.m.
50	426812		Hs.172613	solute carrier family 12 (potassium/chlo	renal	mAb+s.m.
30		AA393167	Hs.41294	ESTs	renal, colon, ovar, uter, stom	CTL
	427239		Hs.356512	ubiquitin carrier protein	lung, blad, test, mela	CTL+s.m.
	427335	AA448542	Hs.251677	Gantigen 7B	tung, headnk, blad, mela, esoph	CTL CTL+s.m.
	427343		Hs.176977	protein kinase C binding protein 2	glio	CTL CTL
55	427722		Hs.180479	hypothetical protein FLJ20116	colon, storn, panc	s.m.
	427747		Hs.180655	serine/threonine kinase 12 FGENESH predicted 11 TM protein	blad, tung, ovar, storn, test, esoph mela	mAb
	427923 427969			epidermal growth factor (beta-urogastron	panc	mAb+diag
	428093		Hs.104830	ESTs	ovar, panc	CTL
60	428141		Hs.182611	solute carrier family 11 (proton-coupled	glio	mAb+s.m.
-	428179	41407770	Hs.279696	serum/glucocorticoid regulated kinase-li	breast	s.m.
	428187		Hs.285529	G protein-coupled receptor 49	ovar, uter, colon, stom	mAb+s.m.
	428242		Hs.2250	leukemia inhibitory factor (cholinergic	ovar, panc, , lung	diag mAb+s.m.
45	428296			solute carrier family 22 (organic cation	renal uter, ovar, fibro, pros, panc, lung, blad, headnk, esoph, mela, storn	mAb+diag+s.m.
65	428330		Hs.2256	matrix metatloproteinase 7 (matrilysin, matrix metatloproteinase 3 (stromelysin	headrik, storn, esoph, colon	diag
	428368 428392		Hs.83326 Hs.2265	secretory granule, neuroendocrine protei	panc	diag
	428450		1 Hs.184339	KIAA0175 gene product	ovar, cerv, panc, lung, blad, mela	s.m.
	428479		Hs.334562	cell division cycle 2, G1 to S and G2 to	lung, blad, colon, uter, ovar	s.m.
70	428484		Hs.184601	solute carrier family 7 (cationic amino	lung, blad, headnk, cerv, esoph, glio, uter, stom, colon, mela	mAb+s.m.
		AW583497		pancreatic polypeptide	panc	diag
	428505		Hs.2281	chromogranin B (secretogranin 1)	pane, tung	diag mAb
	428513		Hs.184697	plexin C1	meta, panc, storn, neactix	mAb+s.m.
75	428579		6 Hs.184942	G protein-coupled receptor 64 similar to SALL1 (sal (Drosophila)-like	ovar, EWS, uter blad, ovar, pros, lung, stom, test	CTL+s.m.
13	428664			similar to SALL1 (sai (Urosophila)-like KIAA1866 protein	breast, coton, tung, panc, stom, headnik, ovar, EWS	mAb
	428698 428748			Ksp37 protein	lung	diag
	428756			CA125 entigen; mucin 16	over, cerv, lung, panc, stom, renal	diag
	428778			fibroblast growth factor receptor-like 1	ovar	mAb+s.m.
80	428784	Y12851	Hs.193470	purinergic receptor P2X, ligand-gated to	glio, meta	mAb+s.m.
	428841		Hs.104935	ESTs	renal	mAb+s.m.+CTL mAb+diag
	428953			tumor necrosis factor receptor superfami	cerv, panc, colon, stom, headrik, renal	diag
	42896	AF120274	Hs.194689	artemin	lung, cerv	
					(20	

	428970	E276891	Hs.194691	retinoic acid induced 3 (RAIG1); metabo	tom. Danc. Colon. Ovar	mAb+s.m. mAb+s.m.
			Hs.197962	Homolog of mouse ADP-ribosylation factor	pio	mAb+s.m.
		\F052693		and large to be seem a feeting a	and insolution can each and inco	mAb+s.m.
	429263			Lett administ connected and result to to man	ung angio, blad, glio	mAb+s.m.
5	429276				hreast, pros	mAb+s.m.
				FGENESH predicted novel secreted protein	paric, ricauric, rong, orai	diag
			Hs.211092	LUNX protein; PLUNC (palate lung and nas	turig, italio	mAb+diag s.m.
	429903			Comi achourem imparation of columnia.	lung, mela	mAb+s.m.
10		NM_000867		2-11/010X/01/PODITION (GCT COMMEN) 100-01-10-	leio glio	s.m.
		R60704	Hs.234434	hairy/enhancer-of-split related with YRP interleukin 7 receptor	mela, lung, panc, stom, esoph, headnk	mAb+s.m.+CTL
		AA361258 NM_001922	Hs.237868	attended to coopie	mela	CTL
		BE062109	Hs.241551	chloride channel, calcium activated, fam	lung, blad, headnk, cerv, esoph	mAb+s.m. s.m.
15		AJ005371	Hs.248017	glyceraldehyde-3-phosphate dehydrogenase	mela	mAb+s.m.
•-		X54232	Hs.2699	glypican 1	glio, lung, cerv, blad, esoph glio	mAb
	431053	\$40369	Hs.249141	Glutamate receptor subunit HE4; epididymis-specific, whey-acidic pr	ovar, uter	diag
		NM_006103 AW583672		granin-like neuroendocrine peptide precu	panc, lung, glio, test	diag
20	431462 431515	NM_012152		EDG-7 (endothelial differentiation, lys	ovar, pros, lung, blad	mAb+s.m. CTL+s.m.
20	431620	AA126109	Hs.264981	Z-5-oligoadenylate synthetase 2 (69-71	esoph, cerv	mAb+diag
	431629	AU077025	Hs.265827	interferon, atpha-inducible protein (clo	panc, uter, cerv, storn, esoph, mela ovar, panc, blad, headnk, mela, renal	mAb+s.m.
	431630	NM_002204		integrin, alpha 3 (ansigen CD49C, alpha	test, renal, blad	CTL
25	431840	AA534908	Hs.2860	POU domain, class 5, transcription facto uroplakin 1B	tung, blad, headnik, uter, cerv, storn, ovar	mAb+diag
25	431846 431870	BE019924 AW449902	Hs.271580 Hs.105500	ESTs	renal	mAb+s.m.+CTL
	431939	AW008061	Hs.231994	ESTs	renal, colon	mAb+s.m.+CTL mAb+diag
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	lung, blad, cerv, headnik, ovar, colon, pros. panc, breast, esoph, test, mela	CTL
	432196	AW300888	Hs.273230	hypothetical protein FLJ10830	renal breast, colon, ovar, stom, panc, uter, cerv, lung	mAb+diag+s.m.
30	432201	AI538613	Hs.298241	Transmembrane protease, serine 3	renal	CTL
	432579	AF043244	Hs.278439 Hs.278461	nucleolar protein 3 (apoptosis repressor matrilin 3	panc, breast	diag
	432596 432606	AJ224741 NM_002104		granzyme K (sarine protease, granzyme 3;	renal, breast, lung, storn, hepC, fibro	CTL mAbus m
	432800	BE391046	Hs.278962	AIM-1 protein	mela, pros	mAb+s.m. CTL+s.m.
35	432829		Hs.57772	ESTs	blad	mAb+s.m.+CTL
	432867	AW016936		ESTs	stom, colon panc, stom, mela	diag
	432874		Hs.279651	melanoma inhibitory activity tumor necrosis factor receptor superfami	pros, renal	m.a+dAm
	432990	AL036071	Hs.279899 Hs.279905	clone HQ0310 PRO0310p1	colon, breast, lung, blad, cerv, uter, test, mela	s.m.
40	433001 433447	AF217513 U29195	Hs.3281	neuronal pentraxin II	meta, esoph, colon, renal	diag s.m.
70	433848	AF095719	Hs.93764	carboxypeptidase A4	headnk, esoph, lung	CTL
	433867		Hs.3618	hippocalcin-like 1	renal	CTL+s.m.
	434206			ESTs, Weakly similar to S69890 mitogen i	storn, colon mela	s.m.
15	434276		Hs.93605	leucine zipper, putative tumor suppresso NM_020142:Homo sapiens NADH:ubiquinone		CTL
45	435013 435472		Hs.110024 Hs.283022	triggering receptor expressed on myeloid	glio	mAb
	435505			interleukin-1 homolog 1	lung, headnk	diag mAb
	435869			junctional adhesion molecule 2	angio, glio	mAb+s.m.
	436456			melanin-concentrating hormone receptor (	mela, glio	mAb+s.m.
50	436480			putative acid-sensing ion channel	glio lung, blad, colon, ovar, uter, headrik, test	s.m.
	436481			HSPC150 protein similar to ubiquitin-con ESTs	renal, panc, headnk, tung	mAb+s.m.
	436576 436608			down syndrome critical region protein DS	blad, lung	CTL+s.m. mAb+s.m.
	43689			carbonic anhydrase XII	breast, renat, ovar, glio	CTL
55	43696		4 Hs.156704	ESTs	tung, panc, renat, uter, colon	diag
	43698			spondin 1, (f-spondin) extracellular mat guanine monphosphate synthetase	ovar, fibro tung, blad, cerv, esoph, headnk	s.m.
	43701			differentially expressed in Fanconi's an	headrik, cerv, lung, blad, breast, pros, ovar, stom, esoph	CTL
	43704 43710			Homo sapiens cDNA: FLJ22314 fis, clone H	panc, renal	mAb+s.m.+CTL mAb+s.m.+CTL
60	43721			ESTs	renal, uter, ovar	CTL
•	43778		Hs.127812	ESTs, Wealtly similar to T17330 hypotheti	lung	mAb+s.m.
	43785			putative GPCR gb:wq05c02.x1 NCI_CGAP_Kid12 Homo sap	blad, lung	mAb+s.m.+CTL
	43793			gb:wq05c02.x1 NCI_CGAP_Rid12 Homo sap chondroitin sulfate proteoglycan BEHAB/b	glio, mela	diag
65	43838		Hs.6194 1 Hs.21858	trinucleotide repeat containing 3	mela	CTL+diag
05	43854 43885			Homo sapiens mRNA for KIAA1647 protein,	renal	mAb+s.m.+CTL mAb+s.m.+CTL
	43892			ESTs	renal	mAb+s.m.+CTL
	43896			gb:EST391184 MAGE resequences, MAGP	Ho renal	mAb
=0	43901			membrane-spanning 4-domains, subfamily A	uter, stom, pros. fibro lung, headnk, cerv, esoph, blad, colon	mAb
70	4392			UL 16 binding protein 2 ESTs, Moderately similar to GFR3_HUMAN		mAb+s.m.
	43947				breast, AWPC, pros, blad	diag
	43956 4396			G protein-coupled receptor 87	tung, blad, headnk, cerv, esoph	mAb+s.m.
	4397			sema domain, immunoglobulin domain (lg),	blad, lung, cerv, renal	mAb+s.m. mAb+s.m.+CTL
75	4397	59 AL3590	55 Hs.67709	Homo sapiens mRNA full length insert cDN	colon, stom, panc, lung	mAb
	4399	79 AW6002	91 Hs.6823	hypothetical protein FLJ10430	renal, cerv, pros, headnk, colon, test btad, ovar, tung, headnk, test	s.m.
		06 AK0005		NALP2 protein; PYRIN-Containing APAF1-li Homo sapiens Fc receptor homolog express		diag
	4400			tumor necrosis factor receptor superfami	glio	mAb
80	4402 4403			5 hopatitis A virus cellular receptor 1	renal, colon, blad	mAb+s.m.
	4403			7 ESTs, Moderately similar to ALUE_HUMAN	! renal	mAb+s.m.+CTL mAb+diag
	4405	16 S42303	Hs.161	cadherin 2, type 1, N-cadherin (neuronal	glio, ovar, uter, renal, hepC	s.m.
	4406	72 AF0838	111 Hs.7345	MAD1 (mitotic arrest deficient, yeast, h	mela	=
					(21	

			Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	tung, blad, headrik, test, mela, esoph	8.M.
			Hs.222119	ESTs, Wealdy similar to S30433 keratin 1	renal	mAb+s.m.+CTL mAb
		AW975183 AW664964	Hs.372210 Hs.128899	ESTs, Weakly similar to S72482 hypotheti ESTs; hypothetical protein for IMAGE:447	fibro, angio breast, tung, blad, panc, headnk, stom, ovar, pros	mAb+s.m.
5		AW874138	Hs.129017	ESTs; type la transmembrane protein	ovar, uter	mAb
-	442438	AA995998		gb:os26b03.s1 NCI_CGAP_Kid5 Homo sapiens	uter, ovar, renal	mAb+s.m.+CTL
	443105		Hs.9004	chondroitin sullate proteoglycan 4 (mela	mela blad, ovar, lung, headnik, stom	mAb+diag mAb+s.m.+CTL
		A1128388 BE614387	Hs.143655 Hs.333893	ESTs c-Myc target JPO1	colon, lung, blad, panc	CTL
10		AF098158	Hs.9329	chromosome 20 open reading frame 1	colon, lung, blad, storn, test, mela	CTL
	443595	AF169312	Hs.9613	PPAR(gamma) angiopoietin related protein	renal	diag
		Al085198	Hs.164226	Thrombospondin 1	angio, panc, uter	diag mAb+s.m.+CTL
		AW449952 NM_013409		basic-halix-loop-helix-PAS protein follistatin	glio, uter, over lung, cerv, headnk, blad, esoph	diag
15		AW163123	Hs.10071	seven transmembrane protein TM7SF3	renal	mAb+s.m.
	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	panc, colon, tung, ovar, renal, esoph, mela, blad, storn, cerv	mAb
	444371	BE540274	Hs.239	forkhead box M1	lung, headnik, blad, gfio, test, mela	8.m.
	444381	BE387335	Hs.283713	hypothetical protein BC014245	breast, colon, blad, lung, panc, headnk, ovar, stom, uter, renal, angio, tast, mela, esoph	diag
20	444488	AW192879	Hs.355660	ancient conserved domain protein 4	renal	mAb+s.m.
20	444527	NM_005408		small inducible cytokine subfamily A (Cy	fibro, esoph	diag
	444781	NM_014400		GPI-enchored metastasis-associated prote	lung, blad, headnk, cerv	mAb+diag CTL+s.m.
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	ovar, tung, blad, headrik, panc, cerv, storn, uter, colon, esoph mela	mAb+s.m.
25	444809 445070	BE207568 NM_000677	Hs.208219 Hs 258	oculospanin adenosine A3 receptor	gio, renal	mAb+s.m.
25	445417	AK001058	Hs.12680	a disintegrin-like and metalloprotease w	panc, headnk, stom, lung, asoph	diag
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	ovar, blad, uter, breast, lung, headink, renal, fibro, panc, cerv	mAb+diag
			Hs.199460	DPCR1 protein	stom, panc, esoph, omuc, esoph	mAb CTL
30		D29954	Hs.13421 Hs.37054	KIAA0056 protein ephrin-A3	pros . colon, breast	mAb+diag
20		BE048061 AA026880	Hs.25252	prolactin receptor	breast, cerv, uter	mAb+s.m.
		AI281848	Hs.194691	retinoic acid induced 3	stom, panc, colon, ovar	mAb+s.m.
		AL040763	Hs.310735	FGENESH prediction similar to multidrug	mela	mAb+s.m.
26		AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	ovar, fibro, panc, headnk, lung, colon, blad, mela, esoph, uter	diag mAb÷s.m.
35	446650		Hs.15813	solute carrier family 22 (organic cation	renal breast, panc, headnk, lung, fibro, mela	diag
	446921 447004		Hs.16530 Hs.157539	small inducible cytokine subfamily A (Cy FGENESH predicted secreted protein	QSQ party recount range and reco	mAb+diag
		AI357412	Hs.157601	Predicted gene: Eos cloned; secreted w/V	colon, pros, fibro, breast, ovar, king, panc	CTL+diag
4.0	447072	D61594	Hs.17279	tyrosylprotein sutfotransferase 1	glio, panc	CTL+s.m.
40	447131			retinoic acid receptor responder (tazaro	renal, breast, stom, tung, mela, ovar	mAb+s.m. CTL+diag
	447208		Hs.237971	hypothetical protein MGC5627 cerebroside (3'-phosphoadenylylsulfate:g	esoph, storn, colon renal	CTL
		NM_004861 A1199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	colon, blad, pros, lung, storn, AWPC, ovar	CTL
	447400		Hs.18457	hypothetical protein FLJ20315	colon, pros, storn, uter	CTL
45		BE270640	Hs.19192	cyclin-dependent kinase 2	meta	s.m. mAb+s.m.+CTL
	447835			ESTs, Wealdy similar to 138022 hypotheti	renal, ovar, uter meta	mAb+s.m.
		AL109716 AW591433	Hs.20034 Hs.298241	Homo sapiens mRNA full length insert cDN Transmembrane protease, serine 3	breast, panc, colon, lung, ovar, storn	mAb+s.m.+CTL
	448243			integrin, beta 8	ovar, uter, tung, stom, headrik, glio, panc	mAb+s.m.
50	448321	NM_005883	3 Hs.20912	adenomatous polyposis coli like	glio .	mAb+s.m.+CTL
	448499		Hs.77550	p53-regulated DDA3	glio	CTL+s.m. mAb+s.m.
	448595		Hs.21572 7 Hs.21602	KIAA0644 gene product nel (chicken)-like 1	breast, glio mela	diag
	448610 448733		9 Hs.187958	solute carrier family 6 (neurotransmitte	lung, renal	mAb+s.m.
55	448844		Hs.177164	FGENESH predicted novel cell surface pr	pane, lung, stom, omuc	mAb+s.m.
	449048		Hs.22920	similar to S68401 (cattle) glucose induc	panc, ovar, uter, glio, headnk, lung	mAb mAb+s.m.
	449444			solute carrier family 16 (monocarboxylic	renal, panc tung, panc, renal, stom, hepC, fibro, mela	mAb+s.m.
	449523 449720		9 Hs.54443 Hs.288708	chemokine (C-C motif) receptor 5 hypothetical protein FLJ21562	colon	CTL
60	449722			cyclin B1	headnk, blad, lung, panc, angio, test, meta, esoph	s.m.
- •	450001		4 Hs.406	solute carrier family 6 (neurotransmitte	renal	mAb+s.m.
•	450375		Hs.352537	a disintegrin and metalloproteinase doma	breast, ovar, headrik, panc, lung, esoph, colon	mAD+0iag+s.m. CTL
	450531			(BC017500) Similar to hypothetical prote	colon lung, headnk, panc, breast, storn, ovar, esoph, colon	mAb+diag
65	450701 450726		Hs.288467 Hs.355462	hypothetical protein XP_098151 (leucine- HUMPSPBA Human pulmonary surfactant-ass		s.m.
05	450931		Hs.25648	tumor necrosis factor receptor superfami	tung, renal	mAb+s.m.
	450983		Hs.25740	ERO1 (S. cerevisiae)-like	trlad, lung, over, panc	diag
	451099		Hs.25954	interteukin 13 receptor, alpha 2	glio, fibro, mela	mAb+s.m. CTL
70	451310			Human DNA sequence from clone RP3-447F: transmembrane 4 superfamily member 7	3 colon, panc renal	mAb
70	451527 451537		Hs.26518 Hs.26550	retinoid X receptor, gamma	meta	CTL+s.m.
	451668		Hs.326444	cartilage acidic protein 1	blad, ovar, lung	mAb+diag
	451939		Hs.27311	single-minded (Drosophila) homolog 2	pros	CTL CTL T
75	451979		Hs.27372	endothelial tyrosine kinase (Etk) (BMX),	angio	CTL+s.m. CTL
75	451988			papillomavirus regulatory factor PRF-1 a disintegrin-like and metalloprotease (	renal ovar	mAb+s.m.+diag
	452097 452190		Hs.27916 Hs.91668	Homo sapiens clone PP1498 unknown mRN/		mAb
	452194		Hs.373599	olfactory receptor, family 2, subfamily	stom, panc, renal, colon, mela, fibro	mAb+s.m.
00	452203	X57522	Hs.352018	transporter 1, ATP-binding cassette, sub	cerv, esoph, blad, storn, mela, renal	mAb+s.m.
80	452281		Hs.28792	Homo sepiens cDNA FLJ11041 fis, clone PL G protein-coupled receptor 34	breast, headnik, panc, slom, lung, esoph, fibro glio, fibro, panc	diag mAb+s.m.
	452355 452401		Hs.29202 15 Hs.29352	tumor necrosis factor, alpha-induced pro	btad, breast, panc, headnk, storn, lung, arth, renal, esoph	diag
	45243		Hs.29499	toll-like receptor 3	renal, hepC	mAĎ
					455	

	452747 8	E153855	Hs.61460	lg superfamily re	ceptor LNIR	breast, blad, lung, headni	t, ovar, stom, uter, panc	mAb mAb+s.m.+CTL
	452795 A		Hs.18878	hypothetical proti	ein FLJ21620	renat, headnk, colon, lung	), panc	CTL
	452838 L	J65011	Hs.30743		ressed antigen in mela	lung, ovar, breast, mela, t	th, lung, blad, esoph, stom	mAb+diag
_	452862		Hs.8687	ADAMIS2 (a di	sintegrin-like and metallo ein DKFZp434K1210	renal	ni, long, alon, over it	CTL
5		BE241876 AA442103	Hs.32352 Hs.33084		nily 2 (facilitated glu	renal, pros		mAb+s.m.
	453642		Hs.34074	dipeptidylpeptida		glio		mAb+s.m.
		AL138387	Hs.256126	baculoviral IAP r	epeat-containing 7 (liv	renal, mela		s.m. mAb+s.m.
		AL080235	Hs.35861		nescence 1 (RIS1)	glio, lung, uter, headnk, o lung, uter, blad, test	zerv, panc, pros	CTL+s.m.
10		AA847843	Hs.62711	High mobility gro	oup (nonhistone chromoso ium channel, subfamily K, m	rung, uter, utau, est Ovar		mAb+s.m.
		A <b>1690321</b> NM_ <b>0</b> 02448	Hs.203845	meh (Dmennhila	i) homeo box homolog 1 (fo	uter, ovar		СП
		NM_002440 BE259150	Hs.127792	delta (Drosophil		glio, lung		mAb+s.m.
	457133		Hs.351221		n rat sarcoma 2 viral on	panc		s.m. diag
15	457489		Hs.127179	cryptic gene		panc, pros, lung		mAb+s.m.
	457561		Hs.286055	chimerin (chima	enn) 2 similar to RIKEN cDNA 28100	glio mela, fibro		mAb
	458079 458435		Hs.54277 Hs.144121	FSTs Weakly s	imilar to T46916 hypotheti	glio		mAb+s.m.+CTL
		AW088642		SRY (sex deten	mining region Y)-box 17 (S	ovar, uter, test		CTL
20	450027	711000012						
	TABLE 66	<b>B</b> :						
	Pkey:	_		eset identifier num	iber			
	CAT numb		Gene cluster nut Genbank access		•			
25	Accession	ı:	Sembaruk access	Sign tiumbers				
23	Pkey		CAT Nur	nber Accession			* * * * * * * * * * * * * * * * * * *	A286833 AA150722 RI007625
	409745	MH1944_	5 BI03099	7 AA921874 AW18	8822 BI027862 AI347618 AI36	1453 Al088754 AW207491	AA077391 BG012775 BG997382 A 106266 B1006991 B1006990 B100776	3 BI007762 BG997377
			BI02786	4 81009100 BI0062	175 B1006270 B1031000 B10298	804 BIOOOZII BIOOIOZI DIO		
20		4040503			818 BG015789 BI033807 AA3			
30	438966 442438	1242593 _. 24590_1				79025 AA828595 AA828577	7 BE935573 AA829588 AI743616 B	E315309 BE047365 AI761053
	442430	24330_1	AW1689	60 AA833900 BG6	79419 BE171071 BF034368 B	F754297 R61781 F08149 F	F07647 T77332 AA897461 AI82971	4 AI376820 AI809991
			AW6618					
35	TABLE 6				on Englandered			
	Pkey: Ref:		Conjugação soute	corresponding to a	mbers in this column are Genta	ank Identifier (GI) numbers.	"Dunham, et al." refers to the public	ation entitled "The DNA
	ret:		sequence of hu	man chromosome	22" Dunham, et al. (1999) Nat	<u>ure</u> 402:489-495.		
	Strand:		Indicates DNA	strand from which	exons were predicted.			
40	Nt_positi	ion:	Indicates nucle	otide positions of p	redicted exons.			
				hu				
	Pkey	Ref 9188605	Strand Flus	Nt_position	7653-7784,8892-9023,9673-98	07.		
	400843 402075	8117407			035,122804-122921,124019-1			
45	402901	889422		175426-175	667			
	404287	2326514	4 Plus	53134-5328				
	404682			40977-4115				
	404875	980132 373834		43081-4322	12,97722-97831 19			
50	404977 405033	- :		142358-142				
50	405547				1520,124914-125050			
	406400	925629	8 Plus	1553-1712,	1878-2140,4252-4385,5922-60	)77		
55	TABLE	£7.						
55	Pkey:	07.	Unique Fos p	robeset identifier n	umber			
	ExAccn	n:	Exemplar Acc	ession number, G	enbank accession number			
	Unigen		Unigene num					
40	Unigen		Unigene gene	e litte Latification Number	linking the information in Table	e 67 to the sequences in Ta	ble 68	
60	Seq ID	NO:	Sequence roo	HUICAUON NUMBER	BINGING THE RUCKLISCOURS ACTOR			
	Pkey	ExAcc	n	UnigenelD	Unigene Title		Seq ID No	
	418007			Hs.83169	matrix metalloproteinase 1	(interstitial	Seq ID No 1 & 199 Seq ID No 2 & 200	
	418007			Hs.83169	matrix metalloproteinase 1	(interstitial	Seq ID No 3 & 201	
65	428368			Hs.83326	matrix metalloproteinase 3 collagen, type XI, alpha 1	(Strainer) and	Seq ID No 4 & 202	
	417866 44438			Hs.82772 Hs.283713	hypothetical protein BC014	1245	Seq ID No 5 & 203	•
	45228			Hs.28792	Homo sapiens cDNA FLJ1	1041 fis, clone PL	Seq ID No 6	
	42869			Hs.334838	KIAA1866 protein		Seq ID No 7 & 204	
70	45286	2 AW37		Hs.8687	ADAMTS2 (a disintegrin-li		Seq ID No 8 & 205 Seq ID No 9 & 206	
	43220			Hs.298241	Transmembrane protease, ESTs, Weakly similar to S		Seq ID No 10 & 207	
	43420			Hs.362915 Hs.105484	regenerating gene type IV		Seq ID No 11 & 208	
	42226 40904			Hs.50081	Hypothetical protein, XP_0	)51860 (KIAA119	Seq ID No 12 & 209	
75	44342		_	Hs.9329	chromosome 20 open rea		Seq ID No 13 & 210	
	44321	1 Al128	388	Hs.143655	ESTs	eeshiin) lika	Seq ID No 14 Seq ID No 15 & 211	
	42866			Hs.189095	similar to SALL1 (sal (Dro interferon-stimulated prote		Seq ID No 16 & 212	
	41327		3085 307115	Hs.833 Hs.29352	turnor necrosis factor, alp		Seq ID No 17 & 213	
80	45240 45240		207115 207115	Hs.29352	tumor necrosis factor, alp		Seq ID No 18 & 214	
	40838			Hs.44532	diubiquitin		Seq ID No 19 & 215	
	41620	09 AA23	6776	Hs.79078	MAD2 (mitotic arrest defic	aent, yeast, n	Seq ID No 20 & 216 Seq ID No 21 & 217	
	4097	57 NM_(	001898	Hs.123114	cystatin SN		and in the state of	
						(22		

	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmilte	Seq ID No 22 & 218
	452194	AI694413	Hs.373599	olfactory receptor, family 2, subfamily	Seq ID No 23 & 219 Seg ID No 24 & 220
	452194 444783	AI694413 AK001468	Hs.373599 Hs.62180	offactory receptor, family 2, subfamily anillin (Drosophila Scraps homolog), act	Seq ID No 25 & 221
5	422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	Seq ID No 26 & 222
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	Seq ID No 27 & 223
	415989 415989	AI267700 AI267700	Hs.351201 Hs.351201	ESTs ESTs	Seq ID No 28 Seq ID No 29
	424252	AK000520	Hs.143811	hypothetical protein FLJ20513	Seq ID No 30 & 224
10	424252	AK000520	Hs.143811	hypothetical protein FLJ20513	Seq ID No 31 & 225
	432867	AW016936	Hs.233364	ESTS	Seq ID No 32 Seq ID No 33
	439759 428970	AL359055 BE276891	Hs.67709 Hs.194691	Horno sapiens mRNA full length insert cDN retinoic acid induced 3 (RAIG1); metabo	Seq ID No 34 & 226
	428953	AA306610	Hs.348183	turnor necrosis factor receptor superfami	Seq ID No 35 & 227
15	428953	AA306610	Hs.348183	tumor necrosis factor receptor superfami	Seq ID No 36 & 228 Seq ID No 37 & 229
	428953 428953	AA306610 AA306610	Hs.348183 Hs.348183	tumor necrosis factor receptor superfami tumor necrosis factor receptor superfami	Seq ID No 38 & 230
	428953	AA306610	Hs.348183	turnor necrosis factor receptor superfami	Seq ID No 39 & 231
20	452203	X57522	Hs.352018	transporter 1, ATP-binding cassette, sub	Seq ID No 40 & 232 Seq ID No 41 & 233
20	428330 436480	L22524 AJ271643	Hs. 2256 Hs. 87469	matrix metalloproteinase 7 (matritysin, putative acid-sensing ion channel	Seq ID No 42 & 234
	407603	AW955705	Hs.62604	Homo saplens, clone IMAGE:4299322, mRNA,	Seq ID No 43 & 235
	425115	R44564	Hs.123956	downstream of. G protein-coupled recept	Seq ID No 44 & 236
25	435472 418870	AW972330 AF147204	Hs.283022 Hs.89414	triggering receptor expressed on myeloid chemokine (C-X-C motif), receptor 4 (fus	Seq ID No 45 & 237 Seq ID No 46 & 238
23	415511	AI732617	Hs.182362	ESTs	Seq ID No 47
	440304	BE159984	Hs.125395	hepatitis A virus cellular receptor 1	Seq ID No 48 & 239
	423161	AL049227 AL049227	Hs.124776 Hs.124776	downstream of cadherin 6 (by 3.3kb) downstream of cadherin 6 (by 3.3kb)	Seq ID No 49 & 240 Sea ID No 50
30	423161 410153	BE311926	Hs.15830	hypothetical protein FLJ12691	Seq ID No 51 & 241
	410153	BE311926	Hs.15830	hypothetical protein FLJ12691	Seq ID No 52 & 242
	410153	BE311926	Hs.15830 Hs.15830	hypothetical protein FLJ12691 hypothetical protein FLJ12691	Seq ID No 53 & 243 Seq ID No 54 & 244
	410153 436895	BE311926 AF037335	Hs.5338	carbonic anhydrase XII	Seq ID No 55 & 245
35	436895	AF037335	Hs.5338	carbonic anhydrase XII	Seq ID No 56 & 246
	421471	U90545	Hs.327179 Hs.183572	solute carrier family 17 (sodium phospha solute carrier family 22 (organic cation	Seq ID No 57 & 247 Seq ID No 58 & 248
	428296 426890	NM_003058 AA393167	Hs.41294	ESTs	Seq ID No 59 & 249
4.0	437212	AI765021	Hs.210775	ESTs	Seq ID No 60
40	438966	AW979074	Un 195107	gb:EST391184 MAGE resequences, MAGP Homo ESTs, Moderately similar to ALUE_HUMAN!	Seq ID No 61 Seq ID No 62
	440311 437100	A1733079 A1761073	Hs.125407 Hs.14535	Homo sapiens cDNA: FLJ22314 fis, clone H	Seq ID No 63
	437100	AI761073	Hs.14535	Homo sapiens cDNA: FLJ22314 fis, clone H	Seq ID No 64
45	450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitte	Seq ID No 65 & 250 Seq ID No 66 & 251
45	419080 443595	AW150835 AF169312	Hs.18878 Hs.9613	hypothetical protein FLJ21620 PPAR(gamma) angiopoietin related protein	Seq ID No 67 & 252
	443595	AF169312	Hs.9613	PPAR(gamma) angiopoietin related protein	Seq ID No 68
	410407	X66839	Hs.63287	carbonic anhydrase IX	Seq ID No 69 & 253 Seq ID No 70 & 254
50	453496 420737	AA442103 L08096	Hs.33084 Hs.99899	solute carrier family 2 (facilitated glu CD70; tumor necrosis factor (ligand) s	Seq ID No 71 & 255
50	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	Seq ID No 72 & 256
	420789	AI670057	Hs.199882	ESTs	Seq ID No 73 Seq ID No 74
	420789 441392	A1670057 AW451831	Hs.199882 Hs.222119	ESTs ESTs, Weakly similar to \$30433 keratin 1	Seq ID No 75 & 257
55	452431	U88879	Hs.29499	to@-like receptor 3	Seq ID No 76 & 258
	431870	AW449902	Hs.105500	ESTs	Seq ID No 77 Seq ID No 78
	431870 449523	AW449902 NM_000579	Hs.105500 Hs.54443	ESTs chemokine (C-C motif) receptor 5	Seq ID No 79 & 259
	409745	AA077391		gb:7814E12 Chromosome 7 Fetal Brain cDNA	Seq ID No 80
60	438859	A1559626	Hs.93522 Hs.55407	Homo sapiens mRNA for KIAA1647 protein, Homo sapiens mRNA; cDNA DKFZp434K0621 (f	Seq ID No 81 Seq ID No 82 & 260
	409637 409637	AA323948 AA323948	Hs.55407	Homo sapiens mRNA; cDNA DKFZp434K0621 (f	Seq ID No 83
	409348	Al401535	Hs.146090	ESTs	Seq ID No 84
65	447269	NM_004861	Hs.17958	cerebroside (3-phosphoadenylylsulfate:g hypothetical protein DKFZp434K1210	Seq ID No 85 & 261 Seq ID No 86 & 262
65	453195 428841	BE241876 Al418430	Hs.32352 Hs.104935	ESTs	Seq ID No 87
	428841	AI418430	Hs.104935	ESTs	Seq ID No 88
	428841	Al418430	Hs.104935	ESTs	Seq ID No 89 Seq ID No 90 & 263
70	409663 409663	A1743750 A1743750	Hs.98306 Hs.98306	KIAA1862 protein KIAA1862 protein	Seq ID No 91 & 264
,,	431939	AW008061	Hs.231994	ESTs	Seq ID No 92 & 265
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	Seq ID No 93 & 266 Seq ID No 94 & 267
	411411 433867	AA345241 AK000596	Ks.55950 Hs.3618	ESTs, Wealdy similar to KIAA1330 protein hippocalcin-like 1	Seq ID No 95 & 268
75	433867	AK000596	Hs.3618	hippocatcin-like 1	Seq ID No 96 & 269
	437938	AI950087	Hs.369628	gb:wq05c02.x1 NCI_CGAP_Kid12 Homo sapien	Seq ID No 97 Seq ID No 98 & 270
	432579 418526	AF043244 8E019020	Hs.278439 Hs.85838	nucleolar protein 3 (apoptosis repressor solute carrier family 16 (monocarboxylic	Seq ID No 99 & 271
	418526		Hs.273230	hypothetical protein FLJ10830	Seq ID No 100 & 272
80	432196	88800EWA	Hs.273230	hypothetical protein FLJ10830	Seq ID No 101 & 273 Seq ID No 102
	438929 410055		Hs.253177 Hs.58241	ESTs gene for serine/threonine protein kinase	Seq ID No 103 & 274
	446650		Hs.15813	solute carrier family 22 (organic cation	Seq ID No 104 & 275
				46.4	

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	426812	AF105365	Hs.172613	solute carrier family 12 (potassium/chlo	Seq ID No 105 & 276 Seq ID No 106 & 277
	447131	NM_004585	Hs.17466	retinoic acid receptor responder (tazaro	Seq ID No 107 & 278
	449444	AWB18436	Hs.351306	solute carrier family 16 (monocarboxylic transforming growth factor, beta-induced	Seq ID No 108 & 279
5	422627 444488	BE336857 AW192879	Hs.118787 Hs.355660	ancient conserved domain protein 4	Seq ID No 109 & 280
,	450931	N25156	Hs.25648	tumor necrosis factor receptor superfami	Seq ID No 110 & 281 Seq ID No 111 & 282
	409220	BE243323	Hs.51233	turnor necrosis factor receptor superfami	Seq ID No 112 & 283
	409220	BE243323	Hs.51233	turnor necrosis factor receptor superfami fibroblast growth factor receptor 4	Seq ID No 113 & 284
10	425998 425998	AU076629 AU076629	Hs.165950 Hs.165950	fibroblast growth factor receptor 4	Seq ID No 114 & 285
10	425009	X58288	Hs.154151	protein tyrosine phosphatase, receptor t	Seq ID No 115 & 286
	443987	AW163123	Hs.10071	seven transmembrane protein TM7SF3	Seq ID No 116 & 287 Seq ID No 117 & 288
	432990	AL036071	Hs.279899 Hs.77542	tumor necrosis factor receptor superfami ESTs	Seq ID No 118 & 289
15	436576 451527	AI458213 AF022813	Hs.26518	transmembrane 4 superfamily member 7	Seq ID No 119 & 290
13	448733	NM 005629	Hs.187958	solute carrier family 6 (neurotransmitte	Seq ID No 120 & 291
	410274	AA381807	Hs.61762	hypoxia-inducible protein 2	Seq ID No 121 & 292 Seq ID No 122 & 293
	125218	H91923	Hs.110024	Empirically selected from AFFX single pr ESTs	Seq ID No 123
20	436961 431630	AW375974 NM_002204	Hs.156704 Hs.265829	integrin, alpha 3 (antigen CO49C, alpha	Seq ID No 124 & 294
20	431630	NM_002204	Hs.265829	integrin, alpha 3 (antigen CD49C, alpha	Seq ID No 125 & 295
	419508	AW997938	Hs.90786	ATP-binding cassette, sub-family C (CFTR	Seq ID No 126 & 296 Seq ID No 127 & 297
	431840	AA534908	Hs.2860	POU domain, class 5, transcription facto gb:os26b03.s1 NCI_CGAP_Kid5 Homo sapiens	Seq ID No 128
25	442438	AA995998	Hs.164129	ESTs, Weakly similar to 138022 hypotheti	Seq ID No 129
25	447835 429276	AW591623 AF056085	Hs.198612	G protein-coupled receptor 51	Seq ID No 130 & 298
	448595	AB014544	Hs.21572	KIAA0644 gene product	Seq ID No 131 & 299 Seq ID No 132 & 300
	440516	\$42303	Hs.161	cadherin 2, type 1, N-cadherin (neuronal	Seq ID No 133 & 301 ·
20	456759	BE259150	Hs.127792	delta (Orosophila)-like 3 FGENESH predicted secreted protein	Seq ID No 134 & 302
30	447004	AW296968 AA663372	Hs.157539 Hs.169395	hypothetical protein FLJ12015	Seq ID No 135 & 303
	425088 409389	AB007979	Hs.301281	Horno sapiens mRNA, chromosome 1 specific	Seq ID No 136 & 304
	448321	NM_005883	Hs.20912	adenomatous polyposis coli like	Seq ID No 137 & 305 Seq ID No 138 & 306
	426344	H41821	Hs.322469	transcriptional activator of the c-fos p	Seq ID No 139 & 307
35	419704	AA429104	Hs.45057 Hs.75090	ESTs KIAA0282 protein	Seq ID No 140 & 308
•	412959 448499	D87458 BE613280	Hs.77550	p53-regulated DDA3	Seq ID No 141 & 309
	458435	AJ418718	Hs.144121	ESTs, Wealty similar to T46916 hypotheti	Seq ID No 142 & 310
	443785	AW449952	Hs.190125	basic-helix-loop-helix-PAS protein	Seq ID No 143 & 311 Seq ID No 144 & 312
40	427343	AI880044	Hs.176977	protein kinase C binding protein 2 FGENESH predicted TM containing protein	Seq ID No 145 & 313
	416857	AA188775	Hs.292453 Hs.197962	Homolog of mouse ADP-ribosylation factor	Seq ID No 146 & 314
	429149 418030	AW193360 BE207573	Hs.83321	neuromedin B	Seq ID No 147 & 315
	457561	AA331517	Hs.286055	chimerin (chimaerin) 2	Seq ID No 148 & 316 Seq ID No 149 & 317
45	457561	AA331517	Hs.286055	chimerin (chimaerin) 2	Seq ID No 150 & 318
	430147	R60704	Hs.234434	hairy/enhancer-of-split related with YRP dipeptidytpeptidase VI	Seq ID No 151 & 319
	453642 453857	Al370936 Al080235	Hs.34074 Hs.35861	Ras-induced senescence 1 (RIS1)	Seq ID No 152 & 320
	449048		Hs.22920	similar to S68401 (cattle) glucose induc	Seq ID No 153 & 321
50	418506		Hs.372651	Unknown protein for MGC:29643 (formerly	Seq ID No 154 & 322 Seq ID No 155 & 323
	416636		Hs.42645	solute carrier family 16 (monocarboxylic absent in melanoma 2	Seq ID No 156 & 324
	421508 421379		Hs.105115 Hs.103982	small inducible cytokine subfamily B (Cy	Seq ID No 157 & 325
	428784		Hs.193470	purinergic receptor P2X, ligand-gated io	Seq ID No 158 & 326
55	431958		Hs.2877	cadherin 3, type 1, P-cadherin (placenta	Seq ID No 159 & 327 Seq ID No 160 & 328
	417542		Hs.82269	progestagen-associated endometrial prote cancer/testis antigen (NY-ESO-1)	Seq ID No 161 & 329
	418678 418678		Hs.167379 Hs.167379	cancer/testis antigen (NY-ESO-1)	Seq ID No 162 & 330
	420208		Hs.95972	silver (mouse homolog) like	Seq ID No 163 & 331
60	430377		Hs.301865	dopachrome tautomerase (dopachrome delta	Seq ID No 164 & 332 Sea ID No 165 & 333
	438549		Hs.21858	trinucleotide repeat containing 3 similar to CABLES [Homo sapiens]	Seq ID No 166 & 334
	412580 417160		Hs.17901 Hs.42146	Paired box protein Pax-3	Seq ID No 167 & 335
	42851		Hs.184697	plexin C1	Seq ID No 168 & 336
65	44793		Hs.20034	Homo sapiens mRNA full length insert cDN	Seq ID No 169 & 337 Seq ID No 170 & 338
	44793		Hs.20034	Homo sepiens mRNA full length insert cDN FGENESH prediction similar to multidrug	Seq ID No 171 & 339
	44634		Hs.310735 Hs.310735	FGENESH prediction similar to multidrug	Seq ID No 172 & 340
	44634 45807		Hs.54277	Homo sapiens similar to RIKEN cDNA 28100	Seq ID No 173 & 341
70	41566		Hs.306814	Homo sapiens lysyl oxidase-like 4 (LOXL4	Seq ID No 174 & 342 Seq ID No 175 & 343
	44767	4 BE270640	Hs.19192	cyclin-dependent kinase 2	Seq ID No 176 & 344
	44767		Hs.19192	cyclin-dependent kinase 2 Homo sapiens Fc receptor homolog express	Seq ID No 177 & 345
	44006 41494		Hs.266331 Hs.77667	lymphocyte antigen 6 complex, locus E	Seq ID No 178 & 346
75	44067		Hs.7345	MAD1 (mitotic arrest deficient, yeast, h	Seq ID No 179 & 347
, ,	41260	9 Z48804	Hs.74124	ocular albinism 1 (Nettleship-Falls)	Seq ID No 180 & 348 Seq ID No 181 & 349
	45383		Hs.256126	baculoviral IAP repeat-containing 7 (liv bacutoviral IAP repeat-containing 7 (liv	Seq ID No 182 & 350
	45383		Hs.256126 Hs.93605	leucine zipper, putative tumor suppresso	Seq ID No 183 & 351
80	4342 4083		Hs.44424	Homo sapiens orphan neurotransmitter tra	Seq ID No 184 & 352
00	4448	09 BE207568	Hs.208219	oculospanin	Seq ID No 185 & 353 Seq ID No 186 & 354
	4159	29 AA724373	Hs.304950	Homo sapiens mucolipin-3 (MCQLN3) endothelin 3	Seq ID No 187 & 355
	4216	66 AL035250	Hs.1408	GINDA ISINI 3	

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W74048
                                                          lymphocyte-specific protein tyrosine kin
                                                                                                           Seq ID No 188 & 356
          424321
                                        Hs.1765
                                                                                                            Seq ID No 189 & 357
          425535
                    AB007937
                                        Hs.158287
                                                           syndecan 3
                                                                                                            Seq ID No 190 & 358
         451537
                                        Hs. 26550
                                                           retinoid X receptor, gamma
                    R56631
                    AA361258
                                        Hs.237868
                                                           interleukin 7 receptor
                                                                                                            Seq ID No 191 & 359
          430280
 5
          418064
                    BE387287
                                        Hs.83384
                                                           $100 calcium-binding protein, beta (neur
                                                                                                            Seq ID No 192 & 360
          448610
                                        Hs.21602
                                                           nel (chicken)-like 1
                                                                                                            Seq ID No 193 & 361
                    NM_006157
                                                                                                            Seq ID No 194 & 362
          432800
                    RF391046
                                        Hs.278962
                                                           AIM 1 protein
                                                                                                            Seq ID No 195 & 363
                                        Hs.189507
                                                           phospholipase A2, group IID
          416350
                    AF188625
                                                                                                            Seq ID No 196 & 364
          405545
                                                           Target Exon
10
                                        Hs.77367
                                                           monokine induced by gamma interferon
                                                                                                            Seq ID No 197 & 365
          414812
                    X72755
                                                                                                            Seq ID No 198 & 366
          432874
                     W94322
                                        Hs.279651
                                                           metanoma inhibitory activity
          Table 68 lists sequences as described in Table 67
15
          Sea ID NO. 1 DNA sequence
          Nucleic Acid Accession #: NM_002421.2
          Coding sequence: 1..1409
                                                         31
                                                                         41
                                                                                         51
                         11
                                         21
20
          ATGCACAGCT TTCCTCCACT GCTGCTGCTG CTGTTCTGGG GTGTGGTGTC ACACAGCTTC
          CCACCGACTC TAGAAACACA AGAGCAAGAT GTGGACTTAG TCCAGAAATA CCTGGAAAAA
TACTACAACC TGAAGAATGA TGGGAGGCAA GTTGAAAAGC GGAGAAATAG TGGCCCAGTG
GTTGAAAAAT TGAAGCAAAT GCAGGAATTC TTTGGGCTGA AAGTGACTGG GAAACCAGAT
                                                                                                           120
                                                                                                           180
25
          GCTGAAACCC TGAAGGTGAT GAAGCAGCCC AGATGTGGAG TGCCTGATGT GGCTCAGTTT
                                                                                                            300
          GTCCTCACTG AGGGAACCC TCGCTGGGAG CAAACACATC TGACCTACAG GATTGAAAAT TACACGCCAG ATTTGCCAAG AGCAGATGTG GACCATGCCA TTGAGAAAGC CTTCCAACTC TGGAGTAATG TCACACCTCT GACATTCACC AAGGTCTCTG AGGGTCAAGC AGACATCATG
                                                                                                            360
                                                                                                            480
          ATATCTTTTG TCAGGGGAGA TCATCGGGAC AACTCTCCTT TTGATGGACC TGGAGGAAAT
                                                                                                            540
          CTTGCTCATG CTTTTCAACC AGGCCCAGGT ATTGGAGGGG ATGCTCATTT TGATGAAGAT GAAAGGTGGA CCAACAATTT CAGAGAGTAC AACTTACATC GTGTTGCGGC TCATGAACTC
30
                                                                                                            600
          GGCCATTCTC TTGGACTCTC CCATTCTACT GATATCGGGG CTTTGATGTA CCCTAGCTAC
                                                                                                            720
          ACCTTCAGTG GTGATGTTCA GCTAGCTCAG GATGACATTG ATGGCATCCA AGCCATATAT GGACGTTCCC AAAATCCTGT CCAGCCCATC GGCCCACAAA CCCCAAAAGC ATGTGACAGT
                                                                                                            780
                                                                                                            840
35
          AAGCTAACCT TTGATGCTAT AACTACGATT CGGGGAGAAG TGATGTTCTT TAAAGACAGA
                                                                                                            900
          TTCTACATGC GCACAAATCC CTTCTACCCG GAAGTTGAGC TCAATTTCAT TTCTGTTTTC
                                                                                                            960
                                                                                                          1020
           TGGCCACAAC TGCCAAATGG GCTTGAAGCT GCTTACGAAT TTGCCGACAG AGATGAAGTC
           CGGTTTTTCA AAGGGAATAA GTACTGGGCT GTTCAGGGAC AGAATGTGCT ACACGGATAC
                                                                                                          1080
           CCCAAGGACA TCTACAGCTC CTTTGGCTTC CCTAGAACTG TGAAGCATAT CGATGCTGCT
40
           CTTTCTGAGG AAAACACTGG AAAAACCTAC TTCTTTGTTG CTAACAAATA CTGGAGGTAT
                                                                                                          1200
          GATGAATATA AACGATCTAT GGATCCAGGT TATCCCAAAA TGATAGCACA TGACTTTCCT
GGAATTGGCC ACAAAGTTGA TGCAGTTTTC ATGAAAGATG GATTTTTCTA TTTCTTTCAT
GGAACAAGAC AATACAAATT TGATCCTAAA ACGAAGAGAA TTTTGACTCT CCAGAAAGCT
                                                                                                          1260
                                                                                                          1320
           AATAGCTGGT TCAACTGCAG GAAAAATTAG
45
           Seg ID NO: 2 DNA seguence
           Nucleic Acid Accession #: NM_002421.2
           Coding sequence: 1..1409
                                          21
                                                                                          51
 50
           ATGCACAGCT TTCCTCCACT GCTGCTGCTG CTGTTCTGGG GTGTGGTGTC ACACAGCTTC
           CCAGCGACTC TAGAAACACA AGAGCAAGAT GTGGACTTAG TCCAGAAATA CCTGGAAAAA
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3660

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15		TGTGGTGGCC					2456
13	GCANTANON	1010010000	ACICITICAL	······································	44000000		
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	CAACACCAAGA	ACATGACCAA	CCTCCTCCAA	TOTOTOCAGO	AGAAGGTGAA	TEGERATECTS	120
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		840
	TOTAL CONCERNATION CARCAGAGA CARCAGAGA CARCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	900 960
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,		140
		200 260
	MANAGRAPORA POROCOGNET CONSCIENCE CLACARCOGI GCCIGCOGI GCCIGCOGI	320
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10		1440 1500
	CONCOCCUTE ANTERECEAR REPORTED CONTRACTOR CO	1560
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15		1680
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	*** COCCOCCC **********************	360
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	TO THE TOTAL ACCURAGE ACACAMACA CONTINUES ACTORISTS OF THE TOTAL ACACAMACA ACACAMACA CONTINUES ACACAMACA CONTINUES ACACAMACA ACACAMACA CONTINUES ACACAMACA A	720 780
40		840
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	comparation of the first aritist Calculated according	960
	THE PROPERTY OF THE PROPERTY O	1020 1080
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	TOTAL CONTROL CONCERN	1260
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	THE PARTY OF THE P	1980
60	A THE COOK ASSESSED ASSESSEDA ASSESSED ASSESSED ASSESSED ASSESSED ASSESSED ASSESSED ASSESSEDA	2040
	TOTAL COMPONENCE CONCENCED TOTAL ACADICUTAL ANGUISMON	2100 2160
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_	THE PROPERTY OF THE PROPERTY O	2880 2940
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	A THE A TOUR ACCORDANCE CONTRACTOR ACCORDANCE ACCORDANCE	780
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75		1320 1380
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PCT/US02/29560

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5	THE TAXABLE TO A CONTRACT A A CACCATOCA CICCAGCA CICCAGCACCACCACCACCACCACCACCACCACCACCACCAC	1380
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		AACGCTGCCA					1860 1920
40		ACAGTCCTGA CGCTGCGGTC					1980
40		GTCCTCACCA					2040
		AGTTGGGTCG					2100
		CCCGAAAGCC					2160
45		CTCCTGGGAA TATTGGTGGA					2220 2280
43	AAAGTTTATT	TCAGGAGGAA	AATGGGTTCA	CACAAAAAGC	AAACTACATT	CTGATCTGCT	2340
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50		CAGGGGAGTT				GGATAATAAA	2520 2580
50		AGAATGGCCT					2640
	TTCCTTCACT	CACCCAGCAG	GTCAGTTTTC	TGTGCAAACA	AACCTGTTTA	GGATTCTTCC	2700
		CCTGGGGTCT					2760
55	TTTTTATTTT	TTCATCCAAC TCATCTCTTA	CATTTOTAL	CACTTTTTAC	ATGATTACTC	TACCTITUT	2820 2880
33	TTTTTTTT	TTTAAAAAAG	AAATAGTCAG	TGTTTTCCTC	CTTTCAACCG	AGACTATTTC	2940
	TGGATTGTGT	GCTCCTCGTC	AGTTGACTTG	TTTTGCACAC	TTTTCTTTAC	TTCATGTCCC	3000
		CCTCCTCCTC					3060
60						GAGTTCACGA	3120 3180
00		TGTTTGGAAT				CIGITONGI	3224
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						ACCCTCCTGG	60
70						GACGGCGGCT	120
70						GCCTTCCCCA TACAGCGACA	180 240
						CTCTGCAGTG	300
	TGTGCGTGAA	CCGCTTTGGC	TGCCGGCCCG	TCATGCTTGT	CCCCCCTCTC	TTTGCGTCGC	360
75						ACCACTGGGG	420
75						CTGAACCGCT	480 540
						CGGGGGGGCT	600
	TCCTCATCCT	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	CTGCTCAACT	GCTGCGTGTG	TGCCGCACTO	ATGAGGCCCC	660
οΛ	TGGTGGTCAC	GGCCCAGCCG	GCCTCCGGGG	CGCCGCGACC	CTCCCGGCG	CTGCTAGACC	720
80						GTCATGGTGC	780 840
						CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	900
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	TCTCCATGTT	CTTCAACGGC	CTCGCGGACC	TGGCGGGCTC	TACGGCGGG	GACTACGGCG	1020

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5	TGATTTTGCT GCTGGGCAAC TTCTTCTGCA TTAGGAAGAA GCCCAAAGAG CCACAGCCTG	1320						
,	AGGTGGCGGC CGCGGAGGAG GAGAAGCTCC ACAAGCCTCC TGCAGACTCG GGGGTGGACT	1380						
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	TT	1982						
^^	Seq ID NO: 105 DNA Sequence							
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	Coding sequence: 53256							
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	CATCHTCC ATGITCTICC TCATGIGCTA CCIGITCGIG AACCIGGCCI GCGCCGIGCA	1800						
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	GGTCACAGA AGCCAGTGAG CCCTTGCCTT GGTTTCTGGA AGTTCTTTTC CTTGGCTGG	3600						
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_	GCTCGGCAGG						3900
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	TGGGAGGTCC	TCAGGCAGCA	GTGGCGCCTG	GTGTCAGGTC	CCCACTCAAC	AGICCCOOC NONTROCCTTT	4380 4440
	GTCCCCTGCC	ATGGCCTGTG	CTTCGGCTGG	AGGCGGCGGT	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	COTTOTOTO	4500
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	ATGAAATCTG	AAAAAAAA					5239
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	î	î.	ī	ī	i .	ī	
	CCTTCAGCAT	AAAAGCTGAT	CCACAAACAA	GAGGAGCACC	AGACCTCCTC	TTGGCTTCGA	60
35	GATGGCTTCG	CCACACCAAG	AGCCCAAACC	TGGAGACCTG	ATTGAGATTT	TCCGCCTTGG	120
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			CCTCCAGTGT				240
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40			GGCCCGTGGA				360
40	TGGTCAGAAG	ATGAAGTACA	GTATTGTGAG	CAGGAACTGT	GAGCACTTTG	TCGCCCAGCT	420
	GAGATATGGC	AAGTCCCGCT	~~× * * ~ * ~ * ~ ~ ~ ~ ~		**************************************		480
			GIMMCMOGI	GGAVAAGGCC	ANGGI IGANG	1000101000	
	CACGGCGCTT	GGAATCCTGG	TTGTTGCTGG	ATGCTCTTTT	GCGATTAGGA	GATACCAAAA	540
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45	CACGGCGCTT AAAAGCAACA GTGGAGATGA TCTCTAGATC	GGAATCCTGG GCCTGAAGCA GCCTCCCCA CTTTCCTCTG	TTGTTGCTGG GCCACAAAAT TGCCTCCAGC TTTCCCTCTC	ATGCTCTTTT CCTGTGTTAG AGCCTGACCC TCGCTGGCAA	GCGATTAGGA AAGCAGCTGT TCGTGCCCTG AAGTATGATC	GATACCAAAA GGGGGTCCCA	540 600 660 720
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	CACGGCGCTT AAAAGCAACA GTGGAGATGA TCTCTAGATC AAGACTGAAG Seq ID NO: Nucleic Ac	GGAATCCTGG GCCTGAAGCA GCCTCCCCCA CTTTCCTCTG GATCAATAAA 107 DNA Se id Accessio	TTGTTGCTGG GCCACAAAAT TGCCTCCAGC TTTCCCTCTC CAGCCATCTG quence n #: NM_004	ATGCTCTTTT CCTGTGTTAG AGCCTGACCC TCGCTGGCAA CCCCTTCAAA	GCGATTAGGA AAGCAGCTGT TCGTGCCCTG AAGTATGATC	GATACCAAAA GGGGGTCCCA TCTCAGGCGT	540 600 660 720
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50	CACGGCGTT AAAAGCAACA GTGGAGATGA TCTCTAGATC AAGACTGAAG Seq ID NO: Nucleic Ac Coding seq 1   CTTGGCTCTT AGAGTAACAT	GGATCCTGG GCCTGAAGCA GCCTCCCCCA CCTTCCTCTG GATCAATAAA 107 DNA Se id Accessio uence: 183. 11   ACAATGCTCA	TTGTTGCTGG GCCACAAAAT TGCCTCCAGC TTTCCCTCTC CAGCCATCTG Quence n #: NM_004 .1646 21   CTTGTTTTCZ CGTGTAATT1	ATGCTCTTTT CCTGTGTTAG AGCCTGACCC TCGCTGGCAA CCCCTTCAAA  696.1  31   CAATGCAGCA ATTTTCTTC	GCGATTAGGA AAGCAGCTGT TCGTGCCCTG AAGTATGATC AAAAAAA  41         AAATGAAATG CTTAATTGCC	GATACCAAAA GGGGGTCCCA TCTCAGGCGT TAATTGAAAC	540 600 660 720 768
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50	CACGGCGCTT AAAAGCAACA GTGGAGATGA TCTCTAGATC AAGACTGAAG Seq ID NO: Nucleic Ac Coding seq 1   CTTGGCTCTT AGAGTAACAT AGGATTACTT TCATGCTGAA	GGAATCCTGG GCCTGAAGCA CCTTCCCCCA CTTCCTCTG GATCAATAAA  107 DNA Se id Accessio uence: 183. 11	TTGTTGCTGG GCCACAAAAT TGCCTCCAGC TTTCCCTCTC CAGCCATCTG Quence n #: NM_004 .1646 21   CTTGTTTTCA CGTGTAATTT CACATCAAAC AAGGTCCAAC	ATGCTCTTTT CCTGTGTTAG AGCCTGACC TCGCTGGCAA CCCCTTCAAA  696.1  31   CAATGCAGCA ATTTTTCTTC GGATCTTCTG CTTACACTAA	GCGATTAGGA AAGCAGCTGT TCGTGCCCTG AAGTATGATC AAAAAAAA  41   AAATGAAATGC CCTTAATTGCC CATTTAAAAT AACCCTGGAT	GATACCAAAA GGGGGTCCCA TCTCAGGGT TAATTGAAAC  51	540 600 660 720 768 60 120 180 240
50	CACGGCGCTTA AAAAGCAACA GTGGAGATGA TCTCTAGATC AAGACTGAAG Seq ID NO: Nucleic Ac Coding seq 1   CTTGGCTCTT AGAGTAACAT AGGATTTCTT TCATGCTGAT	GGATCCTGG GCCTGAAGCA CCTTCCCCCA CTTTCCTCTG GATCAATAAA  107 DNA Se id Accessio usence: 183. 11                 ACAATGCTCA TCCAGAAAAC TCCAGAAAAC TGCTGAACAC TGGTGAACAC TGGTGAACAC	TTGTTGCTGG GCCACAAAAT TGCCTCCAGC TTTCCCTCTC CAGCCATCTG Quence n #: NM_004 .1646 21   CTTGTTTTCC CGGTGTAATTT CACATCAAC AAGGTCCAAC	ATGCTCTTTT CCTGTGTTAG AGCCTGACCC TCGCTGGCAA CCCCTTCAAA  696.1  31   CAATGCAGCA ATTTTTCTTC GGATCTTCTG GGATCTTCTG CTTACACTAA	GCGATTAGGA AAGCAGCTGT TCGTGCCCTG AAGTATGATC AAAAAAAA  41   AAATGAAATG CTTAATTGCC GCATTTAAAAA TGTGATGGGG	GATACCAAAA GGGGGTCCCA TCTCAGGCGT TAATTGAAAC  51   CCTTAGAAAA CCATCTGTGG AGAAGAGGCA GGAGGATGGG ATGACCAAGA	540 600 660 720 768 60 120 180 240 300
50	CACGGCGTT AAAAGCAACA GTGGAGGTGA TCTCTAGATC AAGACTGAAG Seq ID NO: Nucleic Ac Coding seq I I CTTGGCTCTT AGAGTAACAT AGGATTCTT TCATGCTGAAT GATGGATGAT CTTTTGCATT	GGAATCCTGG GCTGAAGCA CCTTCCTCTG GATCAATAAA  107 DNA Se id Accessio uence: 183. 11 12 ACAATGCTCA TCCCGAAAAC TCCCGAAAAC TCCTGAACAC GGGGGGGGG TGTGTTCAT TTTCTTTGTC	TTGTTGCTGG GCCACAAAAT TGCCTCCAGC TTTCCCTCTC CAGCCATCTG Quence n #: NM_004 .1646 21   CCTTGTTTTCC CGTGTAATTI CACATCAAAC AAGGTCCAAAC TTTTCCTGC	ATGCTCTTTT CCTGTGTTAG AGCCTGACCC TCGCTGGCAA CCCCTTCAAA  696.1  31	GCGATTAGGA AAGCAGCTGT TCGTGCCCTG AAGTATGATC AAAAAAAA  41	GATACCAAAA GGGGGTCCCA TCTCAGGCGT TAATTGAAAC  51   CCCTTAGAAAA CCCATCTGTGG AGAAGAGCA GGAGGATGGG ATGACCAAGA AGAGCAAATTG	540 600 720 768 60 120 180 240 360
50	CACGGCGCTT AAAAGCAACA GTGGAGATGA TCTCTAGATC AAGACTGAAG Seq ID NO: Nucleic Ac Coding seq I   CTTGGCTCTT AGAGTAACAT TCATGCTGAA GATGGATATCT TCATGCTGAA GATGGATTGA GTTGGATTGGA	GGAATCCTGG GCCTGAAGCA CCTTCCCCCA CTTCCTCTG GATCAATAAA  107 DNA Se id Accessio uence: 183. 11	TTGTTGCTGG GCCACAAAAT TGCCTCCAGC TTTCCCTCTC CAGCCATCTG Quence n #: NM_004 .1646 21   CTTGTTTTCAAC GGTGTAATT CACATCAAAG AAGGTCCAAC TTTTCCTGC GTCTTTCCAC GTCTTTCAAC	ATGCTCTTT CCTGTGTTAG AGCCTGACC TCGCTGGCAA CCCCTTCAAA  696.1  31	GCGATTAGGA AAGCAGCTGT TCGTGCCCTG AAGTATGATC AAAAAAAA  41	GATACCAAAA GGGGGTCCCA TCTCAGGCGT TAATTGAAAC  51	540 600 660 720 768 60 120 180 240 300
50	CACGGCGCTT AAAAGCAACA GTGGAGATGA TCTCTAGATC AAGACTGAAG Seq ID NO: Nucleic Ac Coding seq 1   CTTGGCTCTT AGAGTAACAT AGGATTTCTT TCATGCTGAT GTTTGGATGAT GTTTGGATTGG TTTGGATTGG	GGATCCTGG GCCTGAAGCA GCCTCCCCCA CTTTCCTCTG GATCAATAAA  107 DNA Se id Accessio usence: 183. 11   ACAATGCTCA TCCAGAAAAC TCCTGAACAC TCCTGAACAC TTCTTGTGAACAC ACTTGGAGAC ACTTGGAGACAC ACTTGGAGACAC ACTTGGAGACAC ACTTGGAGAC	TTGTTGCTGG GCCACAAAAT TGCCTCCAGC TTTCCCTCTC CAGCCATCTG Quence n #: NM_004 .1646 21   CTTGTTTTCC GGTGTAATTT CACATCAAAC TTTTTCCTCC GTTCTTTCAGC TTTTTCCTCC GTTCTTTCAGC TTCTTCCACC TTTTTCCTCC GTTCTTCCACC TTCATCTCTTC GAAACTACCC	ATGCTCTTTT CCTGTGTTAG AGCCTGACCC TCGCTGGCAA CCCCTTCAAA  696.1  31   CCAATGCAGCA ATTTTCTTC GGATCTTCTG CTTACACTAA TGAATGTGTT AAGAGTTTGA GTTTTTTGTGC CCATTCTTGGC	GCGATTAGGA AAGCAGCTGT AAGAAAAAA  41   AAATGAAATG CTTAATTGCC CATTTAAAAA AACCCTGGAT TOTGATGGGG AGGCACCTCC GGGCTTCGTT	GATACCAAAA GGGGGTCCCA TCTCAGGCGT TAATTGAAAC  51   CCTTAGAAAA CCATCTGTGG AGAAGAGGCA AGAGCAAATTG GGTTACCAATTA	540 600 660 720 768 60 120 180 240 300 420
50	CACGGCGTT AAAAGCAACA GTGGAGATGA TCTCTAGATC AAGACTGAAG Seq ID NO: Nucleic Ac Coding seq 1   CTTGGCTCTT TCAGGCTCTT TCAGGCTGAT GGATTCTT TCATGCTGAT GGATGATGAT GTTGGATTGG TTTTGTGAAT GATATCTGAT	GGATCCTGG GCTGAAGCA GCTTCCTCTG GATCAATAAA  107 DNA Se id Accessia uence: 183. 11   ACAATGCTCA TCCTGAACAC GAGGAGGGG TCCTGAACAC GTGTGATCAT TTTCTTTGTGATCAC ACTGGAGAGGG ACCATCTGAACAC ACTGGAGATCATCACC ACTGGAGAGGGGGGGGGG	TTGTTGCTGG GGCACAAAAT TGCCTCCAGC TTTCCCTCTC CAGCCATCTG Quence n #: NM_004 .1646 21   CTTGTTTTCC GGTGTAATTT CACATCAAAC AAGGTCCAAC GTCTTTCCTGC GTCTTTCCAC GTCTTTCAAC GTCTTTCAAC GAAAACTACCTG GCCACAAGT	ATGCTCTTTT CCTGTGTTAG AGCCTGACCC TCGCTGGCAA CCCCTTCAAA  696.1  31	GCGATTAGGA AAGCAGCTGT AAGTATGATC AAAAAAAA  41   AAATGAAATG CATTTAAAAT AACCTGGAT TGTGATGGGG AGGCACCTCP AGGTCCCCTT GGGCTTTCGTT TTTGTGTGACT	GATACCAAAA GGGGGTCCCA TCTCAGGCGT TAATTGAAAC  51   CCTTAGAAAA CCATCTGTGG AGAAGAGGCA GGAGGATGGG ATGACCAAGA GGTACATATTA GTTACTGGTG ATGAGGACTTC	540 600 720 768 60 120 180 240 300 360 420 480
50	CACGGCGCTT AAAAGCAACA GTGGAGATGA TCTCTAGATC AAGACTGAAG  Seq ID NO: Nucleic Ac Coding seq I   CTTGGCTCTT AGAGTAACAT AGGATTACTT TCATGCTGAA GATGATGAT GTTGGATTGG TTTGTACAT GATATCTGT TTGTGAACAT GATATCTGTT TCAAAAAAACCG	GGAATCCTGG GCTTGAGCA GCTTCCTCTG GATCAATAAA  107 DNA Se id Accessio uence: 183. 11	TTGTTGCTGG GCCACAAAAT TGCCTCCAGC TTTCCCTCTC CAGCCATCTG Quence n #: NM_004 .1646 21   CTTGTTTTCA GAGGCAAAAT TATTTCCTCA GAGGCAAAAT TTTTCCTCA GAAACTACAC TTTTTCTCAC GCCCACAAGT TTTTTCTTAACC TCTACACCT TCTACACCT	ATGCTCTTT CCTGTGTTAG AGCCTGACC TCGCTGGCAA CCCCTTCAAA  696.1  31	GCGATTAGGA AAGCAGCTGT TCGTGCCCTG AAGTATGATC AAAAAAAA  41	GATACCAAAA GGGGGTCCCA TCTCAGGGGT TAATTGAAAC  51	540 600 720 768 60 120 180 240 300 360 420 480 540 600 660
50 55 60	CACGGCGTT AAAAGCAACA GTGGAGGTGA TCTCTAGATC AAGACTGAAG Seq ID NO: Nucleic Ac Coding seq I CTTGGCTCTT AGAGTAACAT AGGATTCTT TCATGCTGAT GTTGGATTGAT GTTGGATTGAT GTTTGTGAACAT TACCCGGTTT TCAAAAAACA TTTTGGCACCT TTTGGCACCT TTTGGCACCT TTTGGCACCT TTTGGACAT TTTGGACAT TTTGGACAT TTTGGACAT TTTGGACAT TTTTGGCACCT TTTTGGCACCT TTTTGGCACCT TTTTGGCACCT TTTTGGCACCT TTTTGGCACCT	GGATCCTGG GCCTGAAGCA CCTTTCCTCTG GATCAATAAA  107 DNA Se id Accessio uence: 183. 11   ACAATGCTCA TCCTGAACAC GAGGGAGGGG TTTCATTGTT ACTCATCATCAT ACTTGAGACAC CAGCAGCTGC CAGCAGCTGC CAGCAGCTGC CTTTACAAAAC CTTTACACAAC CTTTACACAC	TTGTTGCTGG GGCACAAAAT TGCCTCCAGG TTTCCCTCTG CAGCCATCTG Quence n #: NM_004 .1646 21   CTTGTTTTCAAAA CAACTCAAAAC GTCTTTCCAGG TTTTCCTGAAAC GTCTTTCAAG GTCTTTCAAG GTCTTTCAAG TTTTCCTGAAAC TCTACAGGTAAT TTCTTACAGGTAAAAC TTCTACAGGTAAAAC TTCTACAGGTAAAAC TTCTACAGGTAAAAC TTCTACAGGTAAAAC TTCTACAGGTAAAAC TTCTACAGGTAAAAC TTCTACAGGTAAAAC TTCTACAGGTAAAAC TTCTCTGAAAAC TTCCTGAAAAC TTCC	ATGCTCTTTT CCTGTGTTAG AGCCTGACCC TCGCTGGCAA CCCCTTCAAA  696.1  31	GCGATTAGGA AAGCAGCTGT AAGTATGATC AAAAAAAA  41  AAATGAAATG CTTAATTGCC GCATTTAAAAT AACCTGGAT TTGTGGCCCTC TGGGTAGCC TTGGTAACT TTGGTAACT TGGGTAGCC AGGCTCGAT	GATACCAAAA GGGGGTCCCA TCTCAGGCGT TAATTGAAAC  51   CCTTAGAAAA CCATCTGTGG AGAAGAGGCA GGACGATGGG ATGACCAAGA GGTCACTGTGG ATGACCAAGA CGTTACTGGTG ATGACCAATACT ACCAAATACT CCGACATTTC	540 600 720 768 60 120 180 240 300 360 420 480 540 600 660 6720
50	CACGGCGTT AAAAGCAACA GTGGAGGTGA TCTCTAGATC AAGACTGAAG Seq ID NO: Nucleic Ac Coding seq I I CTTGGCTCTT AGAGTAACAT AGAGTTCTT TCATGCTGAA GATGGATGGA GTTGGATTCT TTTTTGCAT GATATCTGAT TACCGGTTT TCAAAAAACC TTTTTGGAGC TTTTTGGAGC TTTTTTTTTT	GGAATCCTGG GCTTGAAGCA CTTTCCTCTG GATCAATAAA  107 DNA Se id Accessio uence: 183. 11   ACAATGCTCA TCCTGAACAC AGGGGAGGG TTTCTTTGTACACAC ACTTGATCAT ATTCATCATC ATTGGTTCAT CAGGGTTCGCT ATTGGTTCAT TTTGTTGAGAC CAGCAGCTCC GGGTTCTGCT ATTGGTTCAT TTTGTTGAGACAC TTTGTTGAGACAC TTTGTTGAGACAC TTTGTTGAGACAC TTTGTTGAGACAC TTTGTTGAGACAC TTTGTTGAGACAC TTTGGTTCACAACAC TTTGGCTTTCGCT TTTGGCATTC	TTGTTGCTGG GGCACAAAAT TGCCTCCAGC TTTCCCTCTC CAGCCATCTG Quence n #: NM_004 .1646 21   CCTTGTTTTCC GGTGTAATT CACATCAAAC AAGGTCCAAC TTTTCCTGC GTCTTTCTAAC GTCTTTTCAAC TCTCTAAAC TCTCTTAAC TCTCTAAAC TCTCTAAAC AATTTCCTGAAAC AATTTCGTGGTGC	ATGCTCTTT CCTGTGTTAG AGCCTGACCC TCGCTGGCAA CCCCTTCAAA  696.1  31	GCGATTAGGA AAGCAGCTGT AAGTATGATC AAAAAAAA  41	SATACCAAAA GGGGGTCCCA TCTCAGGCGT TAATTGAAAC  51   CCCTTAGAAAA CCATCTGTGG AGAAGAGGCA GGACGATGGG ATGACCAAGA GGGCAATTG TTACTGGTG ATGACCAAGT ATGCTATTA CTCACTTTTC CTGACTTTTC CTGACTTTTC CTGACTTTTC CTGACTTTTA	540 600 720 768 60 120 180 240 300 420 480 600 660 720 720 780
50 55 60	CACGGCGCTT AAAAGCAACA GTGGAGATGA TCTCTAGATC AAGACTGAAG Seq ID NO: Nucleic Ac Coding seq I CTTGGCTCTT AGAGTAACAT TCATGCTGAT TCATGCTGAT GATGGATGAT GTTGGATTGGA	GGAATCCTGG GCTTGAGCCA CCTTCCTCTG GATCAATAAA  107 DNA Se id Accessio uence: 183. 11	TTGTTGCTGG GCCACAAAAT TGCCTCCTGC CAGCCATCTG Quence n #: NM_004 .1646 21   CTTGTTTTCCTGC GGTGTAATT CACATCAAAG GTCTTCTTCCAGC GTCTTTCCTGC GGCCACAAGT TTCTTCAGC TCACAGCT TTCTTAACC TCTCTATAACC TCTCTATAACC TCTCTATAACC TCTCTATAACC TCTCTATAACC TCTCTGATAAC TCTCTGATAACC TCTCTGATAACC TCTCTGATAACC TCTCTGATAACC TCTCTGATAACC TCTACAGCT ATTCCTGATAAAC TACTTGATAAAC	ATGATCTTT CCTGTGTTAG AGCCTGACC TCGCTGGCAA CCCCTTCAAA  696.1  31	GCGATTAGGA AAGCAGCTGT AAGTATGATC AAAAAAAA  41	GATACCAAAA GGGGGTCCCA TCTCAGGCGT TAATTGAAAC  51   CCTTAGAAAA CCATTCTTGG AGAAGAGCCA GGACGATGG ATTACTGGG ATTACTAGTA GTTTACTAGTTA GTTACTAGTTC ACCAAATACT CTGACTTTC ACCAATACT CTGACTTTTC ACCAATACT CTGACTTTTC ACCAATACT CTGACTTTTC ACCAATACT CTGACTTTTC ACCAATACT CTGACTTTTC ACCAATACT A	540 600 720 768 60 120 180 240 300 360 420 480 540 600 660 720 780 840
50 55 60	CACGGCGTT AAAAGCAACA GTGGAGGTGA TCTCTAGATC AAGACTGAAG Seq ID NO: Nucleic Ac Coding seq I I CTTGGCTCTT AGAGTAACAT AGGATTTCTT TCATGCTGAT CTTTGGCTGAT GTTGGATTGGA	GGATCCTGG GCCTGAAGCA CCTTCCCCCA CTTTCCTCTG GATCAATAAA  107 DNA Se id Accessio uence: 183. 11   ACAATGCTCA TCCAGAAAA TCCAGAAAAC TCCAGAAAAC TTCCTTGTC TTCTTGTC TTCTTTGTC ACCACACTGC CAGCAGCTGC CAGCAGCTGC CAGCAGCTGC CAGCAGCTGC TCTTACAAAA TTCCATCATC TTCCATCATC TTTCTTCTC TTTCACAAA TAGCACATC	TTGTTGCTGG GGCACAAAAT TGCCTCCAGC TTTCCCTCTC CAGCCATCTG Quence n #: NM_004 .1646 21   CTTGTTTTCC GGTGTAATTT CACATCAAAA AAACACTGCT ATTCTTTCAAC TTTTTCCTCAC GCCACAAGT TTCTTATACC TTCTTATACC TTCTTACAGCT ATTCTTACAGCT ATTCTACAGCT ATTCTTACAGCT ATTCTTACAGCT ATTCTTACAGCT ATTCTTACAGCT ATTC	ATGCTCTTTT CCTGTGTTAG AGCCTGACCC TCGCTGGCAA CCCCTTCAAA  696.1  31   CAATGCAGCA ATTTTCTTC GGATCTTCTG GGATCTTCTG CTTACACTAA TGAATGTTTGTG CCATTCTTGG CCATTCTTGG TTCCTTTCT AAGTGGCTGC TTCCTTTCT ATTTCTTCT ATTTCTTCT ATTTCTTCT ATTTCTTCT ATTTCTTCTTCT ATTTCTTCTTCT ATTTCTTTC	GCGATTAGGA AAGCAGCTGT AAGAAAAA  41  AAATGAAATG CTTAATTGCC GCATTTAAAAT AACCTGGAT TOTGATGGCCCTG GGGCTTCGTT TTGTGGACCC TTGGTAACC TTGGTACC TT	SATACCAAAA GGGGGTCCCA TCTCAGGCGT TAATTGAAAC  51   CCTTAGAAAA CCATCTGTGG AGAAGAGGCA AGACCAAGA GGACCAAGA GTTACTGTGT ATCGATCT ACCAATATT ACCCATCTTTA CCCATCTATAT CCCATCCAT	540 600 720 768 60 120 180 240 300 360 420 480 540 660 720 780 840 900
50 55 60	CACGGCGTT AAAAGCAACA GTGGAGGATGA TCTCTAGATC AAGACTGAAG Seq ID NO: Nucleic Ac Coding seq I CTTGGCTCTT AGAGTACAT AGGATTCTT TCATGCTGAT TCATGCTGAT GTTGGATTGT TTTTGTGAAT GTTTGTAAT TACCCGGTTT TCAAAAAACT TTTTGGAGC TTATTTGGAGC TTATTTGGAGC TTATTTGGAGC TTATTTGGAGC TCAAAAAGTGC CAGAGGCACC GTACTTACGCG	GGATCCTGG GCTGAAGCA CTTTCCTCTG GATCAATAAA  107 DNA Se id Accessio uence: 183. 11   ACAATGCTCA TCCTGAACAC GAGGGGGGG TTTCTTTGTGATCATACAC ACTTGATCATCATCATCATCATCATCATCATCATCATCATCATCA	TTGTTGCTGG GGCACAAAAT TGCCTCCAGC TTTCCCTCTC CAGCCATCTG Quence n #: NM_004 .1646 21   CCTTGTTTTCC CAGCTATCTC CAGCTATCTC CAGCTATCTC CAGCTATCTC CAGCTATCTC CAGCTATCTC CAGCTATCTC CAGCTATCTC CAGCTATCTCTC CAGCTATCTC CAGCTATCTC CAGCTATCTC CAGCTATCTC CAGCTATCTC CACACCAGGT CTCTCACAGCT CTCTCACAGCT CTCTCACAGCT CTCTCACAGCT CACACCACAGGT CACACCACAGGT CACACCACAGGT CACACCACAGGT CACACCACAGGT CACACACCTGCC CACACCACAGGT CACACCACAGGT CACACCACAGGC CACACACA	ATGCTCTTT CCTGTGTTAG AGCCTGACCC TCGCTGGCAA CCCCTTCAAA  696.1  31	GCGATTAGGA AAGCAGCTGT AAGTATGATC AAAAAAAA  41   AAAATGAAATG CATTTAAAATA AACCAGGAT TTGTGTGCCTC GGCTTTCGTT TTGTGTGACC TTGGATGGGC CTGATTGGCC TTGGATGGGC TTGGATGGGC TTGGATGGGC TTGGATGGGC TTGGATGGCC TTGGATGGGC TTGGATGGCC TTGGATGCC TTGGATGGCC TTGGATGGCC TTGGATGCC TTGCC TTCC TTGCC TT	SATACCAAAA GGGGGTCCCA TCTCAGGCGT TAATTGAAAC  51   CCTTAGAAAA CCATCTGTGG AGAAGAGGCA GGACGATGGG ATGACCAAGA GGTACTATTA CGTACTATTA CCCATCATTA CCCATCATAT CCCATCCAT	540 600 720 768 60 120 180 240 300 360 420 480 660 660 660 720 780 840 900
50 55 60 65	CACGGCGTT AAAAGCAACA GTGGAGGATGA TCTCTAGATC AAGACTGAAG Seq ID NO: Nucleic Ac Coding seq I CTTGGCTCTT AGAGTAACAT AGGATTCTT TCATGCTGAA GATGGATGGA TTTGTGAAT GATATCTGAT TACCGGTTT TCAAAAAAC TTTTGGAC TATTTGGAC TATTTGAC TATTTGGAC TATTTTGGAC TATTTGGAC TATTTTGGAC TATTTTGAC	GGAATCCTGG GCCTGAAGCA CCTTCCTCTG GATCAATAAA  107 DNA Se id Accessio uence: 183. 11	TTGTTGCTGG GGCACAAAAT TGCCTCCAGC TTTCCCTCTC CAGCCATCTG Quence n #: NM_004 .1646 21   CTTGTTTTCAGC GGTGTAATTT CACATCAAAAC GTCTTTCAAAAC GTCTTTTCAAAAC GTCTTTTCAAAAC TTCTTATAAAC TTCTTATAACC TTCTTATAACC TTCTACAGCTA ACACACTGCC AACACTGGCC AACACTGGCC AACACTGGCC AACACAGGAAAC	ATGCTCTTT CCTGTGTTAG AGCCTGACCC TCGCTGGCAA CCCCTTCAAA  696.1  31	GCGATTAGGA AAGCAGCTGT AAGAAAAA  41	GATACCAAAA GGGGGTCCCA TCTCAGGCGT TAATTGAAAC  51	540 600 720 768 60 120 180 240 300 420 480 540 660 720 780 840 900 960 1020
50 55 60	CACGGCGTTA ANAAGCAACA GTGGAGGATGA TCTCTAGATC ANGACTGAAG Seq ID NO: Nucleic Ac Coding seq I I CTTGGCTCTT AGAGTAACAT AGGATTACTT TCATGCTGAA GTTGGATGAT GTTGGATTGATT TCATACTGAA TTTTGGACAT GATATCTGAT TACCCGGTTTT TCAAAAACG TATTTGGACAC TATTTTGGACAC TATTTGGACAC TATTTGGACAC TATTTGGACAC TATTTGGACAC TATTTTGGACAC TATTTTGGACAC TATTTTGGACAC TATTTGGACAC TATTTTGGACAC TATTTTGGACAC TATTTGGACAC	GGATCCTGG GCCTGAAGCA CCTTCCCCCA CTTTCCTCTG GATCAATAAA  107 DNA Se id Accessio usence: 183. 11   ACAATGCTCA TCCAGAAAAC TCCAGAAAAC TTCCTGAGACAC AGAGGAGGGG GGGTTCTGCT CCTTACAAAA TATCGCATTC ATTCGCATCA TTCCACATCA AGAACAATTCC ATTCGACACAC AGAACAGCAC AGAAGGCTGGC ATTGGACACATCC ATTGGACACACACACACACACACACACACACACACACACA	TTGTTGCTGG GCCACAAAAT TGCCTCCAGC TTTCCCTCTC CAGCCATCTG Quence n #: NM_004 .1646 21   CTTGTTTTCC GGTGTAATTT CACATCAAAC AAAGGTCCAAA TTTCTTAACC GCCACAAGT TTCTTATACC TTCTTATACC TTCTTGTTTCAACC AAATCATCC AAAACTAAAC AACACTAGC AATTTGGTGG AATTTGGTGG AATTTGGTGG AATTTGGTGG AATTTGGTGG AATTTGGTGG AATTTGGTGG AATTTGGTGG AATTTGGTGG AATTTGGTGC AACACTAGC ACCACACTGCC ACCACACTACC AACACTAGCC	ATGCTCTTTT CCTGTGTTAG AGCCTGACCC TCGCTGGCAA CCCCTTCAAA  696.1  31	GCGATTAGGA AAGCAGCTGT AAAAAAAA  41    AAATGAAATG CTTAATTGCC GCATTTAAAAA AACCTGGAT TOTGATGCCCTG GGGTTTCGTT TTGTGGACCTC TTGGTAACC AGACTCTCACA AAAAGATGAT TTCCTCTCTT TTCCTCTCTT	GATACCAAAA GGGGGTCCCA TCTCAGGCGT TAATTGAAAC  51   CCTTAGAAAA CCATCTGTGG AGAAGAGGCA AGAGCAAATTG ATGGACCAAGA GGTGCTATTA CCCATCTTTC ACCAATACT CTGACTTTTC ACCAATACT CTGACTTTTC ACCAATACT CTGACTTTC ACCAATACT CTGACTTTTC ATCAAGGACA AATCAAAGTG GAAGAAAGTG GAAGAAAGTG AAGAAAACTT	540 600 720 768 60 120 180 240 300 420 480 540 600 660 720 780 900 960 1020 1080
50 55 60 65	CACGGCGTT AAAAGCAACA GTGGAGGATGA TCTCTAGATC AAGACTGAAG Seq ID NO: Nucleic Ac Coding seq I I CTTGGCTCTT TCATGCTGAT TCATGCTGAT TCATGCTGAT GTTGGATTGAT GTTGGATTGAT TACCCGGTTT TCAAAAAGTGA TTTTGGACC TATTTGGAC TTTTGGACC TATTTGGAC TATAGGCTA TATAGGTTA TCTTCACAT TCT	GGATCCTGG GCTGAAGCA CTTTCCTCTG GATCAATAAA  107 DNA Se id Accessio usnce: 183. 11   ACAATGCTCA TCCTGAACAC GAGGGAGGGG TTTCCTTGTGATCAATACAC CACAGCATCACACAC ACTAGCACACACACACACACACACACACACACACACACAC	TTGTTGCTGG GGCACAAAAT TGCCTCCAGC TTTCCCTCTC CAGCCATCTG Quence n #: NM_004 .1646 21   CTTGTTTTCC CAGTGAAACT CACATCAAAC AAGGTCCAAC GTCTTTCCAGC GTCTTTCAACCT GCCACAAGT TTCTTACAGCT TTCTTACAGCT TTCTACAGCT TTCTACAGCT AAACTGCCAACAAC ACACTGCCAACACT CTCACAGCAACACT CTCACAGCAACACT CTCACAGCAACACT CTCCACACACACT CTCCACACACACT CTCCACACACA	ATGCTCTTT CCTGTGTTAG AGCCTGACCC TCGCTGGCAA CCCCTTCAAA  696.1  31	GCGATTAGGA AAGAGCTGT AAGAAAAA  41  AAATGAAATG CATTAAATGC CATTAAAATGAAATGA	GATACCAAAA GGGGGTCCCA TCTCAGGCGT TAATTGAAAC  51   CCTTAGAAAA CCATCTGTGG AGAAGAGGCA GGGCATGGGG ATGACCAAGA GTTACTGGTG ATGCAATACT CCCATCCATTA CCCATCCATTA CCCATCCAT	540 600 720 768 60 120 180 240 480 540 600 660 720 780 840 900 960 1020 1080 1140
50 55 60 65	CACGGCGTT AAAAGCAACA GTGGAGGATGA TCTCTAGATC AAGACTGAAG Seq ID NO: Nucleic Ac Coding seq I I CTTGGCTCTT AGAGTAACAT AGAGTTCTT TCATGCTGAA GATGGATGA GATGGATGA TTTGTGAAT GATATCTGAT TCAAAAACC TTTTGGAGC TTATTTGGAGC TATTTGGAGC TATTTGGAGC GTAAAAGTGA CAGAGGCACC GTACTACGGC AAGAGGTCTC ATAAGGTTT TCTCTACACT TTCTCTACAT TTCTCTACAT TTCTCTACAT TTCTCTACAT TTCTCTACAT TTCTCTACAT TTCTCTACAT TTCTCTACAT TTCACCTGGTT TTCTCTACAT TTCACCTGGTT TCTCTACAT TTCACCTGGTT TCACACTGGTT TCTCTACACTT TCACCTGGTT TCACCTGT TCACCTGTT TCACCTGT	GGAATCCTGG GCTTGAAGCA CCTTTCCTCTG GATCAATAAA  107 DNA Se id Accessio uence: 183. 11	TTGTTGCTGG GGCACAAAAT TGCCTCCAGC TTTCCCTCTC CAGCCATCTG Quence II #: NM_004 .1646 21   CCTTGTTTTCC GGTGTAATTI CACATCAAAC AAGGTCCAAC GTCTTCTCTCAAC GTCTTTCTCAAC TTCTCTAAAC TTCTCAAAC TTCTCAAAC AACACACTGC AAATTGGTGG AACACTGC AACAACTGC AACAACTAGC AACAACTGC AACAACTGC AACAACTAGC AACAACAACTAGC AACAACAACTAGC AACAACTAGC AACAACTAGC AACAACTAGC AACAACAACTAGC AACAACTAGC AACAA	ATGCTCTTT CCTGTGTTAG AGCCTGACCC TCGCTGGCAA CCCCTTCAAA  696.1  31	GCGATTAGGA AAGCAGCTGT AAAAAAAA  41    AAAATGAAATG CATTAAAATGACG CATTAAAATGACG CATTAAAATGACG CATTAAAATGACG CATTAAAATGACG CATTAAAATGACGG CAGCTCCCTG GGCTTTCGTT CTGGGACAGGG GCCTTTAGG CTGGACAGGG GCCTTTAGG CAGGACTCCCT CAGGACTCCCT CAGGACTCCCT CTGGACAGGG CAGTTTCTC CAGGACTCCCT CAGGACAGGG CAGTTTCCT CAGGACACT CAGCACACT CAGGACACT CAGGACAC CAGGACACT CAGGACA	GATACCAAAA GGGGGTCCCA TCTCAGGCGT TAATTGAAAC  51   CCCTTAGAAAA CCCATCTGTGG AGAAGAGGCA GGACGATGGG ATGACCAAGA AGACCAAGTTACTGTTACTGTTACTGTTACTGTTACTGTTACTGTTACTGTTACTGTTACTGTACTACAGAAATACT ACCAATCATTACAGCACA AATCAAGAGCA AATCAAGATCAT GAAAAATCCT AAGAAAATCCT AAGAAAACTC AAAAAAAGTG GAAAAACTC AAAAAACTC AAAAAACTC AAAAAACTC AAAAAACTC AAAAAACCT ATCACCTACCT	540 600 720 768 60 120 180 240 300 420 480 540 600 660 720 780 840 900 1020 1020 1140 1200
50 55 60 65	CACGGCGCTTA ANAAGCAACA GTGGAGATGA TCTCTAGATC ANGACTGAAG Seq ID NO: Nucleic Ac Coding seq 1   CTTGGCTCTT AGAGTAACAT AGGATTTCTT TCATGCTGAT GTTGGATGAT GTTGGATGAT GTTGGATGAT GATACCGGTTT TCAAAAAACG TATTTGGACA TATTTGGACA GATATCTGAT TCAAAAAGT CAAAAGTCAAAAGTCAAAAGTCAAAAGTCAAAAGTCAAAAGTCAT TCAAAAGTTATTCACCGTTCTT ATAAGGTTATTCACTGAT TCTCTACACT TTCACCTGAT TCTCTCTACAT TTCACCTGAT TTCTCTACAT TTCACCTGGTT TTCTCTACAT TTCTCTACAT TTCTCTTACAT TTCTCTTACAT TTCTCTTACAT TTCTCTTACAT TTCTGTACGTTAT TT	GGATCCTGG GCCTGAAGCA CCTTCCTCTG GATCAATAAA  107 DNA Se id Accessio usence: 183. 11   ACAATGCTCA TCCAGAAAAC TGCTGAACAC TTCTTGTGG ACTCATCATCAC TTCAGAAAAC TGCTGAACAC TTGTGAGACAC TTTGTGGAGAC TTTGTGGAGAC TTTGTGGAGAC TATTACTTGC TTGTGGAGC TTTGTGGAGC TATTACTTGC TTGGGAGC TATTACTTGC TTGGGAGC TATTACTTGC TTGGGAGC TATTACTTGC TAGCCAGAGC TATTACTTGC TAGCCAGAGC TATTACTTGC TAGCCAGAGC TAGCAGAGC TAGCA	TTGTTGCTGG GGCACAAAAT TGCCTCCAGC TTTCCCTCTC CAGCCATCTG Quence n #: NM_004 .1646 21   CTTGTTTTCC GGTGTAATTT CACATCAAAC TTTTTCTCACC GGCACAAGTI TTCTTATACC CAAACAACACT ACACACAGGC ACTACATAGGT ACACACTGCC ACACCTAGCC CAAACACACC CAAACAACACC CAAAACAACACC CAAAACAAC	ATGCTCTTTT CCTGTGTTAG AGCCTGACCC TCGCTGGCAA CCCCTTCAAA  696.1  31	GCGATTAGGA AAGCAGCTGT AAAAAAAA  41    AAATGAAATG CTTAATTGCC CATTTAAAAA AACCCTGGAT TOTGATGCCCTG GGGTTTCGTT TTTGTGACC TGGGACAGG GCCTTTAAGA CTGGACAGG GCACTTAGA AGAGTCTACC AGACCCTCA AAGAGTCTACC AGACACCTC AGACAGG TTCTCACAA AAGAGTCTACC TTCTGGATACC TTCTGCATGC TTCTCGATGC TTCTCGATGC TTCCTCTT AGACATACTTC CATGGATGGGT TTCTCTCTT CATGGATGGT	GATACCAAAA GGGGGTCCCA TCTCAGGCGT TAATTGAAAC  51   CCTTAGAAAA CCATCTGTGG AGAAGAGGCA AGAGCAAATTG GGTTACTATTA CCCATCCATTA CCCATCCATTA CCCATCCAT	540 600 720 768 60 120 180 240 480 540 600 660 720 780 840 900 960 1020 1080 1140
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	CACGGCGTT AAAAGCAACA GTGGAGGATGA TCTCTAGATC AAGACTGAAG Seq ID NO: Nucleic Ac Coding seq I CTTGGCTCTT AGAGTACAT AGGATTACTT TCATGCTGAT GTTGGATTCT TCATGCTGAT GTTGGATTGT TTGGAACAT GATATCTGAT TACCGGTTT TCAAAAAACT TATTTGGAC GTATTTGGAC TTTTGGAC TATTTGGAC TATTTGAC TTTCACAT TTCACCTGGT TTTCACAT TTCACCTGGGT TTTCACCTGGGT TTTCACCTGGGT TTTCACCTGGGT TTTCACCTGGGT TTTCACCTGGGT TTTCACCTGGGAC AAAACTGGAC	GGATCCTGG GCCTGAAGCA CCTTCCTCTG GATCAATAAA  107 DNA Se id Accessio uence: 183. 11	TTGTTGCTGG GGCACAAAAT TGCCTCCAGG TTTCCCTCTC CAGCCATCTG Quence n #: NM_004 .1646 21   CTTGTTTTCC GGTGTAATTT CACATCAAAC GTCTTTCCTGC GTCTTTCAAC GTCTTTCCTG GTCTTTCAAC GTCTTTACAC GTCTTACAC GTCTTACAC GTCTTTCAAC ACACACTGC AACACCTGC AACACGAAC GTCTTTTCTC AAAACACTGC CAACACC GTCAACACAC GTCAACACAC GTCTTTTCTCC CAAAACACTGC CAACACC	ATGCTCTTTT CCTGTGTTAG AGCCTGACCC TCGCTGGCAA CCCCTTCAAA  696.1  31	GCGATTAGGA AAGCAGCTGT AAGAAAAA  41  AAATGAAATG CCTTAATAGCC CATTTAAAAT AACCTGGAT TTGGTGACCT TTGGTAGCC AGGTCCCTC TTGGTAGCC AGGTCTTAAGA CCTGATTGGTC AGGTCTTAAGA AGGTCTACC AGGTCTTCT TTGGTAACCT AAGAGTGAC AAGAGTGAC AAGAGTGAC AAGAGTGAC TTCCTCTCT TAGGAACCTC TTCTGATAGCC CATCTCCTCT CATGGAACCTC CATCTCCTCT CATGGAACCTC TTCTGGAACCT CATCTCTCGATGC TTCTGGAACCT CATCTCTCGATGC TCCTTCGAATGCC TTCTCGAATGCC TTCTCGAATGCC TCTTCTGGATGCC TCTCTCGATGC	GATACCAAAA GGGGGTCCCA TCTCAGGCGT TAATTGAAAC  51   CCTTAGAAAA CCATCTGTGG AGAAGAGGCA GGACGATGGG ATGACCAAGA GGACCAAGA AGGCAAATACT CTGACTTTTA CCCATCCATA ACCAATACT CTGACTATTA CCCATCCATA ACCAAAAACT CAACAAAAGT GAAGAAAGT GAAGAAAGT GAAGAAAGT GAAGAAAGT AAACAAACT TATCACTTC TCTTACCTTC TCTTTC TCTTTT TCTTTT TCTTTC TCTTTC TCTTTT TCTTTT TCTTTT TCTTT TC	540 600 720 768 60 120 180 240 300 360 420 480 540 960 960 1020 1080 1140 1200 1260
50 55 60 65	CACGGCGTT AAAAGCAACA GTGGAGGATGA TCTCTAGATC AAGACTGAAG Seq ID NO: Nucleic Ac Coding seq I I CTTGGCTCTT AGGATTCTT TCATGCTGAA GATGAACAT AGGATTTCTT TCATGCTGAA GATGATTGG TTTGTGAAT GATATCTGAT TACACGGTTT TCAAAAACG TATTTGGAC CAGAGGCACC GTACTACGC AAGAGTTCT ATAAGGTTAT TCTCTACAAT TCTCTCACAG AAAACTGGA ACCTGCTTTTGGACC CACTGCTTTTTTTTTT	GGAATCCTGG GCTTGAAGCA CCTTTCCTCTG GATCAATAAA  107 DNA Se id Accessio uence: 183. 11    ACAATGCTCA TCCAGAAAAC TCCAGAAAAC TCCAGAAAAC TCCTGAACAC GAGGGAGGGG TGTGATCAT ACTTGATCAT ACTTGATCAT ACTTGATCAT ACTTGACACAC GAGGTGTGC ATTGCACACAC TTACAAAAA TATTCTTGC TATTGCACCTCT ATTGCACACAC ACGAGCTGC ATTGCACACAC ACGACACGC ACCACACGC ATTACATCT ATTACTTGC ATTACTTACACAC ACAATGCCT TTACACACAC ACAATGCCT TTCGTGGAGC ACAATGCCT TTCGTGGAGC ACAATGCCT TTCGTGGAGC ACAATGCCT TAAGAACTAC TAAGAACTAC TAAGAACTAC TAAGAACTAC TAAGAACTAC TTAAGAACTAC TTAAGAACTAC TTAAGAACTAC TTAAGAACTAC TTCGTGGAGC TTCGTGAGC TTCGTGGAGC TTCGTGGAGC TTCGTGGAGC TTCGTGGAGC TTCGTGGAGC TTC	TTGTTGCTGG GGCACAAAAT TGCCTCCAGC TTTCCCTCTC CAGCCATCTG Quence n #: NM_004 .1646 21   CTTGTTTTCCT CAGCTATTTCAAAA AAAGTACAAA TTCTTTCAAAAA TTCTTATAAAA AAACTACCT CACAAACTAGC AAAACTAGCT AAAACAACTAGC AAAACAACTGC CAAAAACTAGCT CAAAACACTGC CACACATTTC CCTGGCATTG CTGGCATTG CTGCCATTG C	ATGCTCTTT CCTGTGTTAG AGCCTGACCC TCGCTGGCAA CCCCTTCAAA  696.1  31	GCGATTAGGA AAGCAGCTGT TCGTGCCCTG AAGTATGATC AAAAAAAA  41	GATACCAAAA GGGGGTCCCA TCTCAGGCGT TAATTGAAAC  51	540 600 720 768 60 120 180 240 300 360 420 780 840 600 720 780 840 900 960 1020 1080 1140 1220 1220 1220
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	CACGGCGTT AAAAGCAACA GTGGAGGATGA TCTCTAGATC AAGACTGAAG Seq ID NO: Nucleic Ac Coding seq 1   CTTGGCTCTT AGAGTACAT AGGATTACTT TCATGCTGAT GTTGGATCTT TCATGCTGAT GTTGGATTGT TTTTGGACAT GATATCTGAT TACCCGGTTT TCAAAAAACC TATTTGGAC GTACTACGC AAGAGTTCTA ATAAGGTTA TCTCTACAT TCACCTGGT TTTCACCTGGT ATAAGGTTA ATAAGGTTA TCTCTACAT TCACCTGGT TTTCACCTGGT TTTCACCTGGT TTTCACCTGGT TTTCACCTGGT TTTCACCTGGT AAAACTGGAA AAACTGGAA AACCTGCTTGC CCACCTTTGC CACCTTTGC CCACCTTTGC CCACCTTTGC CCACCTTTGC CCACCTTTGC CCACCTTTGC CCACCTTTTCACACA ATTCTTACAGT A	GGATCCTGG GCCTGAAGCA CCTTCCTCTG GATCAATAAA  107 DNA Se id Accessio uence: 183. 11	TTGTTGCTGG GGCACAAAAT TGCCTCCAGG TTTCCCTCTC CAGCCATCTG Quence n #: NM_004 .1646 21   CTTGTTTTCC GGTGTAATTT CACATCAAAA AAAACTACCT AAACTACCAA AAACACTGCAA ACACACTGCAAACAAACACTGC CTCACACAACAACAACACACTCTTCCAAAACAACACTGC AAAACACTGCCAAACAACACCCAACTTCTTCCAAAACAACACTGCCAAAACAACACTGCCAAAAACACTGCCAAAAACACTGCCAAAAACACTGCCAAAAAACACTGCCAAAAAACACTGCCAAAAAACACTGCCAAAAAACACTGCCAAAAAACACTGCCAAAAAAACACTGCCAAAAAACACTGCCAAAAAACACTGCCAAAACAACACCCAACACTTCCCAAAAAAACACTGCCAAAAAACACTGCCAACAACTTCCCCAAAAAACACTGCCAACAACAACACCCAACACTTCCCCAAAAAACACTGCCAACAACAACACCCAACACACTCCCAACAACAACACCCAACACACACACTCCCCACACACACCCCAACCACACTCCCCACACACACCCCAACCACACTCCCCACACACACCCCACCA	ATGCTCTTT CCTGTGTTAG AGCCTGACCC TCGCTGGCAA CCCCTTCAAA  696.1  31	GCGATTAGGA AAGCAGCTGT AAAAAAAA  41    AAATGAAATG CTTAATAGCC CATTTAAAAT AACCTGGAT TOTGGTACCC CAGTTCGTT TTGGTGACCC CAGTTCGTT TTGGTACCC AGGCTCTCACA AAGAGTGAC AGGCTCTCCT AGCATTGCCC TTGGGTACCC AGGCTCTCCT AGCATCCCC TTCCGGTTGAC TTCCTCGGTGC TTCCGGTGGA CATCCTCTGG ACCTACCC ACTGGTTGACC TTCCGGTTGACC TTCCGGGTGC ACTGGTTGACC TTCCTGGATGC TTCCTGGATGC TTCCTGGATGC TTCCTGGATGC TTCCTGGATGC TTCCTGGATGC TTCCTGGATGC TTCTGGATGC TTCTGTGT TTCTGGATGC TTCTGGATGC TTCTGGATGC TTCTGGATGC TTCTGGATGC TT	GATACCAAAA GGGGGTCCCA TCTCAGGCGT TAATTGAAAC  51   CCTTAGAAAA CCATCTGTGG AGAAGAGGCA GGACGATGGG ATGACCAAGA GGCCATTCTTC ACCAATACT ACCAATACT CCCATCCATA ACCAATACT CACAATACT CACAATACT CACAATACT CACAATACT CACAATACT CACAATACT CTACACTTTC CACAATACT CATCACTTTC CACAATACT CATCACTTTC CATCACTTTC CATCACTTTC CATCACTTTC CATCACTTTC CATCACTTC CATCACT CATCACTTC CATCACT CATCACTTC CATCACT CATCACTTC CATCACTTC CATCACTTC CATCACT CATCACTTC CATCACT	540 600 720 768 60 120 180 240 360 420 480 900 660 660 660 660 1020 1020 1020 1140 1200 1260 1320 1380
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	CACGGCGTT AAAAGCAACA GTGGAGGATGA TCTCTAGATC AAGACTGAAG Seq ID NO: Nucleic Ac Coding seq I CTTGGCTCTT TCAGATCATC AGGATTACTT TCATGCTGAT TCATGCTGAT GTTGGATTGT TTTTGGAAT GATATCTGAT TACCCGGTTT TCAAAAACG TTTTGGACC TATTTGGACC TATTTGGACC AGAGGTACT ATAAGGTTAT TCTACAT TCTACCTGGT TTTCTACAT TCTACCTGGT TTTCTACAT TCTACCTGGT TTTTGGACC AGAGGTCT ATAAGGTTAT TCTACCTGGT TTTCTACAT CCTGGTTGG CCATCTTTCG ATTCTACAG CTGGACCACC	GGATCCTGG GCTTGAAGCA CCTTTCCTCTG GATCAATAAA  107 DNA Se id Accessio uence: 183. 11   ACAATGCTCA TCCTGAACAC GAGGGAGGGG TTTCCTTGTGAACAC GAGGAGGGGGGG TTTCCTTGTGAACAC TTTCCTTGTGAACAC TTTCCTGAACAC GAGAGATCCTCA TTTCGTGAAC TTTAGGAGGCT TTAGGAGGCT TTAGGAGGCT TTAGGAGGCT TTAGGAGGCT TAGGAACAGT TTAGGAGGCT TAGGAGGCT TAGGAGAGT TTAGGAGGCT TAGGAGGCT TAGGAGGCT TAGGAGGCT TAGGAGGCT TAGGAGGCT TAGGAGGCT TAGGAGGCT TAGCACACAC TTAGGAGGCT TAGGAGGCT TAGCAGAGCT TAGGAGGCT TAGGAGGCT TAGGAGGCT TAGGAGGCT TAGGAGGCT TAGGAGAGCT TAGGAGGCT TAGGAGAGCT TAGGAGGCT TAGGAGGCT TAGGAGAGCT TAGGAGGCT TAGGAGGCT TAGGAGGC TGTTTAGCC TGTGTGAACACAGGTT TAGGAGGCT TAGGAGGC TGTTTAGCC TGTTTAGCC TGTTTAGCC TGTTTAGCC TGTTTAGCC TGTTTAGCC TGTGT TAGGAGGC TGT TTTCTTTTGT TGT TTTCTTTGT TGT TTTCT TTTTCT TTTTTT	TTGTTGCTGG GGCACAAAAT TGCCTCCAGG TTTCCCTCTC CAGCCATCTG Quence n #: NM_004 .1646 21   CTTGTTTTCCTC GGTGTAATTI CACATCAAAC GAAGTCCAAC GTCTTTCAAC GTCTTCTCTC GTCAACACAC GTCTTAAC GTCAACACAC GTCTACACACAC CTACCTAGC AACACCTGC AACACCTGC AACACCTGC AACACCTGC CACACATTT CTCACCACATTT CTCTGGGATTT CTCTGGGATTT CTCTGGGATTT CTCTGGGATTT CTCTGGGATTT CTTGGGATTT CTTGGTATT CTTGGGATTT CTTGGGATTT CTTGGTATT CTTGGTATT CTTGGGATTT CTTGGTATT CTTGGGATT CTTGGTAT CTTGGTAT CTTGGTAT CTTGGTAT CTTGGTAT CTTGGTAT CTTGTT CTTGTT CTTGT CTTTT CTTGT CTTT CTTGT CTTT CTTT CTTT CTTT CTTT CTTT CTT C	ATGCTCTTT CCTGTGTTAG AGCCTGACCC TCGCTGGCAA CCCCTTCAAA  696.1  31	GCGATTAGGA AAGCAGCTGT AAGTATGATC AAAAAAAA  41	GATACCAAAA GGGGGTCCCA TCTCAGGCGT TAATTGAAAC  51   CCTTAGAAAA CCCTTAGAAAA CCATCTGTGG AGAAGAGGCA GGAGGATGGG ATGACCATA CCTTACTGTG ATGACTTTC ACCAAATACT CTGACTTTC ACCAAAAAGTG GACAAAAGTG GACAAAAGTG AAAAAAGTG AAAAAAGTG AAAAAAGTG AAAAAAGTG AAAAAAGTG CATCAAAAAGTG CATCAAAAAGTG CATCAAAAAGTG CATCAAAAAGTG CATCACTATA CATCAAAAGTG CATCAAGAAAGTG CATCACTATATCCTTCCTTCCTTCCTTCCTTCCTTCCTT	540 600 720 768 60 120 180 240 480 540 600 660 660 900 1020 1020 1140 1200 1140 11500 11500
50 55 60 65 70 75	CACGGCGTT AAAAGCAACA GTGGAGGATGA TCTCTAGATC AAGACTGAAG Seq ID NO: Nucleic Ac Coding seq I I CTTGGCTCTT AGAGTAACAT AGAGTTCTT TCATGCTGAA GATGGATGGA TCTTTGTGAAC GATGGATGGA TTTGTGAAT TACCGGTTT TCAAAAACC TATTTGGAG CAGAGGCACC TATTTGGAG GTACTACCGG TATTTGGAG GTACTACGG AAGAGTTCT ATAAGGTTAT TCTCTTCTGAG ACTCCTTGG ACTCCTTGG ATTCTGAGC ACTCCTTGG ATTCTCTGGACCAC CTGGACCACC CTGGACCACC CTGGACCACC CTGGACCACC CTGGACCACC CTGGACCACC CTGGACCACC CTGCACCACC CTGGACCACC CTGCACCACC CTCTTGGACCACC CTGGACCACC CTCTCTTGGACCACC CTGGACCACC CTCTCTTGGACCACC CTCTCTTGGACCACC CTCTCTTCTTGAGC ACTCCTTTGC ACTCTCTTGC ACTCTTCTTGTAGC ACTCCTTCTTGC ACTCTCTTGC ACTCTTCTTGCACCACC CTCTCTTCTTGTAGC ACTCTTCTTGCACCACC ACTCTTCTTGCACCACC ACTCTTCTTGCACCACC CTCTTCTTGTAGC ACTCTTCTTGCACCACC ACTCTTCTTGCTTCTTTCTTTTCT	GGAATCCTGG GCTTGAAGCA CCTTTCCTCTG GATCAATAAA  107 DNA Se id Accessio uence: 183. 11	TTGTTGCTGG GGCACAAAAT TGCCTCCAGC TTTCCCTCTC CAGCCATCTG Quence n #: NM_004 .1646 21   CCTTGTTTTCC CAGCTAAAC AAGGTCCAAC TTTTTCCTGAAAC TTCCTCATCAAC AACACTGCC CACACAACAAC AACACTGCC AACACTGCC CACACAACAC CTCCTTTTTTCTGAACCTCC CACACACTCC CACACACTCC CACACACTCC CACACACTCC CACACACTCC CACACACTCC CACACACTCC CACACACTCC CACACACTTCC CACCACACTTCC CACACACTTCC CACACACTCC CACACACTC CACACACTCC CACACACTC CAC	ATGCTCTTT CCTGTGTTAG AGCCTGACCC TCGCTGGCAA CCCCTTCAAA  696.1  31	GCGATTAGGA AAGCAGCTGT TCGTGCCCTG AAGTATGATC AAAAAAAA  41	GATACCAAAA GGGGGTCCCA TCTCAGGCGT TAATTGAAAC  51	540 600 720 768 60 120 180 240 360 420 480 540 600 660 720 1080 1140 1260 1320 1140 1560 1560 1620
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	CACGGCGTT AAAAGCAACA GTGGAGGATGA TCTCTAGATC AAGACTGAAG Seq ID NO: Nucleic Ac Coding seq I I CTTGGCTCTT AGAGTAACAT AGGATTACTT TCATGCTGAT GTTGGATCTT TCATGCTGAT GTTGGATTGT TTGTGAAT GTTTGGACAT GATATCTGAT TACCCGGTTT TCAAAAACT TATTTGGACC TATTTGGACC TATTTGGACC TATTTGGACC TATTTGGACT TCAAAAGTTAT TCACAGGTACT ATAAGGTTAT TCTCTACAT TTCACTGGT TTTCTTCACAT TTCACTGGT TTTCTTCACAT TTCACTGGT TTTCTTCACAT TTCACTGGT TTTCTTCACAT TTCACTGGT TTTCTTCACAT TTCACTGGT AAAACTGGAT ACTGCTTTGC CTGGACCAC ACTTCTTTGA AAAACTGGAT AAAGTGAACTGGAT ATTCTACAGG CTGGACCAC ACTTCTTTGA	GGATCCTGG GCCTGAAGCA CCTTCCTCTG GATCAATAAA  107 DNA Se id Accessio uence: 183. 11	TTGTTGCTGG GGCACAAAAT TGCCTCCAGG TTTCCCTCTC CAGCCATCTG Quence n #: NM_004 .1646 21   CTTGTTTTCC GGTGTAATTT CACATCAAAA AAACACTCGT AATTTGTTCTCTG AAACACTAGGAACA ACACACTAGGAACA CTCTTTTCTCTGCAGGAACAAACACTGC CAGAACAAACACTGCC CACACACTTTCCCTGCAAACACACTTCTTCTCCCCACACTTTCCCCCCACACTTTCCCCCC	ATGCTCTTTT CCTGTGTTAG AGCCTGACCC TCGCTGGCAA CCCCTTCAAA  696.1  31    CAATGCAGCA ATTTTCTTC GGATCTTCTG CTTACACTAG TGATTGTGT TAAAGGCTTCAG ATTTTCTTCT AAGAGATTAAAG CCTTCTAGTAT ATAAAGGCAC ATTGCCTGTTCT GATTGTAGAT ATAAAGCAC ATGATCAGTTCAG ATCTGTAGAT ATCTGCCTGT CGTTTGACAT CTCAGTTAAAAGCAC ATGAGACAGT AAGACTTTACCC CACTACTTAC CCACTACTTAC CCACTTCTAGTAT ATACTGCCTG CCAGTTTCT AAGAGACACT AAGAGACCT AAGAGACACCT AAGAGACCT AAGAGACACCT AAGAAGACCT AAGACACCT AAGAGACACCT AAGAGACCT AAGAGACACCT AAGAGACACCT AAGACACCT AAGAGACACCT AAGACACCT AACACCT AAGACCT AAG	GCGATTAGGA AAGCAGCTGT AAGAAAAA  41    AAATGAAATG CTTAATTGCC GCATTAAAAA  AAATGAAATG	GATACCAAAA GGGGGTCCCA TCTCAGGCGT TAATTGAAAC  51   CCTTAGAAAA CCATCTGTGG AGAAGAGGCA AGACCAAGA GGACCAACATTC ACCATCATTA CCCATCCATTA ACCCATCCAT	540 600 720 768 60 120 180 240 300 420 480 540 600 660 720 780 840 900 9140 1140 1120 11320 1140 11500 11500 1160 1160
50 55 60 65 70 75	CACGGCGTT AAAAGCAACA GTGGAGGATGA TCTCTAGATC AAGACTGAAG Seq ID NO: Nucleic Ac Coding seq I I CTTGGCTCTT TCAGGCTCTT TCAGGCTCTT TCATGCTGAT AGGATTACTT TCATGCTGAT GTTGGATTGAT TTTTGGAAT GTTTGGATTGAT TACCCGGTTT TCAAAAAAGTTGA TATTTGGACC TATTTGGACC TATTTGGACC TATTTGGACC TATTTGGACC AAGAGTTCTA ATAAGGTTAA TCTCTCTGAA AACTTGGT TCACCTGGT TTTCTGACAT TCACCTGGT TTTCTGACAT CCATCTTTGGACCAC CCATCTTTGGACCAC ACTTCTTCTGAAAAAGTGAA AACTTCACAG AAAAGTGAAAAAAGTGAA AACTTCTCTGAAAAAAGAAAACAAAAACAAAAACAAAAAACAAAAAACAAAAAA	GGATCCTGG GCCTGAAGCA GCCTCCCCA CCTTCCTCTG GATCAATAAA  107 DNA Se id Accessio uence: 183. 11   ACACATGCTCA TCCTGAACAC GAGGGAGGGG TTCCTGAACAC TTCCTTGAACAC GAGGGAGGGG TTTCCTTGTGA TTCCTTGACAC CACACACACAC TATGGCTCT TATGGCTCT TATGGCAC TATGGGCCT TATGGGCCT TATGGGCC TATGTGGAACAC TATGTGGCAC TATGTGGCAC TATGTGGCCT TATGTGACAC CACACAGAC TATGTGGCCT TAGGACACAGC TATGTGGCCC TAGGACACAC TATGTGCAC TAGGACACAC TATGTGCAC TAGGACACAC TATGTGCAC TAGGACACAC TAGGACACAC TAGACACAC TAGACACAC TAGACACAC TAGACACAC TAGACACAC TAACACAC TAGACACAC TAACACAC TAACACAC TAACACAC TAACACAC TAACACAC TAACACAC TATACCC CTAAACACAC AAACACC CTAAACACAC CCTAAACACAC CCTAAACAC CCTAAACAC CCTAAACAC CCTAAACACAC CCTAAACAC CCCC CCCAC CCCC CCCAC CCCC CCCAC CCCC CCCC CCCC CCCC CCCC CCCC CCCC CCCC	TTGTTGCTGG GGCACAAAAT TGCCTCCAGC TTTCCCTCTC CAGCCATCTG Quence n #: NM_004 .1646 21   CTTGTTTTCCTC GGTGTAATTI CACATCAAAC GTCTTTCAACC GTCTTCAACC GTCTTACACC GTCTTACACC CTACACACACT CTACACCACAC GTCTACACC CACACTTTC CTGCAATT CTCTGCAATT CTCTGCTATT CTCTCTCTCT CTTGCTAATT CTCTCTCTTCT CTCTCTTTT CTCTCTCTTCT GTCTTTTTCT CTCTCTTTT CTCTCTCT	ATGCTCTTT CCTGTGTTAG AGCCTGACCC TCGCTGGCAA CCCCTTCAAA  696.1  31	GCGATTAGGA AMGCAGCTGT TCGTGCCCTG AMGTATGATC AMAAAAAA  41  AAATGAAATG CCTTAATTGCC CATTTAAAAT AACCTGGAT TTGGTGACCTC TGGGTGACCT TTGGTGACCT CTGGATGGGC AGGCTCTTCGTT TTGGTGACCT AGGTTCTT TTGGTGACCT AGGTTCTT AGGATGGGC ACTGCCCTC AGGTTCTT TTGTGTACCT CATCTCCTCT CATCTCCTCT TGGTAGCT CATCTCCTCT TGGTAGCT CATCTCCTCT TGGTAGCT TTCTCGATGG TTCTCGATGG TTCTCGATGG TTTTTTGGATGCT TTTTTTGGATGCT TTTTTTGGATGCT TTTTTTGGATGCT TTTTTTTGGATGCT TTTTTTTGGATGCT TTTTTTTTGT AGGATACAATT TTTTTTTTTT	GATACCAAAA GGGGGTCCCA TCTCAGGCGT TAATTGAAAC  51   CCTTAGAAAA CCATCTGTGG AGAAGAGGCA GGGCATATTG AGACCAAGA GGACCAAGA GGACCAAGA GACCAAGA ATCAAATACT CCCATCCATA CCCATCCATA ACCAATACT ACCAATACT TCTACATTTC ATCAAGACA AATCAAAGTG GAAGAAAGTG GAAGAAAGTG GAAGAAAGTG TCTTACCTT CTTACCTTG TCTTACCTT CTTACCTTG TCTTACCTT CTTACCTTTC TCTTACCTT CGCCTTCTTACTA CGCCTTCTTACTA CGCCTTCTTACTT CGCCTCTTTTC TCTTTACCTT CGCCTCTTTTC TCTTTACCTT CGCCTCTTTTC TCTTTACCTT CGCCTCTTTC TCTTTACCTT CGCCTCTTTC TCTTTACCTT CGCCTCTTTC TCTTTACCTT CGCCTCTTTC TCTTTACCTT CGCCTCTTTC TCTTTACCTT CGCCTCTTTC TCTTTACCTT CGCCTCTTCT CGCCTCTTTC CGCATCCCTT CGCCTCTTC CGCATCCCT CCATTCCCCT CCATTCCCT CCATTCCCCT CCATTCCCCT CCATTCCCCT CCATTCCCCT CCATTCCCCT CCATTCCCT CCATTCCCCT CCATTCCCT CCATTCCCCT CCATTCCCT CCATTCCT CCATTCCCT CCATTCC	540 600 720 768 60 120 180 240 480 600 660 660 720 780 840 900 960 1020 1140 1200 1320 1380 1440 1560 1620 1620 1620 1630
50 55 60 65 70 75	CACGGCGTT AAAAGCAACA GTGGAGGATGA TCTCTAGATC AAGACTGAAG Seq ID NO: Nucleic Ac Coding seq I I CTTGGCTCTT AGAGTACAT AGATTCTT TCATGCTGAA GATGGATGA GATGGATGA TTTGTGAAT GATATCGAT TCAAAAACC TATTTGGAGC TATTTGGAG TCAAAAGTGA TCAAAAGTGA TCAAAGTGA TCAAAGTGA TCAAAGTGA TCAACGC TATTTGGAG AAAACTGGA AAAACTGGAC TCTTCTTGAGA AAACTGGGTTT TCACCTGGTTTTCTTCTGAGA AAACTGGACACA ACTTCTTCTGAAAAAACAAAAACAAAAAAAAAA	GGAATCCTGG GCTTGAAGCA CCTTTCCTCTG GATCAATAAA  107 DNA Se id Accessio uence: 183. 11	TTGTTGCTGG GGCACAAAAT TGCCTCCAGC TTTCCCTCTC CAGCCATCTG Quence n #: NM_004 .1646 21   CCTTGTTTTCC CAGCTATCAAAC AAGGTCCAAAC TTTTCCTGC GTCTTTCTAAAC TTCTCTAAAC TTCTCTAAAC ACACACTGC AAAACTACCA AACACTGCC CACCACTATCC CACCACTTTCC CACCACTTTCC CACCACTTTC CTGGCATTGC TTTGGGACTTTC CTGGCATTGC TTTGGGACTTC CTGGCATTGC TCTGCTAAAAG TCTTCTCTCTG AACCTGCAACAGG TCTTTTCTCC CACCACTTTC CTGGCATTGC TCTGCTTAAAT TCTCCTCTCTT GACCTGCAAGG TCTCTCTCTT TTGGTAAAAG TCTCTCTCTCT GACCTGCAAGG TCTCTCTCTCT TTGGTAAAAG TCTCTCTCTCT TTGGAAAAAG TCTCTCTCTCT TTGGAAAAAA TCTCTCTCTCTCT TTGGAAAAAAG TCTCTCTCTCT TTGGAAAAAA TCTCTCTCTCT TTGGAAAAAA TCTCTCTCTCT TTGGAAAAAA TCTCTCTCTCT TTGGAAAAAAT TCTCTCTCTCT TTGGAAAAAAT TCTCTCTCTCT TTGGAAAAAAT TCTCTCTCTCTCT TTGGAAAAAAT TCTCTCTCTCTCT TTGGAAAAAAT TCTCTCTCTCTCT TTGGAAAAAAT TCTCTCTCTCTCT TTGGAAAAAAT TCTCTCTCTCTCT TTGGAAAAAAT TCTCTCTCTCTCTCT TTTTTTTTTT	ATGCTCTTT CCTGTGTTAG AGCCTGACCC TCGCTGGCAA CCCCTTCAAA  696.1  31	GCGATTAGGA AAGCAGCTGT AAGAAAAAA  41	GATACCAAAA GGGGGTCCCA TCTCAGGCGT TAATTGAAAC  51   CCTTAGAAAA CCCATCTGTGG AGAAGAGGCA GGACGATGGG ATGACCAAGA GGACGAATTG ATCAGGACTTC ACCAAATACT ACCAAATACT ACCAATCATTA ACCAATCATTA ACCAATCATTA ACCAATCATTA ACCAATCATTA ACCAATCATTA ACCAATCATTA ACCAATCATTA ATCAGGACA AATCAAGATC ATCAAGGACA AATCAAGATC ATCAGGTC CTGTGTGGGACACA CTGCACTTTC CTGTGTAGGA GGCTCACTT CTGTGTAGGA GGCTCACTT CTGTGTAGGA GGCTGTCCTTT CGGCTCTTTCT ACCATTGCCCG AGAGCTTAAC CATTGCCCT CTGTGTAGGA CGCTGTCCTTT CGCTGTTACCTT CGCTGTTACCTT CGGCTCACT CTGTGTAGGA CGCTGTCCTTT CGCTGTTTCT CGCTGTTTCT CGCTGTTACCTT CGCTGTCTTCT CGCTGTCTTCT CGCTGTCTTCT CGCTGTCTTCT CGGCGTCACT CGGAGGTCTCC CGGGGTCTCCC CGGAGGTCTCC	540 600 720 768 60 120 180 240 300 600 600 600 720 780 840 900 1020 1020 1140 1200 1260 1320 1440 1560 1620 1680 1740 1680
50 55 60 65 70 75	CACGGCGCTTA AAAAGCAACA GTGGAGATGA TCTCTAGATC AAGACTGAAG Seq ID NO: Nucleic Ac Coding seq 1   CTTGGCTCTT AGAGTAACAT AGGATATCTT TCATGCTGAT GTTGGATGAT GTTGGATGAT GTTGGATGAT TACCCGGTTTT TCAAAAAGT TATTTGGACAT GTAAAAGTGA CAGAGGCACAC GTACTACCC AAAACTGGAT ATTTCACTGGT TTTCACTGGACAC CCTGGACCAC ACTTCTTCACA AAAACTGGAT AAAAGTGAAAACTGGAT AAAACTGGAT AAAACTGGAT CCTGGACCAC ACTTCTTCGAAAAGGAAAAACACACTTCTCGAAAAGGAAAAAACACACAC	GGATCCTGG GCCTGAAGCA GCCTCCCCA CCTTCCTCTG GATCAATAAA  107 DNA Se id Accessio usence: 183. 11   ACAATGCTCA TCCAGAAAAC TCCAGAAAAC TCCAGAAAAC TGCTGAACAC AGATGCTCA TTTCTTTGTC ATCCACATTC ATTGGAGAC CAGCAGCTGC ATTGGCTCT TTACAAAA TATTGCATTC ATTGGAGAC AGAACAGCTCT AGAACAGCTCT TTAGAGAGCTGG CAGTTGGCCT TTAGAGAGCTGG CAGTTGGCCTCT TTAGAGAGCTGG CAGTTGGCCTCT TTAGAGAGCTGG CAGTTGTGCCTCT TTAGAGAGCTGC CAGTTTCTCTCTTAGAGAGCT CTTTAGCAGGCC CAGTTTCTTCTCT TTAGAGAGCTCT CCTAAACTTACT AAAACAGCTCT CCTAAACTTACT AAAACAGCTCT CCTAAACTTACT CCTAAACTACT CCTAAACTTACT CCTAAACTTACT CCTAAACTTACT CCTAAACTTACT CCTAAACTA	TTGTTGCTGG GGCACAAAAT TGCCTCCAGC TTTCCCTCTC CAGCCATCTG Quence n #: NM_004 .1646 21	ATGCTCTTTT CCTGTGTTAG AGCCTGACCC TCGCTGGCAA CCCCTTCAAA  696.1  31    CAATGCAGCA ATTTTTCTTC GGATCTTCTG CCATTCACATAA CTTTCCTTTC	GCGATTAGGA AAGCAGCTGT AAAAAAAA  41    AAATGAAATG CTTAATTGCC GCATTAGAATA AACCTGGAT AACCTGGAT TOTGATGGCC CTGGACAGGG CCGTCTTAAGG AGGACCTCA AGGACTCAC AGGACTCAC AGGACTGAC TTGGTAACT TTGGTAACT TTGGTACT TTGGTGACT TTGTGGTGACT TTGTGGTGACT TTGTGGTGACT TTGTTGATG TTGTTGATG TTGTTGATG TTGTTGATG TTGTTGATG TTTTTGATG CAATCAGTT TTGTTGATG TTGTTGATG TTGTTGATG TTGTTGATG TTTTTGATG CAATCAGTT TTTTTTGATG CAATCAGTT TTTTTTGATG CAATCAGTT TTTTTTGATG CAATCAGTT TTTTTTGATG CAATCAGTT TTTTTTGATG CAATCAGTT TTTTTTTGATG CAATCAGTT TTTTTTGATG CAATCAGTT TTTTTTGATG CAATCAGTT TTTTTTTGATG CAATCAGTT TTTTTTGATG CAATCAGTT TTTTTTTGATG CAATCAGTT TTTTTTTGATG CAATCAGTT TTTTTTGATG CAATCAGTT TTTTTTGATG CAATCAGTT TTTTTTTGATG CAATCAGTT TTTTTTTGATG CAATCAGTT TTTTTTGATG CAATCAGTT TTTTTTGATG CAATCAGTT TTTTTTTGATG CAATCAGT TTTTTTTGATG CAATCAGT TTTTTTTGATG CAATCAGT TTTTTTTGATG CAATCAGT TTTTTTTGATG CAATCAGT TTTTTTTGATG CAATCAGT TTTTTTGATG CAATCAGT TTTTTTTGATG CAATCAGT TTTTTTTGATG CAATCAGT TTTTTTTGATG CAATCAGT TTTTTTTGATG CAATCAGT TTTTTTTGATG CAATCAGT TTTTTTTGATG CAATCAGT TTTTTTTTTT	GATACCAAAA GGGGGTCCCA TCTCAGGCGT TAATTGAAAC  51   CCTTAGAAAA CCATCTGTGG AGAAGAGGCA GGGCATATTG AGACCAAGA GGACCAAGA GGACCAAGA GACCAAGA ATCAAATACT CCCATCCATA CCCATCCATA ACCAATACT ACCAATACT TCTACATTTC ATCAAGACA AATCAAAGTG GAAGAAAGTG GAAGAAAGTG GAAGAAAGTG TCTTACCTT CTTACCTTG TCTTACCTT CTTACCTTG TCTTACCTT CTTACCTTTC TCTTACCTT CGCCTTCTTACTA CGCCTTCTTACTA CGCCTTCTTACTT CGCCTCTTTTC TCTTTACCTT CGCCTCTTTTC TCTTTACCTT CGCCTCTTTTC TCTTTACCTT CGCCTCTTTC TCTTTACCTT CGCCTCTTTC TCTTTACCTT CGCCTCTTTC TCTTTACCTT CGCCTCTTTC TCTTTACCTT CGCCTCTTTC TCTTTACCTT CGCCTCTTTC TCTTTACCTT CGCCTCTTCT CGCCTCTTTC CGCATCCCTT CGCCTCTTC CGCATCCCT CCATTCCCCT CCATTCCCT CCATTCCCCT CCATTCCCCT CCATTCCCCT CCATTCCCCT CCATTCCCCT CCATTCCCT CCATTCCCCT CCATTCCCT CCATTCCCCT CCATTCCCT CCATTCCT CCATTCCCT CCATTCC	540 600 720 768 60 120 180 240 480 540 660 660 720 780 840 900 960 1020 1140 1200 1320 1380 1440 1560 1620 1620 1630 1740

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                                                                                          1980
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                                                                                                                                               180
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						405	

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	TGTGTGTTTT TTARARARA RAATGGARAR RAARAGCTT TTARACTGG GAGACTTCTG	4020
	101010111 11111111111111111111111111111	

	ACAACAGCTT GTTCTGAATA				GATACACCTC AA	TGACCCCAGC	4080 4122
5	Seq ID NO: Nucleic Aci Coding sequ		#: NM_0169	41.1			
	1	11	21	31	41	51	
	1	ł	1		Chan CTCTCh	 	60
10	CATTTTCCTC	CCCCAC	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	COTCOTO	CAGACTGTGA CTGCAGATCC	ACTOTTTOGG	60 120
					GCCCGGCTCC		180
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					GAGCAGCCCG		300
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13					TTGGCAGCCG		480
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		134 DNA Sec		H prediction	n		
4 ==	Coding sequ	uence: 14		•			
45	Coding sequ			31	41	51	
45	1	pence: 14 11 	11 21 	31 		1	60
45	1   ATGTGCCAGG	uence: 14 11       CTTTCCTCTG	11 21     GGTGCTAGGG	31   ACACTGTGGC	 TTCTCAAAAA	 TGCCCGTTGT	60 120
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<b>45</b> <b>50</b>	1   ATGTGCCAGG CTGCAGCCAT CAGGCCCAGT AAAAGGTTGG	Dence: 14 11   CTTTCCTCTG ACCCACCTGA TACCACTTGG AAAGGAAGTA	11 21   GGTGCTAGGG ACATGCCCAA ATGGGTGAAG CCCCAGCCTA	31   ACACTGTGGC TCTTGCCTGA TGGCCCTTGC TTGAATGGGG	TTCTCAAAAA TCTCAGAAGC ACTTGAGGAG AAATTGAAGC	TGCCCGTTGT TAAGCAGGGT CTCACTGTCC ACAGATATGT	120 180 240
	I   ATGTGCCAGG CTGCAGCCAT CAGGCCCAGT AAAAGGTTGG AAAACATCTT	Dence: 14  11  CTTTCCTCTG ACCCACCTGA TACCACTTGG AAAGGAAGTA CTCTAGAGTT	11 21   GGTGCTAGGG ACATGCCCAA ATGGGTGAAG CCCCAGCCTA ACCCAGCTGT	31   ACACTGTGGC TCTTGCCTGA TGGCCCTTGC TTGAATGGGG GATCTGGTGA	TTCTCAAAAA TCTCAGAAGC ACTTGAGGAG AAATTGAAGC CAGCTGATGG	TGCCCGTTGT TAAGCAGGGT CTCACTGTCC ACAGATATGT TTCCACTGAA	120 180 240 300
	I   ATGTGCCAGG CTGCAGCCAT CAGGCCCAGT AAAAGGTTGG AAAACATCTT GTAACTATCT	JERCE: 14  11  CTTTCCTCTG ACCCACCTGA TACCACTTGG AAAGGAAGTA CTCTAGAGTT CGGAAAATCT	11 21 GGTGCTAGGG ACATGCCCAA ATGGGTGAAG CCCCAGCCTA ACCCAGCTGT	31   ACACTGTGGC TCTTGCCTGA TGGCCCTTGC TTGAATGGGG GATCTGGTGA GGATTCCATA	TTCTCAAAAA TCTCAGAAGC ACTTGAGGAG AAATTGAAGC CAGCTGATGG TCTGTCAACA	TGCCCGTTGT TAAGCAGGGT CTCACTGTCC ACAGATATGT TTCCACTGAA GCAGGACTCT	120 180 240
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	1   ATGTGCCAGG CTGCAGCCAT CAGGCCCAGT AAAAGGTTGG AAAACATCTT GTAACTATCT CATGTAGAAG Seq ID NO:	Dence: 14  11  CTTTCCTCTG ACCCACCTGA TACCACTTGG ANAGGAAGTA CTCTAGAGTT CGGAAAATCT GCATGGTTAA  135 DNA Se	11 21   GGTGCTAGGG ACATGCCCAA ATGGGTGAAG CCCCAGCCTA ACCCAGCTGT CCCTGCTGTT CATCTCCAAA	31   ACACTGTGGC TCTTGCCTGA TGGCCCTTGC TTGAATGGGG GATTCGTGA GGATTCCATA GCCTCTTCTG	TTCTCAAAAA TCTCAGAAGC ACTTGAGGAG AAATTGAAGC CAGCTGATGG TCTGTCAACA	TGCCCGTTGT TAAGCAGGGT CTCACTGTCC ACAGATATGT TTCCACTGAA GCAGGACTCT	120 180 240 300 360
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50 55	1   ATGTGCCAGG CTGCAGCCAT CAGGCCCAGT AAAAGGTTGG AAAACATCTT GTAACTATCT CATGTAGAAG Seq ID NO: Nucleic Ac Coding seq 1	Dence: 14  11  CTTTCCTCTG ACCCACTGA TACCACTGG ACACTGGA ACAGGAGTA CTCTAGAGTT CGGAAAATCT GCATGGTTAA  135 DNA Se id Accessio uence: 184. 11  j	11 21	31   ACACTGTGGC TCTTGCCTGA TGGCCCTTGC TTGAATGGG GATTCCATA GCCTCTTCTG  812.1 31	TTCTCAAAAA TCTCAGAAGC ACTTGAGGAG AAATTGAAGC CAGCTGATGG TCTGTCAACA GCCAAATGTA	TGCCCGTTGT TAAGCAGGGT CTCACTGTCC ACAGATATGT TTCCACTGAA GCAGGACTCT G	120 180 240 300 360 411
50	1   ATGTGCCAGG CTGCAGCCAT CAGGCCCAGT AAAAGGTTGG AAAACATCTT GTAACTATCT CATGTAGAAG Seq ID NO: Nucleic Ac Coding seq 1   GAGAGGGCCC CGGGAGGGGGC	Dence: 14  11  CTTTCCTCTG ACCACCTGA TACCACTTGA TACCACTTGA CTCTAGAGTT CGGAAAATCT GCATGGTTAA  135 DNA Se id Accessio uence: 184.  11  GGACTAGGGG GACGGATGT	11 21	31   ACACTGTGGC TCTTGCCTGA TGGCCCTTGC TTGAATGGGG GATCTGGTGA GCTCTTCTG  812.1 31   GCGCAGGAGCT GCGCCTTGCC	TTCTCAAAAA TCTCAGAAGC ACTTGAGGAG AAATTGAAGC CAGCTGATGG TCTGTCAACA GCCAAATGTA  41	TGCCCGTTGT TAAGCAGGGT CTCACTGTCC ACAGATATGT TTCCACTGAA GCAGGACTCT G  51   GCAGGCGCGGG TGCGCCTCCG	120 180 240 300 360
50 55	1   ATGTGCCAGG CTGCAGCCAT CAGGCCCAGT AAAAGGTTGG AAAACATCTT GTAACTATCT CATGTAGAAG Seq ID NO: Nucleic Ac Coding seq I   GAGAGGGCCC CGGGACGGG GGGCTGAGCCGGGGGGGGGG	Dence: 14  11  CTTTCCTCTG ACCCACCTGA TACCACTTGG AAAGGAAGTA CTCTAGAGTT CGGAAAATCT GCATGGTTAA  135 DNA Se id Accessio uence: 184.  11    GGACTAGGGG GGACTAGGGG GACCCAGAG	11 21 21	31   ACACTGTGGC TCTTGCCTGA TGGCCCTTGC TTGAATGGG GATTCCATA GCCTCTTCTG  812.1 31   CGCAGGAGCT GCCTCCTTGC AGCAGCCGCT	TTCTCAAAAA TCTCAGAAGC ACTTGAGGAG AAATTGAAGC CAGCTGATGG TCTGTCAACA GCCAAATGTA  41   CCGCGCGGGGCTGGGCGGGCGGGGGGGGGGGGGGGGG	TGCCCGTTGT TAGCAGGGT CTCACTGTCC ACAGATATGT TTCCACTGAA GCAGGACTCT G  51   GCAGGCGCGGG TGCGCCTCCG GCCGCCAGG	120 180 240 300 360 411
50 55	1 ATGTGCCAGG CTGCAGCCAT CAGGCCCAGT AAAAGGTTGG AAAACTATCT CATGTAGAAG Seq ID NO: Nucleic Ac Coding seq 1   GAGAGGGCCC GAGAGGGGCCC CGGGACCGGG AGGATGGGCT ATGTAGACC AGGATGGGCT ATGTAGACC AGGATGGGCT ATGTAGACC ATGTAGACC AGGATGGGCT AGGATGGGCT ATGTAGACC AGGATGGGCT AGGATGGCT AGGATGGGCT AGGATGGCT AG	Dence: 14  11    CTTTCCTCTG ACCCACTTGG AACGAACTA TACCACTTGG AAAGGAAGTA CTCTAGAGTT CGGAAAATCT 135 DNA Se id Accessio uence: 184. 11    GGACTAGGGG GACGGATGGGGAGGGACGGATGGGGGAGGGATGGGGGAGGGA	11 21	31   ACACTGTGGC TCTTGCCTGA TGGCCCTTGC TTGAATGGGG GATCTCATA GCCTCTTCTG  812.1 31   CGCAGGAGCTC GCCTCCTTGC AGCAGCAGCTC	TTCTCAAAAA TCTCAGAAGC ACTTGAGGAG AAATTGAAGC CAGCTGATGG TCTGTCAACA GCCAAATGTA  41	TGCCCGTTGT TAAGCAGGGT CTCACTGTCC ACAGATATGT TTCCACTGAA GCAGGACTCT G  51   GCAGCGCGGG TGCGCCTCGG CCGCGCGAGG CCGAGAGCTCGG	120 180 240 300 360 411
50 55 60	I ATGTGCCAGG CTGCAGCCAT CAGGCCCAGT AAAAGGTTGG AAAACATCTT GTAACTATCT CATGTAGAAG Seq ID NO: Nucleic Ac Coding seq I GAGAGGGCCC CGGGAGCGGG GGGTGAGCC AGGATGGGCT ACCCGGGAGA	Dence: 14  11  CTTTCCTCTG ACCCACCTGA TACCACTTGA TACCACTTGG AAAGGAAGTA CTCTAGAGTT CGGAAAATCT GCATGGTTAA  135 DNA Se id Accessio uence: 184.  11  GGACTAGGGG GACGCATGT GCACGGGCGGAGG GACGCGCAGAG GCGCGCGGAGG CAGAATCCAC	11 21	31   ACACTGTGGC TCTTGCCTGA TGGCCCTTGC TTGAATGGGG GATCTGGTGA GCATCTCTG  812.1 31   CGCAGGAGGCT GCCTCCTTGC AGCAGCAGGAGCT ACACCGACCT TACACCGACCT	TTCTCAAAAA TCTCAGAAGC ACTTGAGGAG AAATTGAAGC CAGCTGATGG TCTGTCAACA GCCAAATGTA  41    CCGCGCGGGGC GGGCGCTCCC CCCCCTTACTA CGGACGCGCC	TGCCCGTTGT TAAGCAGGGT CTCACTGTCC ACAGATATGT TTCCACTGAA GCAGGACTCT G  51   GCAGCGCGGG GCAGGCCTCCG GCGGCGCAGG CCGAGGCTGG GCCCAGCGCC	120 180 240 300 360 411
50 55	1   ATGTGCCAGG CTGCAGCCAT CAGGCCCAGT AAAAGGTTGG AAAACATCTT GTAACTATCT CATGTAGAAG Seq ID NO: Nucleic Ac Coding seq 1   GAGAGGGCCC CGGGAGCGGG GGGCTGAGCC ACCCGGGAGA ACCCGGGAGA GCCCCCCGGG	Dence: 14  11  CTTTCCTCTG ACCACTGA TACCACTGA TACCACTGA CTCTAGAGTT CGGAAAATCT GCATGGTTAA  135 DNA Se id Accessio uence: 184.  1  GGACTAGGGG GAGGCATGT GCGCCGGAGG GCGGCGGGAG ACAGACCACC ACAGCGCCCCAA	11 21	31   ACACTGTGGC TCTTGCCTGA TGGCCCTTGC TTGAATGGGG GATCTGGTGA GCTCTTCTG  812.1  31   GCCACGAGGCCCT GCCACCGAGCC GCCATCGAGC GCCATCGAGC GCCATCGAGC TACACCGACT GGCCTGCACT	TTCTCAAAAA TCTCAGAAGC ACTTGAGGAG AAATTGAAGC CAGCTGATGG TCTGTCAACA GCCAAATGTA  41 ) CCGGCGCGCGCT CGGCCGCGCCCC CCGCTACTA CGGACGCGCC CCGCGCACCCCC CCGCGCACCCCC	TGCCCGTTGT TAAGCAGGGT CTCACTGTCC ACAGATATGT TTCCACTGAA GCAGGACTCT G  51   GCAGCGCGGG TGCGCCTCGG CCGCGCGAGG CCGAGAGCTCGG	120 180 240 300 360 411
50 55 60	I ATGTGCCAGG CTGCAGCCAT CAGGCCCAGT AAAAGATTCT GTAACTATCT CATGTAGAAG Seq ID NO: Nucleic Ac Coding seq I GAGAGGGCCC CGGGAGCGGG GGGCTGAGC AGGATGGGCT ACCCGGAGA GCCCCCCGG GCGCCCCCGG CTGCCCTCCA AAGACGAACT	Dence: 14  11  CTTTCCTCTG ACCCACCTGA TACCACTTGA TACCACTTGA TACCACTTGA TACCACTTGA TACCACTTGA TACCACTTGA TACCACTTGA CTCTAGAGTT CGGAAAATCT GCATGGTTAA  135 DNA Se id Accessio uence: 184. 11  GGACTAGGGG GACGCATGT GCCGCCAGAG GCGCCCAGAG CAGGATCTCAC ACAGCGCCC ATGGTGTGCCC ATGGTGTGCCC ATGGATGACCCA	11 21	31   ACACTGTGGC TCTTGCCTGA TGGCCCTTGC TTGAATGGGG GATCTGGTGA GCTCTTCTG  812.1 31   CGCAGGAGGCT GCCTCCTTGC AGCAGCAGCT TACACCGACT GCCATCGAGC TACACCGACT GCCCAGAGCCC CCCCAGAGCCC CCCCAGAGCCC	TTCTCAAAAA TCTCAGAAGC ACTTGAGGAG AAATTGAAGC CAGCTGATGG TCTGTCAACA GCCAAATGTA  41	TGCCCGTTGT TAAGCAGGGT CTCACTGTCC ACAGATATGT TTCCACTGAA GCAGGACTCT G  51   GCAGGCGCGGG GCGCGCAGG CCGAGAGGTCGG GCCCAGCGCC GGAAGATTGAA CCCCAGAAGAC CCCCAGAAG	120 180 240 300 360 411 60 120 180 240 300 360 420 420 480
50 55 60	1   ATGTGCCAGG CTGCAGCCAT CAGGCCCAGT AAAAGTTGG AAAACATCTT GTAACTATCT CATGTAGAAG Seq ID NO: Nucleic Ac Coding seq 1   GAGAGGGCCC CGGGAGAGGGGC GGGCTGAGCC ACGGAGAGGGC ACCCGGAGA GCCGCCCCGG CTGCCCTCCA AAGACAAACA	Dence: 14  11  CTTTCCTCTG ACCCACCTGA TACCACTTGA TACCACTTGA CTCTAGAGTT CGGAAAATCT GCATGGTTAA  135 DNA Se idd Accessio uence: 184.  11    GGGACTAGGGG GACGGATGT GCAGGGGCGGAGG GCGGCGGAGG GCGGCGGAGG CAGAATCCAC ACAGCGCCC ATGGTGTGCCA ATGGCCTTCA	11 21	31   ACACTGTGGC TCTTGCCTGA TGGCCCTTGC TTGAATGGGG GATCTGGTGA GCATCTCTG  812.1 31   GCCTCCTTGC AGCAGCAGCT GCCTCCTTGC AGCACCGACT GCCACCAGCC TACACCGACT GCCCCAGGGC GCCCAAGAGCC GCCCAAGAGCC GCCCAAAAAGAG	TTCTCAAAAA TCTCAGAAGC ACTTGAGGAG AAATTGAAGC CAGCTGATGG TCTGTCAACA GCCAAATGTA  41  CCGCGCGCGCT GGGCCGCGCC CCGCTACTA CGGACGGCC CCGGCATGCT CGGCCGCGCT CCGCATACTA ATGAGAG ATGCTAAGAG ATGCTAAGAG	I TGCCCGTTGT TAGCAGGGT CTCACTGTCC ACAGATATGT TTCCACTGAA GCAGGACTCT G  51   GCAGGCGCGG GCGCGCAGG CCCAGGAGATGGA CCCAGAGAAGC CCAGAGAGCGC AATGCCTCCA AATGCCTCCA	120 180 240 300 360 411 60 120 180 240 360 420 480 540
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	1   ATGTGCCAGG CTGCAGCCAT CAGGCCCAGT AAAAGGTTGG AAAACATCTT GTAACTATCT CATGTAGAAG Seq ID NO: Nucleic Ac Coding seq 1   GAGAGGGCCC CGGGAGCGGG GGGCTGAGCC AGGATGGGCT ACCCGGGAG GCCCCCGGG CTGCCCTCCA AAGACGAACTA AAAGAACTCA	Dence: 14  11  CTTTCCTCTG ACCCACTGA TACCACTTGA TACCACTTGG AAAGGAAGTA CTCTAGAGTT CGGAAAATCT GCATGGTTAA  135 DNA Se id Accessio uence: 184. 11	11 21 21 21 31 GGTGCTAGGG ACATGCCCAA ATGGGTGAAG CCCCAGCTTT CATCTCCAAA  Quence n #: NM_024 .621 21   CGGCGGGGGAT CCGGACGCCCCCGCCGCCCCCCCCCCC	31   ACACTGTGGC TCTTGCCTGA TGGCCCTTGC TTGAATGGGG GATCTGGTGA GGATCCATA GCCTCTTCTG  812.1   CGCAGGAGCT GCCTCCTTGC AGCAGCCGCT ACACCGACT GCCCAGGGGC TACACCGACT GCCCAGGGGG ATCCAACAGACT GCCCAAGGCG GCTAAAAGAG	TTCTCAAAAA TCTCAGAAGC ACTTGAGGAG AAATTGAAGC CAGCTGATGG TCTGTCAACA GCCAAATGTA  41   CCGGCGCGGCT GGGCCGGCCC CCGGTACTA CGGACGCCCC CCGGACGCCC CCGGACGCCC CCGGCATGCT GAATACAGAG ATGCTAAGAG	TGCCCGTTGT TAGCAGGGT CTCACTGTCC ACAGATATGT TTCCACTGAA GCAGGACTCT G  51   GCAGCGCGGG GCGCCCCGG GCGCCACGGC CGAAGACTGGA CCCAGGACCCCGCAGAGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCCACGCCACGCCACGCCACGCCACGCCACGCCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACGCACACACACACACACACACACACACACACACACACACACA	120 180 240 300 360 411 60 120 180 240 300 420 480 540 600
50 55 60	1   ATGTGCCAGG CTGCAGCCAT CAGGCCCAT AAAAGGTTGG AAAACATCT GTAACTATCT CATGTAGAAG Seq ID NO: Nucleic Ac Coding seq 1   GAGAGGGCCC CGGGAGCGGG GGGCTGAGCC AGGATGGGCT ACCCGGAGGAG GCCCCCCGG CTGCCCCCGA AAGACGAACT CAGAAACAGAACTA ACAAAGAACTA	Dence: 14  11  CTTTCCTCTG ACCCACTTGA TACCACTTGA TACCACTTGA TACCACTTGA TACCACTTGA TACCACTTGA TACCACTTGA TACCACTTGA CTCTAGAGTT CGGAAAATCT GGATGATTAA  135 DNA Se id Accessio uence: 184. 11  GGACTAGGGG GACGCATGT GCCCCAGAG GCGGCAGAG CAGAATCCAC ACAGCGCCC ATGGTTGTGCC GTGAGACCCA ATGGCCTTCACC ATGGCTTTCACC CTGTTACACTA CTTTCACTACTACTACTACTACTACTACTACTACTACTAC	11 21 1 21 1 GGTGCTAGGG ACATGCCCAA ATGGGTGAAG CCCAGGCTA ACCCAGCTGT CCTTGCTGTT CATCTCCAAA  quence n #: NM_024 .621 21 1 CGGCGGGGAC CCGACGGCGCCCCGCCCCCCCCCCC	31   ACACTGTGGC TCTTGCCTGA TGGCCCTTGC TTGAATGGGG GATCTGGTGA GGATCCATA GCCTCTTCTG  812.1   CGCAGGAGCCT GCCTCCTTGC AGCAGCCGCT AGCAGCCGCT GCCTCAGGC TACACCGACT GCCCCAGGTG CCCCAGGGCC ATCCAAGGAC CCCAAGAGAC ATCCAACAGAA	TTCTCAAAAA TCTCAGAGG ACTTGAGGAG AAATTGAAGC CAGCTGATGG TCTGTCAACA GCCAAATGTA  41	TGCCCGTTGT TAAGCAGGGT CTCACTGTCC ACAGATATGT TTCCACTGAA GCAGGACTCT G  51   GCAGCGCCGCG GCCGCGCGCGCCCCG GCGCGCCAGGCCCCCG GGAAGATGGA CCCAGAGAAG CCCAGAGAAG CCCTCTGACC AATGCCTTCACT CTCCTTCAGT	120 180 240 300 360 411 60 120 180 240 360 420 480 540
<ul><li>50</li><li>55</li><li>60</li><li>65</li></ul>	1   ATGTGCCAGG CTGCAGCCAT CAGGCCCAGT AAAAGGTTGG AAAACATCTT GTAACTATCT CATGTAGAAG Seq ID NO: Nucleic Ac Coding seq 1   GAGAGGGCCC CGGGAGCGGG GGGCTGAGCC ACGCTGAGCA ACGACAGA AAAGACAACT CTCAGAAACAGA AAAAGAACTC GTCCTTCACA	Dence: 14  11  CTTTCCTCTG ACCCACTGA TACCACTTGA TACCACTTGA TACCACTTGA TACCACTGA TACCACTGA CTCTAGAGTT COGAAAATCT GCATGGTTAA  135 DNA Se id Accessio uence: 184.  11    GGACTAGGGG GGACGCAGAG GCGGCGGAGA GCGCCGGAGA GCGCCGGAGA CAGAATCCAC ACAGCGCCC ATGGTGTGCC ATGGCCTTCA CCATTAATGT GTGCACTGAT ACTGACTCCA TACCACTGATAC ACTGACTCCA TACTGCACTAC ACTGACTCCA TACTGCACTAC TACTGCACTAC TACTGACTCCA TACTGACTCA TACTGACTCCA TACTGACTCA TACTGACTCCA TACTGACTCCA TACTGACTCCA TACTGACTCCA TACTGACTCCA TACTGACTCCA TACTGACTCCA TACTGACTCCA TACTGACTCA TACTGACTCCA TACTGACTCA TACTGACTCA TACTGACTCCA TACTGACTCA TACTGACTCCA TACTGACTCCA TACTGACTCCA TACTGACTCCA TACTGACTCCA TACTGACTCA TACTGACTCCA TACTGACTCCA TACTGACTCA TACTGACTA TACTGACTCA TACTCA T	11 21 21 21 GGTGCTAGGG ACATGCCCAA ACTGCCCAA ACCGGCTA ACCCAGCTGT CATCTCCAAA  quence n #: NM_024 .621 21   CGGCGGGGCAC CCGACAGCGC CCGACAGCGG CCGACAGCGG CCGACAGCGG CCGACAGCGGGAA GACCACAGAG AACAGATAGC CGCAGAGAGGG CCCATCAAAAG	31   ACACTGTGGC TCTTGCCTGA TGGCCCTTGC TTGAATGGGG GATCTGGTGA GGATCCATA GCCTCTTCTG  812.1  31   GCCTCCTTGC AGCAGGAGCT GCCTCCTTGC AGCAGCAGCT GCCCACAGCC GCCAACAGC ACCCAACAGA ACCCAACAGA ACCTTGAACAGA ACCTTGAACAGA ACCTTGAACAGA	TTCTCAAAAA TCTCAGAAGC ACTTGAGGAG AAATTGAAGC CAGCTGATGG TCTGTCAACA GCCAAATGTA  41   CCGCGCGGGCT CGGCCGGCTCCC CCGCTACTA CGGACGCGCC CCGGCACGCCC CCGGCACGCCC CCGGCACGCCC CGGGCATCCA GAATACACA TCAGCTCAGG ATGCTAAGAG ATGGACAGAACG GGCAGATGCA AGTGGCTGCC GGCAGCACCCC	TGCCCGTTGT TAGCAGGGT CTCACTGTCC ACAGATATGT TTCCACTGAA GCAGGACTCT G  51   GCAGCGCGGG GCGCCCCGG GCCGCCAGGC CCAGAGCTGG CCCAGCGCCC GGAAGATGA CCCAGAGATGA CCCAGAGATGA CCCAGAGATGA CCCAGAGATGA CCCAGAGATGA CCCAGAGATGA CCCTCTCAGC AATGCCTGCA CTTCTTCAGT CCTTCTGCAGT CCTTGCTGGA GCTGCCTGAA	120 180 240 300 360 411 60 120 180 240 420 480 660 660 720 720
50 55 60 65	1   ATGTGCCAGG CTGCAGCCAT CAGGCCCAGT AAAAGGTTGG AAAACATCTT GTAACTATCT CATGTAGAAG Seq ID NO: Nucleic Ac Coding seq 1   GAGAGGGCCC CGGAGCGGG GGGCTGAGCC AGGATGGGCT ACCCGGAGAG GCCCCCCGG CTGCCCTCCA AAGACGAACT AAAAGAACT ACAAAGAACT ACAAAGAACT TGTTTGGGAC CTGAATCT TTGTTGGGAC	Jence: 14  11  CTTTCCTCTG ACCCACCTGA TACCACTTGA TACCACTTGG TACCACTTGG TACCACTTGG TACCACTTGA TACCACTTGG GCATGGTTAA  135 DNA Se id Accessio Lucnce: 184.  11  GGACTAGGGG GACGGATTGA GCGCCACAGG CAGAATCCAC ACAGCGCCTC ATGGCCTTCA ACTGCCTTCAGCC CCTTCTGAGCC CTTCTGAGCC CCTTCTGAGCC CTTCTGAGCC CCTTCTGAGCC CCTTCTGACC CCTTCTGACC CCTTCTGACC CCTTCTGACC CCTTCTGACC CCTTCTGACC CCTTCTGACC CCTTCTCTCACC CCTTCTCTCACC CCTTCTCTCACC CCTTCTCTCACC CCTTCTCTCACC CCTTCTCTCACC CCTTCTCTCC CCTTCTCTCACC CCTTCTCTCACC CCTTCTCTCACC CCTTCTCTCACC CCTTCTCTCC CCTCTCTCT	11 21 21 31 31 GGTGCTAGGG ACATGCCCAA ATGGGTGAAG CCCAGGCTA ACCCAGCTGT CCTTGCTGTT CATCTCCAAA  quence n #: NM_024 .621 21 1 CGGCGGGGCAC CCGACGCGGCCCGCCCCC CCGACGCGGAC CCGACGCGGCAC CCGACGCGGCAC CCGACGCGGCAC CCGACAGAC GCCCACAGAC GCCCACAGAC GCCCACAGAC GCCCACAGAC GCCACAGAGC TCGCACAGAC GCCAGAGAGTC CCATCAAAG TCGCAAGAC TTGCAAGAC TTCAACTTAT	31   ACACTGTGGC TCTTGCCTGA TGGCCCTTGC TTGAATGGGG GATCTGGTGA GGATCCATA GCCTCTTCTG  812.1   CGCAGGAGCT GCCTCCTTGC AGCAGCCGCT AGCAGCAGCT GCCTAGAGGA CCCCAGGGCC ATCAACAGA CCTTAAACAG ACCTTGAAGAG ACCTTGAAGAG ACCTTGAAGAG ACCTTGAAGAG CCATTGAAGAG CCATTGAAG CCATTGAAGAG	TTCTCAAAAA TCTCAGAAGC ACTTGAGGAG AAATTGAAGC CAGCTGATGG TCTGTCAACA GCCAAATGTA  41	TGCCCGTTGT TAAGCAGGGT CTCACTGTCC ACAGATATGT TTCCACTGAA GCAGGACTCT G  51   GCAGGCGCGGG TGCGCCTCCG GCCGCGCAGGCCCCGGAAGAAGGCCCAGGCCCCCCCC	120 180 240 300 360 411 60 120 180 240 360 420 480 540 660 720 780 840
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	I   ATGTGCCAGG CTGCAGCCCAGT AAAAGATTCT GTAACTATCT CATGTAGAAG Seq ID NO: Nucleic Ac Coding seq I   GAGAGGGCCC CGGGAGCGGG GGGTGAGCC AGGATGGGCT ACCCGGAGACAGA AAAAAAGAACT CAGAAACACA ACAAAGAACTCA CCTGAATTCT TTGTGGGCTTCATTGTTGGGCTTCATTGTTGAGCA ATGTTAATAA	Dence: 14  11  CTTTCCTCTG ACCCACCTGA TACCACTTGA TACCACTTGG AAAGGAAATTA CTCTAGAGTT CGGAAAATCT GGATGGTTAA  135 DNA Se id Accessio uence: 184.  11  GGACTAGGGG GACGCATGG GCGCCCAGAG GCGCCCAGAG CAGGATCAC ACAGCGCCC ATGGTGTGCC CCATTAACTT GTGTCAACTA GCACTGGATCC ACTGGATCCC ACTGGATCCC ACTGGATCCC ACTGGATCCC ACTGGATCCC ACTGGATCCC CCTTCTGAGCC CCTTCTGAGCC ACTGCAAATCC ACTGCAAATCC ACTGCAAATCC CCTTCTGAGCC ACTGCAAATCC ACTGCAAATCC CCTTCTGAGCC CCTTCTGAGC CCTTCTGAGCC CCTTCTGAGCC CCTTCTGAGC CCTTCTGAGC CCTTCTGAGC CCTTCTGAGC CCTTCTGAGC CCTTCTGAGC CCTTCTGAGC CCTTCTGACC CCTTCTGACC CCTTCTGACC CCTTCTGACC CCTTCTGACC CCTTCTGACC CCTTCTGACC CCTTCTCTCTC CCTTCTCTCTC CCTTCTCTCTC CCTTCTCTCTC CCTTCTCTCTC CCTTCTCTCTC CCTTCTCTCT CCTTCTCTCTC CCTTCTCTC CCTTCTCTCTC CCTCTCTCTCTC CC	11 21 21 31 31 GGTGCTAGGG ACATGCCCAA ACTGCCAAA ACGGGCTA ACCCAGCTGT CCTTGCTGTT CATCTCCAAA  quence n #: NM_024 .621 21   GGGGGGGGAC CGGCGGGGAC CCGACAGCCG CCGACAGCCG CCGACAGCCG CCGACAGCCG CCGACAGCAG GTGCCCAAAT GACCACAGAG GTGCCCAAAT GCCCAAAT GCCACAGAGGGGC CCGAGAGGTC CCGAGAGAGTC CCGAGAGAGTC CCATCAAAGAT GCCACACAGAG TTGCACACCTTCTACTTATI TTCAGTTCACT TTCCAGTTCACT	31   ACACTGTGGC TCTTGCTGA TGGCCCTTGC TTGAATGGGG GATCTGGTGA GCATCTCTG  812.1   CGCAGGAGGCT GCCTCCTTGC AGCAGCAGCT TACACCGACT GCCTCAGGC TACACCGACT CCCCAGAGGC ATCCAACAGG ATCCAACAGG ATCCAACAGG ATCCAACAGG CATCCAACAGG CATCCAACAGG CATCCAACAGG CATCCAACAGG CATCCAACAGG CATCTAACTG CATCTAACTG CATCTAACTG CATCTAACTG CATCTAACTG TTTGTCTCTT	TTCTCAAAAA TCTCAGAAGC ACTTGAGGAG AAATTGAAGC CAGCTGATGG TCTGTCAACA GCCAAATGTA  41	TGCCCGTTGT TAAGCAGGGT CTCACTGTCC ACAGTATGT TTCCACTGAA GCAGGACTCT G  51   GCAGGCGCGGG GCGCGCGGG GCGCGCAGG CCGAGAGATGG CCCAGAGATG CCCAGAGAAG CCCCAGAGAAG CCCTCTGACC AATGCCTGAC TCGAAGATCG CTTCTTCAGT CCTTGCTGGA GCTGCCTGACT GTGCTTACAT GTGATACCGT	120 180 240 300 360 411 60 120 180 240 300 360 420 540 660 720 780 840 900
50 55 60 65	I   ATGTGCCAGG CTGCAGCCAT AAAGGTTGG AAACATCTT GTAACTATCT CATGTAGAAG Seq ID NO: Nucleic Ac Coding seq I   GAGAGGGCCC GGGAGAGGGGG GGGCTGAGCC AGGATGGGCT ACCCGGAGA GCCGCCCCGG CTGCCCTCCA AAGACAACAC GTCTTCACA CCTGAATTCT TTGTTGGGAC ATGTTAATAA CTCGTGTAAA	Dence: 14  11  CTTTCCTCTG ACCCACCTGA TACCACTTGA TACCACTTGA TACCACTTGA TACCACTTGA TACCACTTGA CTCTAGAGTT CGGAAAATCT GCATGGTTAA  135 DNA Se idd Accessio uence: 184.  11    GGACTAGGGG GGACGGATGT GGACTGAGGG GCGCGCGAGG GCGCGCGAGG CAGAATCCAC ACAGCGCCC ATGGTGTGCCC ATGGTGTACCC ATGGCTTCACTA GCACTGGATC CCTTCTAGCC CTTCTAGCCC CTCTCTAGCCC CTCTCTAGCCC CTCTCTAGCCC CTCTCTGAGCCC ACTGGATCCC CTCTCTAGCCC CTCTCTAGCCC CTCTCTAGCCC CTCTCTAGCCC CTCTCTAGCCC CTCTCTAGCCC CTCTCTAGCCC ACTGCAACTG ACTGCAACTG ACTGCAACTG ACTGCAACTG ACTGCACTG	11 21 21 31 GGTGCTAGGG ACATGCCAAA ATGGGTGAAG CCCCAGCTGT CCTGCTGTT CATCTCCAAA Quence n #: NM_024 621 21   GGGCGGGGCAC CCGACAGCCG CCGACAGCCG CCGACAGCCG CCGAAGCAGGGG CCGAAGCAGGGG CCGAAGAGGGGG CCGATCTACA GACCACAGAG AACAGATAGG TGCCCAAAT GACCAAAGAG TTGCTAAACAG TTGCTAAACAG TTGCCAAACAG TTGCCAAACAG TTGCCAAACAG TTGCCAAACAG TTGCAAGAGCC TTCTACTTAAT TGAAAGCTTACAG TGAAAGCTTACAG TGAAAGCTTACAG TTAAAGCTTACAG TTAAAGCTTACAG TTAAAGCTTACAG TTAAAGCTTACAG TTAAAGCTTACAG TTAAAAGCTTACAG TTAAAAGCTTACAG TTAAAGCTTACAG TTAAAGCTTACAG TTAAAAGCTTACAG TTAAAAAGCTTACAG TTAAAAAGCTTACAG TTAAAAGCTTACAG TTAAAAGCTTACAG TTAAAAAGCTTACAG TTAAAAAGCTTACAG TTAAAAAGCTTACAG TTAAAAAAAAAA	31   ACACTGTGGC TCTTGCCTGA TGGCCCTTGC TTGAATGGGG GATCTGGTGA GGATCCATA GCCTCTTCTG  812.1  31   GCGAGGAGCT GCCTCCTTGC AGCAGCAGCT GCCCCAGAGC GCCCAGAGC GCCCAGAGC GCTAAAAGAG ACCTTGAAAA CAAGCAGAAG ACCTTGAAGAG TTTGTCTCTT GCGTCAGTTTA	TTCTCAAAAA TCTCAGAAGC ACTTGAGGAG AAATTGAAGC CAGCTGATGG TCTGTCAACA GCCAAATGTA  41  CCGCCGCGCGCGCT CGGCCTCCC CCCGCTACTA CGGACGCGCC CCGGCATGCT GAAATCCCAA TCAGCTCAGG ATGCTAAGAG ATGGACAAACT GCAAACTCCT GCAGCAAACT TATTGGCACA TGCAACACCC TGAAACAGAA	TGCCCGTTGT TAAGCAGGGT CTCACTGTCC ACAGATATGT TTCCACTGAA GCAGGACTCT G  51   GCAGGCGCGGG TGCGCCTCCG GCCGCGCAGGCCCCGGAAGAAGGCCCAGGCCCCCCCC	120 180 240 300 360 411 60 120 180 240 360 420 480 540 660 720 780 840
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	I ATGTGCCAGG CTGCAGCCCAGT AAAAGATTCT GTAACTATCT CATGTAGAAG Seq ID NO: Nucleic Ac Coding seq I GAGAGGGCCC CGGGAGCGGG GGGTGAGCC AGGATGGGT ACCCGGAGAACAGA AAAAGAAGTCA ACAAAGAACT CTGTTGTGGGAC ATGTTAATAA CTGGTGTAATAC CATTTTCTG	Jence: 14  11  CTTTCCTCTG ACCCACCTGA TACCACTTGA TACCACTTGA TACCACTTGA TACCACTTGA TACCACTTGA TACCACTTGA CTCTAGAGTT CGGAAAATCT GCATGGTTAA  135 DNA Se id Accessio uence: 184.  1  GGACTAGGGG GACGCATGG GGCCCAGAG GCGCCCAGAG CAGGCGCCC ATGGCTCCA ATGGCTTCA CCATTAATGT GCTGTAACTA GCACTGGATC ACTGGATCACTA CCTTCTAGCC CCTTCTAGCC ATGGATCACTA ACTGGATCACTA ACTGGATCACTA ACTGCAACTA ACTGCAA	11 21 21 31 31 GGTGCTAGGG ACATGCCCAA ACTGCCAAA ACGCAGCTA ACCCAGCTGTCTT CATCTCCAAA (Quence n #: NM_024 .621 21 1 GGGCGGGCAC CGGCGGCGCCCCGCACCCCCGCACCCCCCCC	31   ACACTGTGGC TCTTGCCTGA TGGCCCTTGC TTGAATGGGG GATCTGGTGA GCTCTTCTG  812.1 31   CGCAGGAGCT GCCTCCTTGC AGCAGCAGCT TACACCGACT GCCAAGGCG TACACCGACT GCCCAGGGC CCCAGGGC CCCAGGGC CCCAGGGC CCCAGGCC CCTTGAAGA ACCTTGAAGA TCTCTACTT GGTCATTAAAC TTTGTCTCTT GTGCTATAAC TCCTTCATTT	TTCTCAAAAA TCTCAGAAGC ACTTGAGGAG AAATTGAAGC CAGCTGATGG TCTGTCAACA GCCAAATGTA  41	TGCCCGTTGT TAAGCAGGGT CTCACTGTCC ACAGTATGT TTCCACTGAT GCAGGACTCT G  51   GCAGGCCCCGG GCAGGCCCCGG GCAGGCCCCGG GCCCGCAGG CCCAGGCCCC GAAGATGCT CCCAGAGAAG CCCCAGAGAAG CCCTTCTCAGT CCTTCTTCAGT CCTTCTCAGT GTGCTTACAT GTGATAACAGT AAGTAGGAAT ATGATACGAT ATGATACAAT	120 180 240 300 360 411 60 120 180 240 300 360 420 540 660 720 780 840 900 960 1020 1080
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50 55 60 65 70 75	1   ATGTGCCAGG CTGCAGCCAT CAGGCCCAGT AAAAGGTTGG AAAACATCTT GTAACTATCT CATGTAGAAG Seq ID NO: Nucleic Ac Coding seq 1   GAGAGGGCCC CGGAGCGGG GGGCTGAGCC AGGATGGGCT ACCCGGAGG CTGCCCTCCA AAGACGAACT CAGAAACT ACAAAGAACT ACAAAGAACT TTGTTGGGAC ATGTTAATAA CTGGTGTAAA CCATTTCTGTTCC ATTCTTTCCC ATTCTTTCCC TTACCAGGT TCAAGGTACAG TCA	Jence: 14  11  CTTTCCTCTG ACCCACTGA TACCACTTGA TACCACTTGA TACCACTTGA AAAGGAAACTA  135 DNA Se id Accessio Jence: 184.  11  GGACTAGGGG GACGGATGA GCGCCAGAG GACGGATGA CAGGGCATGAT GCGCCAGAG GCGCCAGAG GCGCCAGAG GCGCCAGAG CAGAATCCAC ACAGCGCCC GTGAGACCCA ATGGCTTCAC ATGGCTTCAC CCTTCTAGACC CTTCTGAGCC CTTCTGAGCC CTTCTGAGCC CTCCTAGACC CTTCTGAGCC CTTCTTAGACC CTTTCTTAGACC CTTCTTTAGACC CTTCTTAGACC CTTCTTAGACC CTTCTTAGACC CTTTTAGACC CTTCTTAGA	11 21 21 21 31 32 31 32 32 32 32 32 32 32 32 32 32 32 32 32	31   ACACTGTGGC TCTTGCCTGA TGGCCCTTGC TTGAATGGGG GATCTGGTGA GGATCCATA GCCTCTTCTG  812.1   CGCAGGAGCT GCCTCCTTGC AGCAGCAGT AGCACCAGAGCC GCTAAAAGAG CCCCAGAGCC GCTAAAAGAG CCCCAGAGCC GCTAAAAGAG CCCCAGAGCC GCTAAAAGAG CCCCAGAGCC TACACCAGT CCCCAGAGCC CCCAGAGCC GCTAAAAAGA CCTTGAAGAG CAACTTGAAGAG CTTTTACTTC TTGTTCTTTATTT ATCCAACTCT TATTTCCTTTA	TTCTCAAAAA TCTCAGAAGC ACTTGAGGAG ACTTGAGGAG AAATTGAAGC CAGCTGATGG TCTGTCAACA GCCAAATGTA  41   CCGCGCGGGGC GGGCGGCGC CCGGCTACTA CGGACGGCG CCGGCATGGT AATTCCTAACA TCAGCTAGAG TGGAACTCCT TGAAACAGAA TTTTGGCACAC TTGAACTCCT TGAAACCACACAT AAACCCACACAT AAACCCACACACACA	TGCCCGTTGT TAGCAGGGT CTCACTGTCC ACAGATATGT TTCCACTGAA GCAGGACTCT G  51   GCAGCGCGGG GCGCGGGG TGCGCCTCCG GCGCGCGCAGGCCCCGGAGGATGGA CCCAGAGAATGCCTGCA TCCGAAGAATC CTTCTTCAGT GTGCTTACAT GTGATACGGT AATGAGATGA TCGAAGAAT ATGAAAAAA AGACAGATCG TAGACAGATCG	120 180 240 300 360 411 60 120 180 240 480 600 660 720 780 840 960 1020 1080 1180 1180
<ul><li>50</li><li>55</li><li>60</li><li>65</li><li>70</li></ul>	I ATGTGCCAGG CTGCAGCCCAGT AAAAGAGTTGG AAACATCTT GTAACTATCT CATGTAGAAG Seq ID NO: Nucleic Ac Coding seq I GAGAGGGCCC AGGATGGGCT ACCCGGAGA GCCCCCGG CTGCCCTCCA AAGAACAGAAC	Jence: 14  11  CTTTCCTCTG ACCCACCTGA TACCACTTGA TACCACTTGA TACCACTTGA TACCACTTGA TACCACTTGA TACCACTTGA TACCACTTGA CTCTAGAGTT CGGAAAATTT 135 DNA Se idd Accessio uence: 184. 11  GGACTAGGGG GACGCATGT GCCCCCAGAG GCGGCGGGGG CAGGATCACCA ACAGCGCCCC ATGGCTTCA CCATTGATCTCACTTAATGT GCTCTCAACTA CCATTGAATG ACTGCATCA ACTGCAACTG CTTCTGAGCC ACTGCAACTG CTTCTGAGCC ACTGCAACTG CTCTCTAGGCC ACTGCAACTG CTCTCTAGGCC TCACTTAAATGT CTCTCTAGACC ACTGCAAATG CACTGCAACTG CTCTCTAGGCC CTCTCTAGGCC ACTGCAAATG CGGAAAAGTC CCCATTGCAACTC CGGAAAACTC CCCATTGCACC CCATTGCACC CCATTGCACC CCATTGCACC CCATTGCACC CCCATTGCACC CCATTGCACC CCATTGCACC CCATTGCACC CCATTGCACC CCATTGCACC CCATTGCACC CCATTGCACC CCATTGCACC CCATTGCACC CCATTCCACC CCATTGCACC CCATTGCACC CCATTGCACC CCATTCCACC CCATTGCACC CCATTGCACC CCATTGCACC CCATTCCACC CCATTGCACC CCATTGCACC CCATTGCACC CCATTCCACC CCA	11 21 21 21 31 31 31 31 31 31 31 31 31 31 31 31 31	31   ACACTGTGGC TCTTGCCTGA TGGCCCTTGC TTGAATGGGG GATCTGCTGA GGATCCATA GCCTCTTCTG  812.1 31   CGCAGGAGCT GCCTCCTTGC AGCAGCAGCT GCCAAGGAGC TACACCGACT GCCCAGGGC CCCAGGGC CCCAGGGC CCCAGGCC GCTAAAAGAG ACCTTGAAGA CCTTGAAGA TTTGTCTCTT GGTCATTAAAC TCCTTCATTT CATCCAACTCT TGTTCCTTTA TTTCCTCTT TTTTCCTTTT CCCATGGCATT CTTTCCTTTT TTTTCCTTTT CCCATGGCATT TTTTCCTTTT CCCATGGCATT CCCTTCATTT CTTTTCCTTTT CCCATGGCATT CCCATGCCATT CCC	TTCTCAAAAA TCTCAGAAGC ACTTGAGGAG AAATTGAAGC CAGCTGATGG TCTGTCAACA GCCAAATGTA  41	TGCCCGTTGT TAAGCAGGGT CTCACTGTCC ACAGTATGT TTCCACTGAT GCAGGACTCT G  51   GCAGGCCCGG GCAGCCCGG GCGCGCGGG CGAGAGATGGA CCCAGAGAAG CCCAGCCCC AATGCCTCGG ACCAGGAGATCG CCTTCTGACC AATGCCTTCAGT CCTTCTCAGT CTTCTTCAGT GTGATACAGT ATGAAAAAA ATGAAAAAT ATTGAAAAAAT ATGAAAAAAT ATGAAAAAAT ATGAAAAAAT ATGAAAAAAT ATGAAAAAAT ATGAAAAAAT AGACAGATCG GTGTTCTTGAG GTGTTCTTGAG	120 180 240 300 360 411 60 120 180 240 600 660 660 660 720 780 840 900 960 1020 1080
50 55 60 65 70 75	I  ATGTGCCAGG CTGCAGCCAT CAGGCCCAGT AAAAGGTTGG AAAACATCTT GTAACTATCT CATGTAGAAG  Seq ID NO: Nucleic Ac Coding seq I  GAGAGGGCCC GGGAGCGGG GGGCTGAGCC AGGATGGGCT ACCCGGGAGA ACAGAACAGA	Jence: 14  11  CTTTCCTCTG ACCCACCTGA ACCCACCTGA TACCACTTGG AAAGGAAGTA CTCTAGAGTT CGGAAAATCT CGGAAAATCT 135 DNA Se id Accessio Jence: 184. 11  GGACTAGGGG GACGGATGA GCGCCAGAG GCGCCAGAG GCGCCAGAG GCGCCAGAG GCGCCCAGAG CAGAATCCAC ACAGCCCCC TTGAGCCTCA ACTGACTC CCTTCTGAGCC CTTCTGAGCC CTTCTGAGCC CTTCTGAGCC CTTCTGAAAAT GGCAACTG CACTGAATC CCCATCAAAAT GGGAAAACTCC CCCATCACC CCCTGCACC CCTTCTAAAA CGGAAAACTCC CCCATGCACC CCTTCTAAAA CGGAAAACTCC CCCATGCACC CCTTTTAATTTAA	11 21 21 21 31 32 31 32 32 32 32 32 32 32 32 32 32 32 32 32	31   ACACTGTGGC TCTTGCCTGA TGGCCCTTGC TTGAATGGGG GATCTGGTGA GGATCCATA GCCTCTTCTG  812.1  31   CGCAGGAGCT GCCTCCTTGC GCTCCTTGC GCTCCTTGC GCCAGGAGCC GCAATGGAGA ACCTTGAAGA ACCTTGAAGA CAACCAGAT CGTTAAAATG TTTTGTCTTT GGTCAACTTG TATCCTTATTT ATCCAACTCT TGTTTCCTTT CCTTCATTTT ATCCAACTCT TGTTTCCTTT CCTTGATTAACT TGTTTCCTTT TATCAACTCT TGTTTCCTTT TATCAACTCT TGTTTCCTTT TATCAACTCT TGTTTCCTTT CCTTGAAGTCT TGTTTCCTTT TATCAACTCT TGTTTCCTTT TAACAACTCT TAAAAGTCCTCC TGCCAATGCAT	TTCTCAAAAA TCTCAGAAGC ACTTGAGGAG ACTTGAGGAG ACATTGAAGC CAGCTGATGG TCTGTCAACA GCCAAATGTA  41   CCGGCGCGGCT CGGGCGGCC CCGGTACTA CGGACGCGC CGGGCATGCT GAATACCCAA TGGACACCAC TATTGGCACA TTGAACTCCT TGAAACACAA TCTCCTGCCC TAAATATTCT TAAACACAAT CTTTTGGGAC CTTTTTGGGAC CTTTTTGGGACC CTTTTTGGGACC CTTTTTTTTTT	TGCCCGTTGT TAGCAGGGT CTCACTGTCC ACAGATATGT TTCCACTGAA GCAGGACTCT G  51   GCAGCGCGGG GCGCCCCGG GCGCCCCGG GCGCCCCGG CCAGGGCCCCGG CCAGAGCTGG CCAGAGATGA CCCAGAGATGA CCCAGAGATGA CCCAGAGATGA CCTTCTCAGT CCTTCTCAGT GTAATACCGT AATGCCTGAC AATGCCTGAC AATGCCTGAC ATGCAGAGATC GTGATACAGAT AATTAGAAAT AAGTAGGAT AATTAGAAAT AAGACAGATCG GTGCTTCTGGG GTGCTTGAGC AATGCCTGAC GTGCTTACAT TATGAAAAT AAGACAGATCG GTGCTTCTGGG GTGCTTGTGA AAGTAGAAT ATGAAAAAA AAGACAGATCG GTGTCTTGGG ATACCCCTCA	120 180 240 300 360 411 60 120 180 240 480 660 660 660 660 720 720 780 840 900 1020 1020 1140 1200 1240 1250 1320 1380
50 55 60 65 70 75	I ATGTGCCAGG CTGCAGCCCAGT AAAAGAGTTGG AAAACATCTT GTAACTATCT CATGTAGAAG Seq ID NO: Nucleic Ac Coding seq I GAGAGGGCCC GGGAGGGGGCTGAGCCCGGGAGAACAGAAC	Jence: 14  11  CTTTCCTCTG ACCCACTTGA TACCACTTGA TACCACTTGA TACCACTTGA TACCACTTGA TACCACTTGA TACCACTTGA CTCTAGAGTT CGGAAAATCT 135 DNA Se id Accessio Luence: 184. 11  GGACTAGGGG GACGCATGG GGACGCATGG GCGCCGGGGG GCGGCGGGGG CAGAATCAC ACTGCCTCAC ATGGCCTTCA CCATTACACT ACTGCACTC ACTGCACTC ACTGCACTC ACTGCACTC ACTGCACTC ACTGCACTC CCCTCTTCAGCC ACTGCACTC CCCTCTTCAGCC ACTGCACTC CCCTCTTCAGCC ACTGCACTC CCCTCTCACC CCCTCCTCC CCCTCCTCC CCCTCCTCC CCCTCCT	11 21 21 21 31 31 31 31 31 31 31 31 31 31 31 31 31	31   ACACTGTGGC TCTTGCCTGA TGGCCCTTGC TTGAATGGGG GATCTGCTGA GGATCCATA GCCTCTTCTG  812.1  31   CGCAGGAGCT GCCTCCTTGC AGCAGCAGCT TCCAACGAC CCCAGGAGCC GCTAAAAGAG ACCTTGAAGA CAACCAGAAG CTCTTACTA CTCTTACTT CGTCTACTT CTTTCCTTT CTTTCCTTT CCCATGGCAT CCCATGGAGC TTTCCACTT CTTTCCTTT CCCATGGCAT CCCTCATTT CTTTCCTTT CCCATGGCAT CCCATGAGGC TTTCCACT CCCTCATTT CTTTCCTTT CCCTTCATTT CCCATGGCAT CCCATGGCAT CCCATGGCAT CCCATGGCAT CCCATGGCAT CCCATGGCAT CCCATGGCAT CCCATGGCAT CCCATGCAT CCCCATGCAT CCCCATGCAT CCCATGCAT CCCCATGCAT CCCCATGCAT CCCCATGCAT CCCCATGCAT CCCCAT	TTCTCAAAAA TCTCAGAAGA ACTTGAGGAG ACTTGAGGAG ACTTGAGGAG ACTTGAGCAG CAGCTGATGA GCCAAATGTA  41	I TGCCCGTTGT TAGCAGGGT CTCACTGTCC ACAGATATGT TTCCACTGAA GCAGGACTCT G  51   GCAGGCCGCG GCGCCCCG GCGCCCAGCGCCCGC GCAGAGATGA CCCAGAGATGA CCCAGAGATGA CCCTCTGAC AATGCCTGCA CCTTGTCGGA GCTGCTTGACAT GTACATACGT AAGTAGGAAT ATTGAAAAAA AGAGAATCG GTGTTGAAAAA ATTGAAAAAA AGAGAATCG GTGTTTGGAG GTGCTTGGA GTGCTTGCAG CCTTGCTGGA GTACATTACAAAT ATTGAAAAAA AGAGAATCG GTGTTTGGGG GTGCTTGGA	120 180 240 300 360 411 60 120 180 240 600 660 6720 780 840 600 1020 1080 1140 1200 1200 1320

	AGGAGAGGGA GATGATCCAG AGACATGTGG CAGCAGGCAT GGCTTCCCCT TGGCCTCTCT	1560
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	ACCTGGTTGA TGTGTATTCA TACTGACATT AGATTGATGT GCACTGCATT AGAAATGAGG	1680
•	TAGCTGACAC AGAAAAAGGA TGTTTTGATA GGAATAATTT TCTAGTATGT CTTGAAACAT	1740 1800
5	GTTCATCTGG AAGTATTTTC CTCCAAAGTA ATGTAGCATG ATTTTTCAAG GATTGTTAAC ATGCCTGGGA TTGGGAAAGA TAGGACTAAA GTTGTGCCAA ACTATATCAA TAAATTCCAT	1860
	GTTTAGCAGA AATAGGCAGC CTATTGGTGT TATGTTTATG TAACATAGTC CAGAGAACTG	1920
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	ACACAAGTOG GTAGTGTCAT TTTTCCTTCC TTCCTTCCAT TGGCAGATTG TATATTTATT	2040
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	TCTGGTTAGT CGTGACTATC TATCCTGAAT CTAACAGTGA CTTCATAACT AGGAGACTGA	2160 2220
	ATTAGACCCT TRAGGTATAG TGTGTGTTGC ARATCACTCT GCARTGGARA CTTTTATATT CAGGGTAGGT TTGTGTCTTA ARCTAGGTGT TCTRATCART GTACARGACT TTACCATACA	2280
	CGCAACTATA GTTTTTCTAA ACCTTCATCA TTTTGTGATT CTTTGAGAAA GGGCTTTTAG	2340
15	CARCTITATO TICTAARRA TOTTITTARC RATRATAGA TARRAGARRA ACCTOTGATI	2400
	CATATGTCCC CACTGGCATT ACTCAGCAGG AGCCCCCAGC TGCCAAAGGT TGGCAGTGAT	2460
	CCTGCAAGTT CAAGGGCTCT TTCTCCCTGG GGATGTGCTT TGTGGCTTCT CTTTACAGCT	2520
	TIGITICIGE ATCAGITCAC TGCTGCATGT TGTTTGGAAT TTATCACCTT AAGAAAGTGT	2580 2640
20	CTCTGTTTTA TATAGAAACA CTTTCTCACT TACAGGGGAG AAGGAAATGC AGGGCACATG ATCTGGCCCT CCCCAGAACA ATCTGGATTT CACGGGGACA GCAACCAGAA GTTAAACCAT	2700
20	GTGACTAAAA ATGCATCTGG CTACTTTTTC ATGTATGTAT GAGACAGAAA CTAATCCTTA	2760
	CTATCCTATT AGGATACCAC TITTCATTGC AAAGTTTGTG TCAATAAAGT CATTAATTTT	2820
	AAACAT	2826
25	Seq ID NO: 136 DNA Sequence	
	Nucleic Acid Accession #: XM_040550.1	
	Coding sequence: 824158 1 11 21 31 41 51	
	1 11 21 31 41 31	
30	COTTOCTTC COTTGCAGAT TOCCACACT COATGCTGTG TGCTGCAGGC TGGTCCTGAA	60
	CCLEGATOTO TOGOTGAGAG GATGGGGGCA GATGGGGAAA CAGTGGTTOT GAAGAACATG	120
	CTCATTGGCA TCAACCTGAT CCTTCTGGGC TCCATGATCA AGCCTTCAGA GTGTCAGCTG	180
	GAGGTCACCA CAGAAAGGGT CCAGAGACAG TCAGTGGAGG AGGAGGGAGG CATTGCCAAC	240
25	TACAACACAT CCAGCAAAGA GCAGCCTGTG GTCTTCAACC ACGTGTACAA CATTAACGTG	300 360
35	CCCTTGGACA ACCTCTGCTC CTCAGGGCTA GAGGCCTCTG CTGAGCAGGA GGTGAGTGCA GAAGACGAGA CTCTGGCAGA GTACATGGGC CAGACCTCAG ACCACGAGAG CCAGGTCACC	420
	GAAGACGAGA CTCTGGCAGA GTACATGGGC CAGACCTCAG ACCACGAGAG CCAGGTCACTTTTACACACAC GGATCAACTT CCCCAAAAAG GCCTGTCCAT GTGCCAGTTC AGCCCAGGTG	480
	CTGCAGGAGC TGCTGAGCCG GATCGAGATG CTGGAGAGGG AGGTGTCGGT GCTGCGAGAC	540
	CACTOCAACT CCAACTGCTG CCAAGAAAGT GCTGCCACAG GACAACTGGA CTATATCCCT	600
40	CACTOCAGTO GCCACGGGA CTTTAGCTTT GAGTCCTGTG GCTGCATCTG CAACGAAGGC	660
. •	TOOTTTOOCA AGANTTOOTO GGAGCCCTAC TGCCCGCTGG GTTGCTCCAG CCGGGGGGTG	720
	TETETERATE GOOGTGOAT CTGTGACAGC GAGTACAGCG GGGATGACTG TTCCGAACTC	780
	CGGTGCCCAA CAGACTGCAG CTCCCGGGGG CTCTGCGTGG ACGGGGAGTG TGTCTGTGAA	840
AE	GAGCCCTACA CTGGCGAGGA CTGCAGGGAA CTGAGGTGCC CTGGGGACTG TTCGGGGAAG	900 960
45	GGGAGATGTG CCAACGGTAC CTGTTTATGC GAGGAGGGCT ACGTTGGTGA GGACTGCGGC CAGCGGCAGT GTCTGAATGC CTGCAGTGGG CGAGGACAAT GTGAGGAGGG GCTCTGCGTC	1020
	TGTGAAGAGG GCTACCAGGG CCCTGACTGC TCAGCAGTTG CCCCTCCAGA GGACTTGCGA	1080
	GTGGTTGTA TCAGGGACAG GTCCATTGAG CTGGAATGGG ACGGGCCGAT GGCAGTGACG	1140
	GANTATGTGA TCTCTTACCA GCCGACGGCC CTGGGGGGCC TCCAGCTCCA GCAGCGGGTG	1200
50	CCTGGGGGTT GGGGTGTGT CACCATCACG GAGCTGGAGC CAGGTCTCAC CTACAACATC	1260
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	CAGTOGGAGC CCTTCTCATT TTCCTTCGAT GGGTGGGAAA TCAGCTTCAT TCCAAAGAAC AATGAAGGG GAGTGATTGC TCAGGTCCCC AGCGATGTTA CGTCCTTTAA CCAGACAGGA	1500
55	CTARAGCCTG GGGAGGATA CATTGTCAAT GTGGTGGCTC TGARAGAACA GGCCCGCAGC	1560
33	CCCCCTACCT CGGCCAGCGT CTCCACAGTC ATTGACGGCC CCACGCAGAT CCTGGTTCGC	1620
	GATGTCTCGG ACACTGTGGC TTTTGTGGAG TGGATTCCCC CTCGAGCCAA AGTCGATTTC	1680
	ATTITTICA ANTATIGICIT GGTGGGCGG GAAGGTGGGA GGACCACCTT CCGGCTGCAG	1740
<b>~</b>	CCTCCCCTGA GCCAATACTC AGTGCAGGCC CTGCGGCCTG GCTCCCGATA CGAGGTGTCA	1800
60	GTCACTGCCG TCCGAGGGAC CAACGAGAGC GATTCTGCCA CCACTCAGTT CACAACAGAG ATCGATGCCC CCAAGAACTT GCGAGTTGGT TCTCGCACAG CAACCAGCCT TGACCTCGAG	1860 1920
	TEGGATACA GTGAAGCCGA AGTTCAGGAG TACAAGGTTG TGTACAGCAC CCTGGCGGGT	1980
	GAGCAATATC ATGAGGTACT GGTCCCCAGG GGCATTGGTC CAACCACCAG GGCCACCCTG	2040
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	AAGGACAGGA CCTCATACAC ACTAACAGAT CTAGAGCCTG GGGCAGAGTA CATCATTTCC	2340 2400
70	GTCACTGCTG AGAGGGGTCG GCAGCAGAGC TTGGAGTCCA CTGTGGATGC TTTCACAGGC TTCCGTCCCA TCTCTCATCT GCACTTTTCT CATGTGACCT CCTCCAGTGT GAACATCACT	2460
70	TEGGAGTGATC CATCTCCCC AGCAGACAGA CTCATTCTTA ACTACAGCCC CAGGGATGAG	
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	CTGCAACCAG CCACAGAGTA TATTGTGAAC CTTGTGGCTG TCCATGGCAC AGTGACCTCT	2640
	GAGCCCATTG TGGGCTCCAT CACCACAGGA ATTGATCCCC CAAAAGACAT CACAATTAGC	2700
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	TACCGAGTAT CATATCGACC CACCCAAGTG GGACGACTAG ACAGCTCAGT GGTGCCCAAC	2820 2880
	ACTGTGACAG AATTCACCAT CACCAGACTG AACCCAGCTA CCGAATACGA AATCAGCCTC	
	AACAGCGTGC GGGGCAGGGA GGAAAGCGAG CGCATCTGTA CTCTTGTGCA CACAGCCATG GACAACCCTG TGGATCTGAT TGCTACCAAT ATCACTCCAA CAGAAGCCCT GCTGCAGTGG	3000
80	MAGGCACCAG TGGGTGAGGT GGAGAACTAC GTCATTGTTC TTACACACTT TGCAGTCGCT	
30	GGAGAGACCA TCCTTGTTGA CGGAGTCAGT GAGGAATTTC GGCTTGTTGA CCTGCTTCCT	3120
	AGCACCCACT ATACTGCCAC CATGTATGCC ACCAATGGAC CTCTCACCAG TGGCACCATC	3180
	AGCACCAACT TITCTACTCT CCTGGACCCT CCGGCAAACC TGACAGCCAG TGAAGTCACC	3240
	AGACAAAGTG CCCTGATCTC CTGGCAGCCT CCCAGGGCAG AGATTGAAAA TTATGTCTTG	

	ACCTACAAAT C	CACCGATGG	AAGCCGCAAG	GAGCTGATTG	TGGATGCAGA	AGACACCTGG	3360
	ATTCGACTGG A	AGGCCTGTT	GGAGAACACA (	GACTACACGG	TGCTCCTGCA	GGCAGCACAG	3420
	GACACCACGT C	GAGCAGCAT	CACCTCCACC	GCTTTCACCA	CAGGAGGCCG	CGTGTTCCCT	3480
-	CATCCCCAAG A	CTGTGCCCA	GCATTTGATG	AATGGAGACA	CTTTGAGTGG	GGTTTACCCC	3540
5	ATCTTCCTCA A						3600 3660
	GGGGGGGGGT C						3720
	AATATACACA (						3780
	CAAGAGGCCG (						3840 .
10	AAACTCCGCA 1	PAGGAAGCTA	CAACGGCACT	GCGGGGGACT	CCCTCAGCTA	TCATCAAGGA	3900
10	CGCCCTTTCT	CACAGAGGA	TAGAGACAAT	GATGTTGCAG	TGACTAACTG	TGCCATGTCG	3960
	TACAAGGGAG						4020
	GAGTCCAGGC A	ACAGTCAGGG	CATCAACTGG	TACCATTGGA	AAGGCCATGA	GTTCTCCATC	4080
	CCCTTTGTGG A	AAATGAAGAT	GCGCCCCTAC	AACCACCGTC	TCATGGCAGG	GAGAAAACGG	4140
15	CAGTCCTTAC	AGTTCTGAGC	AGTGGGCGGC	TGCAAGCCAA	CCAATATTTT	CTGTCATTTG	4200
	TTTGTATTTT /	ATAATATGAA	ACAAGGGGGG	AGGGTAATAG	CAATGTGTTT	TGCAACATAT	4260
	TAAGAGTATG	TGAAGGAAGC	AGGGATGTCG	CAGGAATCCG	CTGGCTAACA	TCTGCTCTTG	4320
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20	CAACCTTCAC	CTCCTTTCCC	ACCAAGGAGG	AGAAGTAGGA	AGTTTTCTTA	AAGGGCCAAT	4440
20	TCAAAGCCAA	GTCGTGGGGT	GCAGATTGTT	ATGGTGACAG	GCACACACAT	TTTTCTACCC	4500
	TTCTTCTGAG	ATGTCCTCTG	CCTTCCAGGT	ATTTGTGATT	TTGTCACAGC	CTGACATGGC	4560
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	CCTTAAAAGG	AAACAGATCA	ACTACACCGC	ATCCCAACAA	CCCAGGTTCT	TTTCCTTCCT	4680 4716
25	TCCTTCCTTC	CTCCCTTCCT	TCTTTCCTGC	CTTCCC			4710
23							
	Seq ID NO:						
	Nucleic Aci			,0,,,			
	Coding sequ	11	21	31	41	51	
30	†	<u> </u>	ï	ī	ï	Ĭ	
50	GCCTTTGGGG	ACCAGGAGGC	AGACATGTGT	TGCTTTGCAC	GTCATCTGGT	CCTTCCACCT	60
	GGCTGGGCAT	GGGATGGTGA	CCTCAGCTGG	AACATGGGGC	TCGAGCCAGA	CCTCAGGGTC	120
	TCCCTGCGTG	TAGCCCCCAA	CCCCAAGCCT	GATCCCCACC	GGAGACCTGA	ACAGCCTTGG	180
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A E	GGGAGGAGGC	GAGCGCTGAT	GGGAAAGGAA	CAAAGAGGGA	AGGGGGGGGG	GAAGGGGGTT	840 900
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	AGGCCAGAGC	CAGAAGACGG	CCAGAGGCAC	AAAGAAGCCA	ACCCTCCCC	GGAGTCAAGG	1020
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	GCCACACAGG	CCCTTCCCTC	CAUCICACO	COCCUTTO	CACAGCTTAG	GTGTCACCCA	1140
50	CTCCCCTTCC	TOTAL	TATTETOTATE	CCCACCACA	GCTGGTGGTC	TGTCTGCCCC	1200
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	TOTOTOTO	CLGLCHGCC	TGTGAGCCTG	GGGGTGCTGG	GCTGGCCAGT	CGGCTTGCTG	1320
	CCTTACCCTC	TCCCAGCTGT	CTGAGTGTTT	GTCCGGCTG1	CAGGATGTGT	CCTGGGGGCT	1380
	GGGAAGGAGA	GGCCGACCCA	TNGTCTGTCC	GTCGACTGGT	CAGTTGGACC	TTCAGCTGTC	1440
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	ACTCCTGCCT	GAGACCCCCC	CCCAACCCAC	GATCAGGCAG	GACGGCTGGC	GCTTAGGTCA	1620
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	ACCUTATION	CCCAGACGCT	GCAGGAGCTC	AAGATGGCG	\ GCTCCGTGGG	GCCCTACGAG	1740
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65	AAGTTCCAGC	CGCCCACCC	GGGCCCGGAC	CCTGCCGCC	TONCOCCO	A GGGCAGCCCA C CACCATCCGG	2100
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	CTGCTGGAGG	TOTOGRACE	CTCTCACCTY	CACCCCCCCC	T CCAAGCGCC	T GGACGAGCTG	2220
	CCCCACCTCC	ACACCCACT	CTCCATCCA	ATTCCACCTG	A TOOGGCAGO	A GCTTGAGTTC	2280
	CCCCACGIGG	ACATOCOCTO	C GCTGATGGA	GAGCGCTTO	GCACCTCGG	A CGAGATGGTG	2340
70	Cyclustry	AGATCCGCG	CTOGOGOCT	GAGCAGATT	G ACAAGGAGC	T GCTGGAGGCG	2400
, 0	CAGGACCGAG	TGCAGCAGA	C GGAGCCCCA	GCCTTGCTG	G CGGTGAAGT	C GGTGCCGGTG	2460
	GACGAGGACC	CCGAGACAG	A GGTCCCCAC	A CACCCTGAG	G ATGGCACCC	C TCAGCCGGGC	2520
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00	GCCCGAGACC	GCCGGCCCCG	A GGGAGGTGG	C GCCGGCAGC	CCCCGATCC	C CATCGAGCCG	2940
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50	GAAGAAGGT ACCTGCTGCT AAAAATAAAG Seq ID NO: Nucleic Ac: Coding seq I   GAATTCCGCC GCGCTGTTCG CGTCTGCCAG TTGTTTTGCT CCATCATCTC	CCTTCCTCT GCTGCTGCTG ACAAATGCTG ACAAATGCTG 149 DNA Seid Accessiouence: 445. 11	CCCCAGACT CTAATCTTCA CGCCTTAAA quence n #: L29126 .1845 21   CAGGTCCTGT TCGAGCCGCA TCCTTGGCCC CTGGCCCGCA	TGGTGTCCTT GGGCACTGCT AAA  .1  31   GCCAGATTGT GCCGCAGCTGGTT GCAGCTGGTT TCTCCTTGAA	41     CCCTCTCAAC   TOGCAGCTCA	S1	2940 3000 3033 60 120 180 240
50	GAAGAAGGT ACCTGCTGCT AAAATAAAG Seq ID NO: Nucleic Ac: Coding sequil GAATTCCGCC GCGCTGTTGG CGTCTGCCAG TTGTTTTGCT CCACACCACTC CCACGGGAGAA	CCTTCCCTCT GCTGCTGCTG ACAAATGCTG  149 DNA Se id Accessio uence: 445.  11    TCACAGTGGC CGTGAGTTGA CTTCGTGGGG GTTCCAGGAA TGCCCGCTCA ATCCACCGGG	CCCCAGACT CTAATCTTCA CGCCTTAAA quence n #: L29126 .1845 21   CAGGTCCTGT TCGAGCCGCA TCCTTGGCCC GCGAACCTTC CTGGCCCGGG GTCCGAGTGCCGCGGGGTCCGGGCCGGG	TGGTGTCCTT GGGCACTGCT AAA  .1  31    GCCAGATTGT GCCGCAGCTC GCAGCTGGTT TCGATGTAGC TCTCCTTGAA AGGGGGCAT	TCCCTCCACT GCTGCCTTA  41	TCTTAGGCC TCTTCCTGCC GTCGCTGAGG  51   CTCCAGCCGG GCCTGGTAGA AGCCAGCGCC GTATTGAGCT AGTGCCCCAG AGAGGCGGGT	2940 3000 3033 60 120 180 240 300
50 55	GAAGAAGGT ACCTGCTGCT AAAAATAAAG Seq ID NO: Nucleic Ac Coding seq 1   GAATTCCGCC GCGCTGTTCG CGTCTGCCAG TTGTTTTGCT CCAGGAGACCCA GCAGGACCCA GCAGGACCCA	CCTTCCCTCT GCTGCTGCTG ACAAATGCTG 149 DNA Seid Accessio uence: 445. 11 † TCACAGTGGC CGTGAGTTGA CTTGGTGGGG GTTCCAGGAA ATCCACCGG AATCCACCGG	CCCCAGACT CTAATCTCA GUENCE n #: L29126 .1845 21   CAGGTCCTGT TCGAGCCGCA TCCTTGGCCCGC GCGAACCTTC CTGGCCCGGG AGGAGCCACG AGGAGCCACG AGGAGCCACG AGGAGCCACG	GCGCACCACA AGGGGGATTGT TCGATGTAGC TCGATGTAGC TCGATGTAGC TCCCTCGAA AGGGGGATTGT ACCCCCCACCA	41	TCTAAGGCC TCTTCCTGCC GTCGCTGAGG  51	2940 3000 3033 60 120 180 240 300 360
50 55	GAAGAAGGT ACCTGCTGCT AAAATAAAG Seq ID NO: Nucleic Acc Coding seq I GAATTCCGCC GCGCTGTTGG CGTCTGCCAG TTGTTTTGCT CCATCATCTC CCAGGGAGAA GCAGGACCGC	CCTTCCTCT GCTGCTGCTG ACAAATGCTG 149 DNA Seid Accessiouence: 445. 11   TCACAGTGGC CGTGAGTTGA CTTGGTGGGA TTGCCGGGA TTGCCGGGA TGCCGCTCA ATCCACCGG GACGCGGCG	CCCCAGACT CTAATCTCA CGCCTTAAA Quence n #: L29126 .1845 21   CAGGTCCTGT TCGAGCCGCA TCCTTGGCCC GTGCAACCTTC CTGGCCCGCA GTGCGAGTCG AGGAGCCAGC AGGAGACCAGC AGGAGCCAGC AGGAGACCAGC AGGAGACCAGC AGGAGACCAGC AGGAGCCAGC AGGACCAGC AGGAGCCAGC AGGAGCCAGC AGGAGCCAGC AGGAGCCAGC AGGAGCCAGC AGGAGACCACC AGGACCACC	TGGTGTCCTT GGGGACTGCT AAA  .1  31   GCCAGATTGT GCCGCAGCTGGT TCGATGTAGC TCTCCTTGAA AGGGGCATT AGGGGCATT CCCCCCACCA CTCCTCTCCACCACCA CTCCTCTCCACCACCACCACCACCACCACCACCACCACCA	41	S1   CTCCAGCCGG GCCTGTAGGCCGG GCCTGTAGA AGCCAGGCCGG GTATTGAGCT AGTGCCCCAG AGAGGGGGGT TGAGGGAGACG CTCCTCCGTG	2940 3000 3033 60 120 180 240 300 360 420
50	GAAGAAGGT ACCTGCTGCT AAAATAAAG Seq ID NO: Nucleic Acc Coding seq I GAATTCCGCC GCGCTGTTGG CGTCTGCCAG TGTTTTGCT CCATCATCTC CCAGGGAGAA GCAGGACCCA TAGGAGCCGA TGCTCCCATC	CCTTCCCTCT GCTGCTGCTG ACAAATGCTG 149 DNA Sei id Accessio uence: 445. 11   TCACAGTGGC CGTGAGTTGA CTTCGGGGG GTTCCAGGAC ATCCACCGG GACGCGCGC GAGCAGCGGGGGGGGGG	CCCAAGACT CTAATCTTCA CGCCTTAAA quence n #: L29126 .1845 21   CAAGGTCCTGT TCGAGCCGCA TCCTTGGCC GCGAACCTTC CTGGCCGGGG GTCGGAGTGG GTCGGAGTGG CAGGCCAGG	TGGTGTCCTT GGGCACTGCT AAA  .1  31   GCCAGATTGT GCCGCAGCTC GCAGTTGTT CCTCTTGAA AGGGGGCATT CCTCCTTCTCCCA ATATGGAAT	41	S1	2940 3000 3033 60 120 180 240 300 360 420 480
50 55	GAAGAAGGT ACCTGCTGCT AAAATAAAG Seq ID NO: Nucleic Ac: Coding seqt 1   GAATTCCGCC GCGCTGTTGG CGTCTGCCAG TTGTTTTGCT CCATCATCT CCATCATCT TAGGAGCCGAC TAGGAGCGAC TAGGAGCGAC TAGGAGGCAC CAAGAGGCAC	CCTTCCCTCT GCTGCTGCTG ACAAATGCTG  149 DNA Seid Accessio uence: 445.  11  TCACAGTGGC CGTGAGTTGA CTTGGTGGGC GTTCCAGGAA ATCCCCCTCA GACGGCGGCCC GAGCAGCGGA CTGAAGAATA CTCGTCCCAA	CCCCAGACT CTAATCTTCA CGCCTTAAA quence n #: L29126 .1845 21   CAGGTCCTGT TCGAGCCGCA TCCTTGGCCC GGGAACCTTC CTGGCCCGCG GTCGGGGTGCC AGGAGCCAGC GGTGATGCGT CCAGGCCTCCI GAGAACATC CAAGACCACC GGTAATGCGT CAAGACCACC GAGAACATC CAAGACCACC GAGAACATC CAAGACCACC CAAGAACATCATC CAAGAACATCATC	TGGTGTCCTT GGGCACTGCT AAA  .1  31    GCCAGATTGT GCCGCAGCTC GCAGCTGGTT TCGATGTAGC TCTCCTTGAA AGGGGGCAT CCCCCACCA CCCCTCTCCCA ATATGGAAA TGTCCTCGCG	41   CCCTCCACT  41   CCCTCTCAAC CCGCTCCAGC CTGGCAGGCCAGGG CGCAGCTCGGCAGGCCAGGGCAGGG	TICTAAGGCC TCTTCTGCC GTCGCTGAGG  51   CTCCAGCCGG GCCTGGTAGA AGCCAGCCCC GTATTGAGCT AGTGCCCCAG AGAGGCGGGT TGAGGAGACG TCAGTTACAG TCAGTTACAG ACAGCACAAAA	2940 3000 3033 60 120 180 240 300 360 420 480 540
50 55	GAAGAAGGT ACCTGCTGCT AAAATAAAG Seq ID NO: Nucleic A: Coding seq I GAATTCCGCC GCGCTGTTGG CGTCTGCCAG GTTTTGCCAG GCAGACCCA TAGGAGCAC TAGTATCGC CAAGAGGCGC TCCTCCGATG CAAGAGGGCGC TATTATGGGA	CCTTCCTCT GCTGCTGCTG ACAAATGCTG 149 DNA Seid Accessiouence: 445. 11   TCACAGTGGC CGTGAGTTGA CTTGGTGGGC GTTCCAGGAA TGCCCGCTCA ATCCACCGGG GACGGCGCCC GAGCAGCGGGAA CTGAAGAATA CTGGTCCGTCCAA	CCCCAGACT CTAATCTICA GUENCE n #: L29126 .1845 21   CAGGTCCTGT TCGAGCCGCA TCCTTGGCCCGCA GTCGGGATGCC AGGAGCCACC GCTGATGCCC CGGTAATGCGT CCAGCTCCT CTGGCCCGGC TCCTGGCCCGCC TCCTGGCCCGCC TCGGGATGCCACC TCGGGATGCCACC TCGGGATGCGT TCGGGATCATT	TGGTGTCCTT GGGGACTGCT AAA  1 31   GCCAGATTGT GCCGCAGCTC GCAGCTGGTT TCGATGTAGAG AGGGGCATT CCCCCCACCA CTCCTTCCA ATATGGAAAT TGTCCTCCGG	41	SI  CTCCAGCCGG GCCTGATGA  SI  CTCCAGCCGG GCCTGGTAGA AGCCAGCGC GTATTGAGCT AGTGCCCCAG AGAGGCGGGT TGAGGAGACG CTCGTCGGTG TGAGGAGACG CTCGTCGGTG TCAGTTACAG CCAGACCAAAA AGCTTCTTGGA	60 120 180 3033 60 120 180 240 300 360 420 480 540 600 660
50 55	GAAGAAGGT ACCTGCTGCT AAAATAAAG Seq ID NO: Nucleic Acc Coding seq I GAATTCCGCC GCGCTGTTGG CGTCTGCCAG TTGTTTTGCT CCATCATCTC CCAGGGAGAA TAGGAGCGCC TCCTCCCGATG CAAGAGGCAC TATTATGAGGGCGA TATTATGAGGGAGA GCGCTGGAGG CAAGAGGCAA GGCCTGGAGG	CCTTCCTCT GCTGCTGCTG ACAAATGCTG ACAAATGCTG 149 DNA Seid Accessiouence: 445. 11   TCACAGTGGC CGTGAGTTGA CTTGGTGGGC GGTCCAGAA TGCCCGGTCA ATCCACCGGA CTGAAGAATA CTGACGGGGA CTGAAGAATA CTGGTCCCAA GAGAGTTCA GGGGGGGA GGGGGGGA GTGAAGAATA	CCCCAGACT CTAATCTICA GCCCTTAAA quence n #: L29126 .1845 21   CAGGTCCTGT TCGAGCCGCA TCCTTGGCCCGCACCTTC CTGGCCCGCG GTCGGAGCTCC GGTGAGTCCC GGTGAGTCCC GGTGAGTCCC GGTGAGTCCC GGTGAGTCCC GGTGAGTCCC GGTGAGTCCC GGTGAGTCCC GGTGATCCT CCAGCCTCCC GGGATCATC CCAGCTCCCC GGGATCATC CCAGCTCCCC GGGATCATC CCAGCTCCCC CCAGCTCCCC CCAGCTCCCCC CCAGCTCCCC CCAGCTCCCCC CCAGCTCCCC CCAGCTCCCC CCAGCTCCCC CCAGCTCCCCC CCAGCTCCCC CCAGCTCCCCC CCAGCTCCCC CCAGCTCCCCC CCAGCTCCCC CCAGCTCCCCC CCAGCTCCCC CCACCCCC CCACCCCC CCACCCCCC CCACCCCCC	TGGTGTCCTT GGGGACTGCT AAA  .1  31    GCCAGATTGT GCCGCAGCTGGT TCGCATGTAGT AGGGGCATT CCCCCACCA ATATGGAAAT TGTCCTGGGG TCTCCTGGGAG AGCCAGCGGG AGCCAGCGGG AGCCAGCGGG AGCCAGCGGG AGCCAGCGGG AGCCAGCGGG AGCCAGCGGG AAACGCAGCGGG AAACGCAGCGGG AAACGCAGCGGGAAAA	41     CCCTCCAAC  TOGCAGCTCAAC TOGCAGCTCAAC TOGCAGCTCAGC GCCAGCATTG GCAGCAGGG GCAGCATTG GAGCCAGGG AGCCAGGG AGCCAGGGAAG AGCCAGGATGAAC AGCAGCAGGAAG AGCAGCAGGGAAG AGCAGCAGGGAAG AACCAGGATGAAC AACCAGGATGAAC AACCAGGATGAAC AACCAGGATGAAC AACCAGGATGAAC AACCAGGATGAACAGGATGAACCAGGATGAACCAGGATGAACAGGATGAACAGGATGAACAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGGATGAACCAGAACCAGGATGAACCAGAACCAGAACCAACAACCAGAACCAACAACCAACAA	S1	2940 3000 3033 60 120 180 240 360 420 540 660 660 6720
50 55 60	GAAGAAGGT ACCTGCTGCT AAAATAAAG Seq ID NO: Nucleic Ac. Coding seq I GAATTCCGCC GCGCTGTTGG CGTCTGCCAG TTGTTTTGCT CCATCATCTC CCAGGAGAAA GCAGGACCCA TAGGAGCGGC TAGTTATGCAAG GCAGGAGAC CAAGAGGCAC TATTATGGAA GCCTGCAGG	CCTTCCCTCT GCTGCTGCTG ACAAATGCTG ACAAATGCTG 149 DNA Seid Accessio Unence: 445. 11	CCCAAGACT CTAATCTCA CGCCTTAAA quence n #: L29126 .1845 21   CAGGTCCTGT TCGAGCCGCA TCCTTGGCC GGAACCTTC CTGGCCGGGGAACCTTC CTGGCGGGGTGGGGGGGGGG	TGGTGTCCTT GGGCACTGCT AAA  .1  31    GCCAGATTGT GCCGCAGCTC GCAGCTGGT TCGATGTAGC TCTCCTTGCAA AGGGGCATT ATATGGAAT TGTCCTCGGGG TTTCGGAGG TGTCCTGGGGG TTTCGGAGGGC TTTCGGAGGGC TTTCGGAGGGC TTTCGGAGGGC TTCAGGAGGGC TTCAGGAGGGC TTCAGGAGGGC TTACAGGCTCC	41	51   CTCCAGCCGG GCCTGAGA  51   CTCCAGCCGG GCCTGGTAGA AGCCAGCCCC GTATTGAGCT AGTGCCCCAG TGAGGAGACG TGAGGAGACG CTCCTCGGTG TCAGTTACAG CCAGCCAAAA AGCTTCTTGGA CCAGACCAAAA AGCTTCTTGGA CCAGACCACGCTG GAAACACTTT	2940 3000 3033 60 120 180 240 420 480 600 660 720 720 780
50 55	GAAGAAGGT ACCTGCTGCT AAAAATAAAG Seq ID NO: Nucleic Ac: Coding sequil GAATTCCGCC GCGCTGTTGG CGTCTGCCGG TTGTTTTGCT CCAGGGAGAA GCAGGACCCA TAGGAGCCGC TCCTCCGATG CAAGAGGCAC TATTATGGAA GGCGTGGAGG GCTTCTCAGGT GTGGGTGAGG	CCTTCCCTCT GCTGCTGCTG ACAAATGCTG 149 DNA Seid Accessiouence: 445. 11   TCACAGTGGC GTTCAGGAA TGCCCGGCTCA ATCACCCGG GAGCAGCGGC GAGCAGCGGC GAGCAGCTGAA CTCGTCCCAA GAGAGTTTCA GGAGATTCA AGAGGTTTCA	CCCCAGACT CTAATCTCA GUENCE n #: L29126 .1845 21   CAGGTCCTGT TCGAGCCGCA TCCTTGGCCCGC GCGAACCTTC CTGGCCGGC GTCGGGTGCC GGGATCCTT TGGGCCAGC GGTGATCCT TGGGCCAGC GGTGATCCT TGGGCCAGC GGTGATCCT TGGGCTCCC AGGACCACC AGGACCACC AGGACCACC GGTGATCAT TGGGATTCAT	TGGTGTCCTT GGGCACTGCT AAA  .1  31    GCCAGATTGT GCCACCAGCTGGTT TTGGATGTAGCG TCTCCTTGAA AGGGGCATT TCGCTCCACCA CTCCTCCACCA CTCCTCCACCA CTCCTCCACCA CTCTCTCGGAGG AGCCAGCGG TTCTCGGAGG AGCCAGCGGG TACAGGCTGT GATCTGGTGG GATCTGGTGG	41	TCTTAGGCC TCTTCTGCC GTCGCTGAGG  51   CTCCAGCCGG GCCTGGTAGA AGCCAGCGCC GTATTGAGCT AGTGCCCCAG TGAGGAGACG TCAGTTACAG TCAGTTACAG CCAGCCACAAAA AGCTTCTTGGA GCTACTTGGAG GCAGACCAAAA GCTTCTTGGA GCAACACTTT GGAAACACTTT GGAAACACTTT	2940 3000 3033 60 120 180 240 300 420 480 540 660 720 840
50 55 60	GAAGAAGGT ACCTGCTGCT AAAATAAAG Seq ID NO: Nucleic Ac Coding seq I GAATTCCGCC GCGCTGTTGG CGTCTGCCAG TTGTTTTGCT CCATGATCATCTC CCAGGGAGAA GCAGGACCG TCCTCCGATG CAAGAGGCAC TATTATGGAG GCAGGACG GCTCTCAGGT TATTATGGAGGAAG GCTCTCAGGT TATTATGAAA	CCTTCCTCT GCTGCTGCTG ACAAATGCTG ACAAATGCTG 149 DNA Seid Accessiouence: 445. 11   TCACAGTGGC CGTGAGTTGA TGCCCGCTCA ATCCACCGG ACCGCGGCGCGC CGAGCAGCGGGCGCGCCCC GAGCAGCGGGGCGGGGCGCGGCGCGGGGGGGG	CCCCAGACT CTAATCTICA GUENCE n #: L29126 .1845 21   CAGGTCCTGT TCGAGCCGCA TCCTTGCCC GGGAACCTTC CTGGCCGGG GTGGGGTGC AGGAGCCAGC CTGGCCCGGG CGTGATGCGT CCTAGAGCC CTGGCCCGGC GGGAACCTTC CTGGCCCGGC GGGAACCTTC CTGGCCCGGC GGGAACCTTC CTGGCCCGGC CGGGAACCTTC CCTGGCCCGGC CGGGAACCTTC CCAGCTCCT CGAGTACAT CCTTAGAGAI AGCCTTAAAC CCGAGTACATC CGGAGTACATC	IGGITICCTT GGGACTGCT ANA  1  31    GCCAGATTGT GCCGCAGCTG TCTGAN AGGGGCATT TCTCCTTGAN AGGGGCAT TCTCCTCCA ATATGGANAT TCTCCTCCGGAG TCTCCTGGAG AGCCAGCGGT TCTCGGGAG AGCCAGCGGT TCTCGGGAG AGCCAGCGGT TAAGGATCT TCTCAGGAGT TCTCAGGAGT TCTCAGGAGT TCTCAGGAGT TCTCAGGAGG TCTCAGGAGT TCTCAGGAGT TCTCAGGAGT TCTCAGGAGT TCTCAGGAGT TCTCAGAAATG	41	SI  CTCCAGCCGG GCCTGAGG  SI  CTCCAGCCGG GCCTGGTAGA AGCCAGCGC GTATTGAGCT AGTGCCCCAG AGAGCCGCG TTAGAGCGCG CTCGTCGGTG AGAGCCGCGG CTCGTCGGTG CTCGTCGGTG CCAGCAGACCAATA CAGCCGCGTG CCACCAGCGCGG CCACCAGCGCGG CCACCACAGCGCGG CCACCACAGCGCGG CCACCACAGCGCTG CCACCACAGCGCTG CCACCACAGCCGCTG CCACCACAGCCGCTG CCACCACAGCCGCTG CCACCACAGCTG CCACCACAGCCGCTG CCACCACAGCCCCCCCCCC	2940 3000 3033 60 120 180 240 360 420 480 540 660 720 780 840 900
50 55 60	GAAGAAGGT ACCTGCTGCT AAAATAAAG Seq ID NO: Nucleic Acc Coding seq I GAATTCCGCC GCGCTGTTGG CGTCTGCCAG TGTTTTGCT CCATCATCTC CCAGGGAGAA GCAGGACCCA TAGGAGCGCG TGCTCCGATG CAAGAGGCAC TATTATGGAA GCCTCGAGG GCTCTCAGGT GTGGGGGGG GTTCTCAGGT TATTATGGAA ACCATAGAGA ACACATTGGAT CACATAGAGA CACATTGGAT	CCTTCCCTCT GCTGCTGCTG ACAAATGCTG ACAAATGCTG 149 DNA Sei id Accessio uence: 445. 11    TCACAGTGGC CGTGAGTTGA CTTGGTGGGG GTTCCAGGA ATCCACCGG GAGCAGCGGCA CTGAAGAATA CTCGTCCAA GAGAGTTTCA GGGAGTTCA GGGGCTACAT TTGGAAACCA AGAGGTTTCA AGAGGTTTCA AGAAGGTTTCA AGAAAGGTTTCA AGAAAGCTACA AGAAGGTTTCA AGAAAGCTGC ATGCCACCCT	CCCCAGACT CTAATCTTCA CGCCTTAAA quence n #: L29126 .1845 21   CAGGTCCTGT TCGAGCCGCA TCCTTGGCC GCGAACCTTC CTGGACCGCA GTCGGATCGC GGTGGATCGG CGAGCTCCT GGGACCTCC GGGGACCTCC GGGACCTCC GGGACCTCC GGGACCTCC GGGATCAGG CCAGCCTCCAGGACCTCC CCTACAGGAC CCCTTAGAGAC GCGATCATCAT CCGAGTACAT CGGATTCAT CGGATTCAT CGGATTCAT CGGATTCAT	IGGTGTCCTT GGGCACTGCT AAA  .1  31    GCCAGATTGT GCCGCAGCTG GCAGATTGT GCCGCAGCTG TCTCCTTGAA AGGGGCATT AGGGGCATT TCTCCTTGCA ATATGGAAT TGTCCTGGCAG TTCTCGGAGC TTCTCGGAGC TTCAGGAGT TGTCTGGGAG TTCAGGAGT TGTCTGGGAG TTCAGAGT AGCCAGCGGG TTCAAAATGAAATG	41   CCCTCCAAC TOGCAGCTCA TOGCAGCTCAAC TOGCAGCTCAGC GCCAGCATTG CAGCCTCAGC CAGCTCAGC CAGCATAGC CAGCATAGC CAGCATAGC CAGCAGAAC CAGCAGATG CAGCAGATG CAGCAGATG CAGCAGATG CAGCAGATG CAGCAGGATG CA	51   CTCCAGCCGG GCCTGGTAGA AGCCAGCCCC GTATTGAGCT AGTGCCCCAG AGAGCAGCAC CTCAGCCGG CTCGTTAGA AGCCAGCAGCCC GTATTGAGCT CTGAGCAGCAGA AGCTTCTTGGA ACTACAGCTG GAAACACTTT GATAACACTT GATAACACTT GATAACACTG CACTCTATGAA CCTCTCATGAA AGCTTCTTAGAA CCTACAGCTG CACTCTTAGAA CCTCTCATGAA CCTCTCATGAA CCTCTCTATGAA CCTCTCTATGAA CCTCTCTATGAA CCAGCTCTAAA	2940 3000 3033 60 120 180 240 300 360 420 480 540 660 660 660 720 780 840 900 900 960
50 55 60	GAAGAAGGT ACCTGCTGCT AAAAATAAAG Seq ID NO: Nucleic Ac Coding seq    GAATTCCGCC GCGCTGTTGG CGTCTGCGCG GTTTTTGCT CCAGGGAGAA GCAGGACCCA TAGGACCGC TCCTCCGATG CAAGAGGCAC TATTATGGAA GCGCTTCTAGGA GCCGTTGAGGT GTCGTCAGGT GTCGTCAGGT ATTATGGAA CACATTGGAA AATGAAAC CACATTGGAA	CCTTCCCTCT GCTGCTGCTG ACAAATGCTG ACAAATGCTG 149 DNA Seid Accessiouence: 445. 11 TCACAGTGGC GTTCAGGAA TGCCCGGTAA TGCCCGGTAA GAGAGTTCA GAGAGGTTCA GAGAGGTTCA ATCACCCGG GAGCAGCGGC GAGCAGCGGAA TTGGAAACCAA AGAGGTTTGAAAGCAA AGAGGTTTGAAACCAA AGAGGTTTGAAAACCAA AGAGGTTTGAAAACCAA AGAGGTTTGAAAACCAA	CCCCAGACT CTAATCTICA GUENCE n #: L29126 .1845 21   CAGGTCCTGT TCGAGCCGCA TCCTTGGCCCGCA GGGAGCCTCCT CTGGCCCGCA GGTGATGCGT CCTGAGTCCCT AGGAGCCACC GGTGATCCT TGGGATTCCT CTGGCCTCCT CTGGCCTCCT CTGGCCTCCT CTGGCCTCCT CTGGCCTCCT CTGGCCTCCT CTGGCCTCCT CTGGCCTCCT AGGAGCTACAC GGTGATCAT CCTTAGAGAI GGCCTTAAAG GGCCTTAAAC GGTCACTTAAC CGTCACACACA CGTCACACAC CGTCACACACA CGTCACACACAC CGTCACACACA CGTCACACACAC CGTCACACACACACAC CGTCACACACACAC CGTCACACACAC CGTCACACACAC CGTCACACACAC CGTCACACACACACACACAC CGTCACACACACACACACACACAC CGTCACACACACACACACACACACACACACACACACACAC	TGGTGTCCTT GGGCACTGCT AAA  1 31   GCCAGATTGT GCCAGCAGTTGT TCGATGTAGCG TCTCCTTGAA AGGGGCATT TCGCTCCACCA CTCCTCCACCA CTCCTCCACCA CTCCTCCACCA CTCCTCCGGGG TCTCCGGGGG TCTCCGGGGG TCTCGGGGGG TCTCGGGGG TCTCGGGGG TCACAGGCTCT GATCTGGTG TCAAAATGG AAATGGAAA AAAGTATCC GAAGAACAC GAAGAACAC GGAGAACAC	41	TICTAAGGCC TCTTCTGCC GTCGCTGAGG  51	2940 3000 3033 60 120 180 240 420 480 660 720 780 840 900 960 1020
50 55 60 65	GAAGAAGGT ACCTGCTGCT AAAATAAAG Seq ID NO: Nucleic Ac Coding seq I GAATTCCGCC GCGCTGTTGG CGTCTGCCAG TTGTTTGCCAG CATCATCTC CCAGGGAGAA GCAGGACCCA TAGGAGCCAC TATTATTGGA GCGTGGAGG GCTCTCAGGT GTOGGTGAGA GATACAATAGAAA CACATTGGAA AATGAACCAA TCCCTGGTTC	CCTTCCTCT GCTGCTGCTG ACAAATGCTG ACAAATGCTG 149 DNA Seid Accessiouence: 445. 11   TCACAGTGGC CGTGAGTTGA CTTGGTGGGC GTTCCAGGAA TGCCCGCTCA ATCCACCCGG GACGAGGGGGC GAGCAGCGGGG CTGAGGATTCA CTGTCCCAC TTGGTAGCAC TTGGAAACCAA CGAAGGTTTCA AGAGGTTTCA AGAGGTTTGA AGAGGTTTGA AGAGGTTTGA AGAGGTTTGA AGAGGTTTGA AGAGGTTTGA AGAGGTTTGA AGAGGTTGG ATGCCACCCT ATGCCACCCT GAAAAACCAAC GAAAACCAAC GAAAACCAAC GAAAACCAAC GAAGGGGTTGG ATGCAACCACCT ATGCCACCCT AGAAAACCAAC GAAAACCAAC GAAGGGGTTGG ATGCAACCACCT AGAAAACCAAC GAAGGGCTTGG AGAAAACCAAC GAAGGGGTTGG AGAAAACCAAC GAAGGGCTTGG AGAAAACCAAC GAAGGGCTTGG AGAAAACCAAC GGAAGGGCTTGG ACGAAAACCAAC AGAGGGCTTGG ACGAAAACCAAC AGAAAACCAAC AGAAAACCAAC AGAAAACCAAC AGAAAACCAAC AGAAAACCAAC AGAAAACCAAC AGAAGGGCTTGG AGAAAACCAAC AGAGGGCTTGG AGAAAACCAAC AGAAGGGCTTGG AGAAAACCAAC AGAAAACCAAC AGAAGGGCTTGG AGAAAACCAAC AGAGGGCTTGG AGAAAACCAAC AGAGGGCTTGG AGAAAACCAAC AGAGGGCTTGG AGAAAACCAAC AGAGGGCTTGG AGAAAACCAAC AGAGGGCTGG AGAAAACCAAC AGAGGGCTGG AGAAAACCAAC AGAGGGCTGG AGAGAAACCAAC AGAGGGCTGG AGAAAACCAAC AGAGGCGCTGG AGAAAACCAAC AGAGGCCTGC	CCCCAGACT CTAATCTICA GUENCE n #: L29126 .1845 21   CAGGTCCTGT TCGAGCCGCA TCCTTGGCCCGCA GTCGGAGTGC AGGAGCCACA CGTGATGCCT CTGGCCCGGC GTCGGATTGCT CTGGCCCGGC GTCGATTGCCC CGGAACCATT CTGGAGTTGCT CTGGCCCGGC GTGAGTAGCT CGTGATGCT CTGGAGTTGCT CTGGAGTTGCT CTGGAGTTCAT CGTGATCAT CGTGATCAT CTGGATTCAT CTGGATTCAT CTGGATTCAT CTGGATTCAT CTGGATTCAT CTGCACACACA CCTCACACAC	TGGTGTCCTT GGGCACTGCT AAA  1 31   GCCAGATTGT GCCGCAGCTG TCGATGTAGAGCGCC TCTCCTTGAA AGGGGCATT TGTCCTCGCG ATATGGAAAT TGTCCTCGGAGC TTCTCGGAGC TCTCCTGGAGC AGCCAGCGGC TACAGGCTCC TCTCAGAAAT TGTCCTGGGAGC AGCCAGCGGC TACAGGCTCC TCAAAAATAGAAAT AAAGTATCCC GAACTAGAACAACC GAACGAACAACC AACGACAACC	41	SI  CTCTAAGGCC GTCGCTGAGG  SI  CTCCAGCCGG GCCTGGTAGA AGCCAGCGC GTATTGAGCT AGTGCCCCAG AGAGGCGCG TAATGAGCT TAAGTACAG AGCAGCACAAA AGCTTCTTGGA CAGACCAAAA AGCTTCTTGGA CAGACCATTT GATAACACTT GATAACACTTG CATCTATGAA AAAGATCTCAAAAAAAAAA	2940 3000 3033 60 120 180 240 360 420 480 540 660 720 780 900 960 1020 1080
50 55 60	GAAGAAGGT ACCTGCTGCT AAAATAAAG Seq ID NO: Nucleic Acc Coding seq I GAATTCCGCC GCGCTGTTGG CGTCTGCCAG TGTTTTGCT CCATCATCTC CCAGGGAGAA TAGGAGCGCA TATTATGGAG GCCTGCGAGG GCTCTCCGATG CAAGAGGCAA TATTATGGAT CACATGGAG ATCATCAGTT ACTAGAAA TACATAGAAA CACATTGAT AATGAACCAA TCCCTGGTTTA	CCTTCCTCT GCTGCTGCTG ACAAATGCTG ACAAATGCTG 149 DNA Seid Accessiouence: 445. 11	CCCCAGACT CTAATCTICA GUENCE  n #: L29126 .1845 21   CAGGTCCTG TCGAGCCGCA TCCTTGGCCCGCA GTCGAGCCTCC GGCAACCTTC CTGGACCTCC GGCAACCTC CCTGGACCCGCA GTCGATCCAT CCTTAGAGAA AGCCTAGAACAT CCTTAGAGAA AGCCTACACACAC CCCTCACACACAC CCTTCACACACAC CCTTCACACACC CGTTCACACACC CGTTCACACACC CGTTCACACACC	IGGITICCTT GGGGCACTGCT AAA  .1  31    GCCAGATTGT GCCGCAGCTG TCGCATGTAT ACGCGCAGCTGGTAT ACGCGCAGCTGTT CCCCCACCAC ATATGGAAAT TGTCCTGGGG TCTCTCCCA AGCCAGCGGC TACAGGCTGT TACAGGCTCT ATATGGAAAT ATATGGAAAT ATACGGAAAC AGCACACC	41	TICTAAGGCC TCTTCTGCC GTCGCTGAGG  51   CTCCAGCCGG GCCTGGTAGA AGCCAGCCCC GTATTGAGCT TGAGGAGCCCCAG AGAGCGCGGT TGAGGAGACCAAAA AGCTTCTTCGT CTCGTCGGT TCAGTTACAGG CTACACGCTG GAAACACTTT GATAACACTG CATCTATGAA AAAGATCTCC ATGAGAAGACA TGCCAATTTC	2940 3000 3033 60 120 180 240 300 360 420 780 660 720 780 840 900 960 1020 1080 1140
50 55 60 65	GAAGAAGGT ACCTGCTGCT AAAATAAAG Seq ID NO: Nucleic Ac Coding seq I GAATTCCGCC GCGCTGTTGG CGTCTGCCAG TTGTTTTTGCT CCAGGAGACA TAGGAGCCCA TAGGAGCCCA TATTATGGAA GGCTGGAGG GCTCTCCGATG CAAGAGGCAC TATTATGGAA GGCTGGAGG TACTAGAAC TACATAGAAA CACATTGGAA TCCCTGGTTC CACACTTTTA AATGAACCAA TCCCTGGTTC CACAACTTTTA ATGTGGGGGG	CCTTCCCTCT GCTGCTGCTG ACAAATGCTG ACAAATGCTG 149 DNA Seid Accessio uence: 445. 11   TCACAGTGGC CGTGAGTTGA CTTGGTGGGG GTTCCAGGAA TCACCCGGTA ATCACCCGG GAGCAGCGGA CTGAAGAATA CTGAGTGCCAA AGAGGTTCAA GAGAGTTTCAA GAAAAGCTGG ATGCCACACA AGAGGTTTGAAACCAA AGAGGTTTGAAACCAA AGAGGTTTGAAACCAA AGAGGTTTGAAACCAA AGAGGTTTGAAACCAA AGAGGTTCAACACCCTAAGAACAAA	CCCCAGACT CTAATCTICA GUENCE n #: L29126 .1845 21   CAGGTCCTGT TCGAGCCGCA TCCTTGGCCCGC GCGAACCTTC GTCGGACTGCC GTCGAGTCCT AGGACTCC AGGATCATC AGGACCACA GTCATTAAA GCCTTAAAA GCCTTAAAA AGGCTTAAAA CCTCACACAC CCTCACCACA CCTCACCACAC CCTTCCACACA AAGGGTTCCGA	GGGACTGCT GGGCACTGCT AAA  1 31   GCCAGATTGT GCCGCAGCTC GGAGTGGTT TCGATGTAGC TCTCCTTGAA AGGGGGCATT GCCCCCCACCA CTCCTCTCCA ATATGGAAAT ACGCGCCT TCTCTGGGAGC TCTCTGGGAGC TCTCTGGGAGC TCTCTGGGAGC TCTCTGGGAGC TCTCAAAATGA AAAGTATCC GAAGAACACC GAAGAACACC GAAGACAACC CAACACTGGG GTGCTAGAACTGGG GTGCTAGAACTGGG GTGCTAGAACTGGG GTGCTAGAACTGGG GTGCTAGAACTGGG GTGCTAGACTGGG GTGCTAGACACCGG GTGCTAGACCACCGG GTGCTAGACACCG GTGCTAGACACCG GTGCTAGACACCG GTGCTAGACACCG GTGCTAGACACCG GTGCTAGACACCG GTGCTAGACACCG GTGCTAGACACCG GTGCTAGACCACCGG GTGCTAGACACCG GTGCTAGACACCG GTGCTAGACACCG GTGCTAGACACCG GTGCTAGACACCG GTGCTAGACACCG GTGCTAGACACCC GTGCTAGACCC GTGCTAGACC GTGCTAGACCC GTGCTAGACC GTGCTAGACC GTGCTAGACC GTGCTAGACC GTGCTAGACC GTGCTAGACC GTGCTAGACC GTGCTAGACC GTGCTAGACC GTGCTAG	41	51	2940 3000 3033 60 120 180 240 360 420 480 540 660 660 660 660 660 1020 1020 1020 1140 1200
50 55 60 65	GAAGAAGGT ACCTGCTGCT AAAATAAAG Seq ID NO: Nucleic A: Coding seq    GAATTCCGCC GCGCTGTTGG CGTCTGCCAG GTTGTTGCCAG GCAGACCCA TAGAGAGCCA TAGTATCTC CAAGAGGCGC TGCTCGATG GCAGACCCA TATATGGAA GCCGTTCAGGT GTCGTCAGGT ATTATGGAA GCCATTGAA ATGAACCAA TCCCTGGTTC CACACTTTA ATGTGGGGC CAGTGTTCCA	CCTTCCTCT GCTGCTGCTG ACAAATGCTG ACAAATGCTG 149 DNA Seid Accessiouence: 445. 11   TCACAGTGGC CGTGAGTTGA CTTGGTGGGC GTTCCAGGAA TGCCCGCTCA ATCACCCGG GACGAGCGGC GAGCAGCGGG CTGAAGAATA CGAGGGTTCA AGAGGTTTCA AGAGGTTTCA AGAGGTTTGA AGAGGTTTGA AGAGGTTGG AGAAAACAAA CGAAAGGGCGC AGGACACCCC AGGACACCCC AGGACACCCC AGGACACCCC AGGACACCC AGGACACCCC AGGACACCCC AGGACACCCC AGGACACCCC AGGACACCCC AGGACACCCC AGGACACCCCC AGGACACCCCC AGGACACCTCC AGCACCCTCC AGCACCCTCC AGCACCCTCC AGCACCCTCC AGCACCCTCC AGCACCCTCC AGCACCCTCC ACCACCCCC AGCACCCTCC ACCACCCCC ACCACCCCC ACCACCCCC ACCACCCCC ACCACC	CCCCAGACT CTAATCTTCA GUENCE n #: L29126 .1845 21   CAGGTCCTGT TGGAGCCGCA TCCTTGGCCCGCA GGGAACCTTC CTGGCCCGCA GGGAGCCACC GGGAACCTTC CTGGCCCGCA GGGAGCCACC GGTGATGCGT CCTTAGAGAT CCTCAGAGAT CCTCAGAGAT CCTCAGAGAT CCTCACACAC CCTCACAC CCTCA	TGGTGTCCTT GGGCACTGCT AAA  1 31   GCCAGATTGT GCCGCAGCTG TCGATGTAGAGCGCTGCT TCGATGTAGAGCGCCT TTCGAGGGCAC TTCTCCCACAC TTCTCCCACAC TTCTCCGGAGC AGCCAGCGGC TACAGGCTCCT TGAAAAATGAAA CAGACCAC CAACTGGTG CAAAAATGAAAC CAAACAAC CAAACTAGCAC CAAACTGGTG	41	TICTAAGGCC TCTTCTGCC GTCGCTGAGG  51	2940 3000 3033 60 120 180 240 300 360 420 480 540 660 720 780 960 960 1020 1140 1200 1260
50 55 60 65	GAAGAAGGT ACCTGCTGCT AAAATAAAG Seq ID NO: Nucleic Ac Coding seq I GAATTCCGCC GCGCTGTTGG CGTCTGCCAG GTGTTTGCTCAG TGTTTTGCT CCAGGGAGAA TAGGAGCGGC TGCTCGGATG CAAGAGGCAG TTATATGGAA GGCGTGGAGG GTCTCAGGT GTCGTTCAGGT TACTAGAAA TCCCTGGTTC CACAACTTTA ATGTGGGGGC CAGTGTTCCC TACTGTTTGTT	CCTTCCTCT GCTGCTGCTG ACAAATGCTG ACAAATGCTG 149 DNA Seid Accessiouence: 445. 11	CCCCAGACT CTAATCTICA GUENCE  #: L29126 .1845 21   CAGGTCCTGT TCGAGCCGCA TCCTTGGCCC GAGACCTTG CCGAACCTTG CCGAGCCCGCA GTGCGAGTCGT CCTGGCCCGCA GTGCGAGTCGT CCTGGCCCGCA GTGCGATCAT CCTTAGAGAT CCTACACACA CGAGTACATC CCTACACACAC CGTTCCAGCACACAC CGTTCCAGGCA CGTTCCAGCACACAC CGTTCCAGAGA AGGGTCCGC CGTTCCAGAGA AGGGTCCGC CCTCAGAGAA CGTCACACACAC CGTTCCAGAGA AGGGTCCGC CCTCAGAGGA AGGGTCCGC CCCCAAGAC CGTTCCAGAGA AGGGTCCGC CCCCAAGAC CGTTCCAGAGC AGGGTCCGC CCCCAAGAC CGTTCCAGGC CCCCCAGCAC CGTTCCAGGC CCCCCAGCC CGTTCCAGCC CGTTCCAGC CGTTCAGC CGTTCCAGC CGTTCACC CGTTCACC CGTTCACC CGTTCACC CGTTCACC CGTTCCACC CGTTCCAGC CGTTCCAGC CGTTCACC CGTTCCAGC CGTTCCAGC CGTTCACC CGTTCCAGC CGTTCACC CGTTCACC CGTTCACC CGTTCCAGC CGTTCACC CGTTCACC CGTTCCAGC CGTTCACC CGTTCACC CGTTCACC CGTTCACC CGTTCACC CGTTCACC CGTTCCACC CGTTCACC	IGGTOTECTT GGGGACTGCT ANA  1  31    GCCAGATTGT GCCGCAGCTGGT TCGATGTAGC TCTCCTTGAA AGGGGCATT TCGATGTAGC TCTCCTTGAA AGGGGCATT TCTCCTCCACCAC ATATGGAAAT TCTCCTCCCACCAC TCTCCGGAGC AGCCAGCGGGT TCTCGGGAGC AGCCAGCGGGG TCTCAGAAATG AAAGTATCCC CAACACCACC CCCACACCGGG TGCTCAGACC CCCACACTGGT TGCTCAGACC CCACACTGGT CCACACTGGT GGGGACCCC CCACACTGGT CCACACTGGT GGGACAACC CCACACTGGT CCACACCTGGT GGGGACCC CCACACTGGT GGGCCCACACCGGGG TGCTCACACCGGGG GGCTCACACCGGGGG GGCCCACACCGGGG GGCCCACACCGGGGG GGCCCACACCGGGGG GGCCCACACCGGGGG GGCCCACACCGGGGG GGCCCACACCGGGGGG GGCCCACACCGGGGGGGG	TCCTCCACT GCTGCCTTA  41    CCCTCTCAAC TCGCAGCTCA GCTGCAGCTCA GCCAGCATGG GCAGCAGGG TCATCTCCCC GCTGTCCGG CATACTTATA GAGGTGAAAA CAGAGGATGA CACAGAATA CTCAAGAGAC CTCAAGAGAC CTCAGAGAC CTCAGAC CTCACAC	TICTAAGGCC TCTTCTGCC GTCGCTGAGG  51   CTCCAGCCGG GCCTGGTAGA AGCCAGCGCC GTATTGAGCT AGTGCCCCAG AGAGGCGGGT CTGGTCGCTG AGAGCCAAAA AGCTTCTTGG CTCAGCCTG CAGACCAAAA AGCTTCTTGG CATCATAGAA CAGACCTAAA AAAGATCTCC ATGAGAAGACA TGCCAATTIC ACGTACACAAAA CAGACCAATTIC CATGAGAAGACA CAGACAAAAA CAGACCAATTIC CATGAGAAGACA CAGACAAAAA CAGAACACC CTGACACAAAA CAAGAAAAGTGC CATGTAGAAGAC CAGGAGAAAAGTGC CATGTAGAAGACTGC CATGTAGAAAAAGTGC CATGGTGGTACACAAAA	2940 3000 3033 60 120 180 240 300 360 420 780 840 650 720 780 840 1020 1140 1200 1200 1320
50 55 60 65 70	GAAGAAGGT ACCTGCTGCT AAAAATAAAG Seq ID NO: Nucleic Ac Coding seq I GAATTCCGCC GCGCTGTTGG CGTCTGCCAG TTGTTTTTGCT CCATCATCTC CCAGGAGACCA TAGGAGCCCA TAGGAGCCGC TATTATGGAA GGCTGGAGG GCTCTCAGGT GTCGGTGAGA GCTCTCAGGT TAGAACCAA TCCCTGGTTC CAAACTTTA AATGAACCAA TCCCTGGTTC CACAACTTTGC TAGTGGGGC CAGTGTTCCC TACTGTTGC GACATTGGT	CCTTCCCTCT GCTGCTGCTG GCTGCTGCTG ACAAATGCTG  149 DNA Sei id Accessio uence: 445.  11  TCACAGTGGC CGTGAGTTGA CTTGGTGGGG GTTCCAGGAA TCCACCGGA ATCCACCGG GAGCAGCGGA CTGAAGATTCA CGAGAGATTCA GAGAGTTCA GAGAGTTCA GAGAGTTCA GAGAGTTCA GAGAGTTCA GAGAGTTCA GAGAGTTCA GAGAGTTCA GAGAGTTCA AGAGGTTCA AGAGGTCCA AGCCCCI AGAAAACCAA CTCATCGCCCI AGCACGTCC AAGCACGTCC AAGCACGTCC ACCTCACACA CTCATCGCCCI AACCCCCCAAACCTCACACA AGCACGTCCC AACCCCCAAACCTCACACAC ACCTCACACAC ATCGGGAAAA	CCCCAGACT CTAATCTCA GUENCE  n #: L29126 .1845 21   CAGGTCCTGT TCGAGCCGCA TCCTGGCCCGCA GTCGGACCTCC GGGAACCTTC GTCGGACCGCA GTGGACCACA GTGATCAT TCGAGCTAA GTCCTTAAGAGA GTCCTTAAGAGA GTCCTTAAGAGA GTCCATCACACA GTCGATTCAT CCTACACACA GTCCACACACA CCTCACACACA CCTCACACACA CCTCACACACA	IGGTGTCCTT GGGCACTGCT AAA  1  31    GCCAGATTGT GCCGCAGCTC GCAGCTGGT TCGATGTAGC TCTCCTTGAA AGGGGCATT GCCCCCCACCA CTCCTCTCCA ATATGGAAAT GCCCCCCACCA CTCTCTCGGAGC TCTCTGGGAGC TCTCTGGGAGC TCTCTGGGAGC TCTCTGGGAGC TCTCTGGGAGC TCTCAGAATTGC TACAGGCTCT GATCTGGTGA TAAAAATTGCA AAAGTATCC GAAGACACC CAACTGGT GAAGACACC CAACTGGT GAACTGAT GAACTGATACA AGGATTAAAA AGGATTAAAA	41	STITATAGGCC TCTTACTGCC GTCGCTGAGG  SI  CTCCAGCCGG GCCTGGTAGA AGCCAGCGCC GTATTGAGCT AGTGCCCCAG AGAGCGCGG TGAGGAGACG CTCGTTGGTA ACCCACCGTG CAGACCAAAA ACCTTCTTGGA CTACACCGTG GAAACACTTT GAAACACTTT GAAACACTTT CATACACCGCTG CATCTATGAA AAAGATCTCC ATGAGAAGACA ACAGAATTCC ATGAGAAGACA CAGGACAAATTC CGTACACAAAT CAAGAAAGTC CATGTGGTA	2940 3000 3033 60 120 180 240 300 360 420 780 840 900 960 1020 1020 1140 1200 1260 1320 1380
50 55 60 65	GAAGAAGGT ACCTGCTGCT AAAAATAAAG Seq ID NO: Nucleic Ac. Coding sequil GAATTCCGCC GCGCTGTTGG CGTCTGCGAGGAGAA GCAGGACCCA TAGGAGCGCC TCCTCCGATG CAAGAGGCAC TATTATGGAA GCAGGAGGAA TACATAGAAA CACATTGAT AATGAACCAA TCCCTGGTTC CACAACTTTA ATGTGGGGGG CACTGTTCCC TACTGTTCCC TACTGGTTCCC TACTGGTTCCC TCTGGGTTCCC TCTGGTTCCC TCTCCC TCTGGTTCCC TCTGGTTCCC TCTGGTTCCC TCTGGTTCCC TCTGGTTCCC TCTGGTTCCC TCTGTTCCC TC	CCTTCCCTCT GCTGCTGCTG ACAAATGCTG ACAAATGCTG 149 DNA Seid Accessiouence: 445. 11   TCACAGTGGC GTTCAGGAA TGCCCGCTCA ATCACCCGG GAGCAGCGGC GAGCAGCGGC GAGCAGCTCA ACAGTGGTTCA GAGAAATA CTGAAAACCA AGAGGTTTCA AGAGGTTTCA AGAGGTTTCA AGAGGTTCA AGAGGTTTCA AGAGGTTTCA AGAGGTTCACACCT AGAAAACCA AGAGGTTCACACCT AGAAAACCA AGAGGTTCACACCT AGAAAACCAA CTCATCGCCCA AGCACGTTCC AGCACCTTCC AGCACCTTCC AGCACCTTCC AGCACCTTCC AGCACCTTCC AGCACCTTCC ACCTCACAAA ACTCACACAA ACTCACACAA ACTCACACAA ACTCACACAA ACTCACACACA	CCCCAGACT CTAATCTICA GUENCE n #: L29126 .1845 21   CAGGTCCTGT TCGAGCCGCA TCCTTGGCCC GGGAACCTTC CTGGCCCGGG GTCGGGTGCGG GGTGATGCGT CCTGAGATCAT TGGGATCCT CTGGCCCGGG GGTGATCCT CTGGCCCGGG GGTGATCCT CTGGCCCGGG GGTGATCCT CTGGCCCGGG GGTGATCCT CCTTAGAGAT CCTTAGAGAT GACCTTAAAG GGCCTTAAAG GGTCATCACAG CCTACACAGG CCAATGATCAT CCTTCGAGGGG CCAATGATCAT CCTTCACACAG CTCCACACAG CTCACACAG CTCACACAG CCTCACACAG CTCACACAG CTCACACAC CTCACACAG CTCACACAC CTCA	TGGTGTCCTT GGGCACTGCT AAA  1 31   GCCAGATTGT GCCACCACCACCACCACCACCTGGTT TCGATGTAGACACACACACACACACACACACACACACACA	41	TICTAAGGCC TCTTCTGCC GTCGCTGAGG  51   CTCCAGCCGG GCCTGGTAGA AGCCAGCGCC GTATTGAGCT AGTGCCCCAG TGAGGAGACG TCAGTTACAG CAGCACCAAAA AGCTCTTGGA CAGCACCAAAA CAGCACAAAA CAGCACTT TGAGAAGACA TGCCAATTCC ATGACACAAA CAGGAAGACA TGCCAATTCC ATGACACAAA CAAGAAAAGTCCC TGAGAAAAGTCCC TGAGAAAAAGTCCC TGAGAAAAGTCCC TGAGAAAAAGTCCC TGAGAAAAAGTCCC TGAGAAAAAGTCCC TGAGAAAAAGTCCC TGAGAAAAAGTCCC TGAGAAAAAGTCCC TGAGAAAAAGTCCC TGAGAAAAAGTCCC TGAGGAAAAAGTCCCATGGAAAAAGTCCCATGGAAAAAGTCCCATGGAAAAAGTCCCATGGAAAAAGTCCCATGGAAAAAGTCCCATGCTGAAAAAGTCCCATGCTGAAAAAGTCCCATGCTGAAAAAAGTCCCATGCTGAAAAAGTCCCATGCTGAAAAAGTCCCATGCTGAAAAAGTCCCATGCTGAAAAAAGTCCCATGCTGAAAAAGTCCCATGCTGAAAAAGTCCCATGCTGAAAAAGTCCCATGCTGAAAAAGTCCCATGCTGAAAAAGTCCCATGCTGAAAAAGTCCCATGCTGAAAAAGTCCCATGCTGAAAAAGTCCCATGCTGAAAAAGTCCCATGCTGAAAAAGTCCCATGCTGAAAAAGTCCCATGCTGAAAAAGTCCCATGCTGAAAAAGTCCCATGCTGAAAAAGTCCCATGCTGAAAAAGTCCCATGCTGAAAAAGTCCCATGCTGAAAAAGTCCCATGCTGAAAAAGTCCCATGCTGAAAAAGTCCCATGCTGAAAAAGTCCCATGCTGAAAAAGTCCCATGCTGAAAAAGTCCCATGCTGAAAAAGTCCCATGCTGAAAAAGTCCCATGCTGAAAAAGTCCCATGCTGAAAAAGTCCCATGCTGAAAAAGTCCATGCTGAAAAAGTCCCATGCTGAAAAAGTCCCATGCTGAAAAAGTCCCATGCTGAAAAAGTCCATGCTGAAAAAGTCCATGCTGAAAAAGTCCATGCTGAAAAAGTCCATGCTGAAAAAGTCCATGCTGAAAAAAGTCCATGCTGAAAAAAGTCCATGCTGAAAAAAGTCCATGCTGAAAAAAGTCCATGCTGAAAAAAGTCCATGCTGAAAAAGTCCATGCTGAAAAAAGTCCATGCTGAAAAAAGTCCATGCTGAAAAAAGTCCATGCTGAAAAAAGTCCATGCTGAAAAAAAA	2940 3000 3033 60 120 180 240 300 360 420 480 540 900 960 1020 1080 1140 1260 1320 1340
50 55 60 65 70	GAAGAAGGT ACCTGCTGCT AAAATAAAG Seq ID NO: Nucleic Ac Coding seq I GAATTCCGCC GCGCTGTTGG CGGCTGTTGCCAG TTGTTTTGCT CCATGATCATCTC CCAGGGAGAA TAGGAGCACA TATTATTGGAGCGG GTCTCAGGT GTCTCAGGT GTCTCAGGT ATATATGGAA CACATTGGAT AATGAACA CACATTGGTT CACAACTTTA ATGGGGGG CAGTGTTCCC TACTGTTCC CACACTTTC CACACTTC CACACTTC CACACTTC CACACTTTC CACACTTC CACACTTC CACACTTC CACACTTC CACACTTC CACACTTC CACACTTTC CACACTTC CACAC	CCTTCCTCT GCTGCTGCTG ACAAATGCTG ACAAATGCTG 149 DNA Se id Accessio uence: 445. 11   TCACAGTGGC CGTGAGTTGA CTTGGTGGGC GTTCCAGGAA TGCCCGCTCA ATCACCCGG GACGAGCGCGC GAGCAGCGGG CTGAGAAAAA TTGGAAAACAA GAGAGTTTGA GAAGGGTTGA AGAGGTTCA AGACAAC ATTGGGAAAA ATTGGGAAAA ATTGGGAAACAA TTGGGAAAACAA	CCCCAGACT CTAATCTICA GUENCE n #: L29126 .1845 21   CAGGTCCTGT TCGAGCCGCA TCCTTGGCCCGCA GTCGGATCCC AGGAGCCACA CGTGATGCCA CGTGATCCC CTGGCCCGGC GTCGGATCCC CTGGCCCGGC AGGAGCCACA CGTGATCCC CCTGCACACA CGTCACACACA CGTCACACACA CGTCACACACA CGTCACACACA CGTCACACACA CGTCACACACA CGTCACACACA CCTTCACACACA CCTCACACACA CCTTCACACACA	TGGTGTCCTT GGGCACTGCT ANA  1  31    GCCAGATTGT GCCGCAGCTGGT CCGCAGCTGGT TCGATGTAGAA AGGGGCAT TGTCCTCGA ATATGGAAAT TGTCCTCGGAG CTCTCTCCA ATATGGAAAT TGTCCTCGGGAG AGCCAGCGGC TTCAGAAATGGAA CAAATGCAAC CCACACTGGT GATCTAGAGACACC CCACACTGGT GAAGACAACC CAACTGGT GGAGCAACC CAACTGGT GGTCAGAAC CAAATGAAATG	41    CCCTCTCAAC    CCCTCTCAAC   CCCTCTCAAC   CCCCTCCAAC   CCCCCCCCCC	STI  CTCTAAGGCC GTCGCTGAGG  SI  CTCCAGCCGG GCCTGGTAGA AGCCAGCGC GTATTGAGCT AGTGCCCCAG AGAGGCGCG TAATGAGCT TAGAGGAGACG CTCAGTCAGT CAGACAAAA AGCTTCTTGGA CAGACAAAA AGCTTCTTGGA CAGACACAAAA CGTTCTAGAA CAGACACAAAA CGTTCTAGAA CAGACACAAAA CGAGTCTAAA CAGACACAATTC CGTACACACAC CTGCCAGACACAATTC CATGACACAAA CAGAGACCAATTC CAGTACACAAA CAGAGACACA CGTACACACAA CAGAGAGACA CCATGACACAAA CCAGGAGAGAC CCTTAAACACG CCTTAAACTG	60 120 180 240 300 360 420 480 540 660 720 780 960 1020 1140 1260 1320 1340 140 1500
50 55 60 65 70	GAAGAAGGT ACCTGCTGCT AAAAATAAAG Seq ID NO: Nucleic Ac Coding seq I GAATTCCGCC GCGCTGTTCG CGTCTGCCAG TTGTTTTTGCT CCATCATCTC CCAGGAAGAC TAGGAGCCGC TATTATGGAA GCAGGACCCA TAGGAGGCAC TATTATGGAA CACATTGGAT AATGAACCAA TCCCTGGTTC CAAACTTTA ATGTGGGGGC CAGTGTTCCC TACTGTTTGCT CACAACTTTTTTTTTT	CTTCCCTCT GCTGCTGCTG GCTGCTGCTG ACAAATGCTG  149 DNA Sei id Accessio uence: 445.  11  TCACAGTGGC CGTGAGTTGA CTTGGTGGGG GTTCCAGGAA TCCACCGGAA ATCCACCGG AGGCGGCCC AGGAGATTCA CGAGAGATTCA CGAGAGATTCA CGAGAGATTCA CTCGTCCCAA CGAGAGGTTCA AGAGGTTCA AGAGGTCCACA AGGCCCCC AGGCACCC AGGCCCCC AGGCACCC AGGCCCCC AGGCACCC AGGCCCCC AGGCACCC AGGCCCCC AGGCACACA ATCCGCACAC ATCCCCACAC ATCCGCACAC ACCTCACACAC ATCGGGAAAT ACTGCCACAC ACCTCACACAC ACCTCACAC ACCTCACACAC ACCTCACAC ACCTCACA	CCCCAGACT CTAATCTICA GUENCE  n #: L29126 .1845 21   CAGGTCCTGT TCGAGCCCGA TCGTGGCCCGG GGAACCTTC CTGGCCCGGG GTGGGGTCCT AGGATCAT TGGACCAGA GTGGATCAT TGGACCAGA GTGGATCAT TGGATCAT TGTGAAGA AGGGTCCCC CAATGACTGT ACTCAGAGAA CGTTCACAGAA TGATCATCAGAGA TTGAAGCAGT TGAAGCAGT	TGGTGTCCTT GGGCACTGCT AAA  1  31    GCCAGATTGT GCCGCAGCTC GCAGCTGGT TCGATGTAGC TCTCCTTGAA AGGGGCATT CCCCCCACCA CTCCTCTCCACA TGTCTCTGGAGC TGTCTCTGGAGC TGTCTCTGGAGC TGTCTCTGGAGC TGTCTCTGGGAGC TGTCTGGGAGC TACAGGCTCT GAAAATGGAAAC TACAGCACACC GGATTGTGTG TGAAAATGGAAAC GAACTGAT GGAGACACC GGATTAAAA GGAGACACC GGATTAAAAC GAAAATGGCA AGGATTAAAA AAAATGGCA AGGATTAAAAC AAAAATGGCA ATAAAACTC AAAAATGGCA ATAAAACTC AAAATGGCA ATAAAACTC AAAATGGCA AAAATGGCA AAAATGACTC AACATTGAT	41	51	2940 3000 3033 60 120 180 240 300 360 420 780 840 600 660 720 780 840 1020 1140 1200 1320 1380 1440 1560
50 55 60 65 70	GAAGAAGGT ACCTGCTGCT AAAAATAAAG Seq ID NO: Nucleic Ac: Coding seqi    GAATTCCGCC GCGCTGTTGG CGTCTGCCAG TTGTTTTTGCT CCAGGGAGAAA GCAGGACCCA TAGGAGCCGC TCCTCCGATG CAAGAGGCAC TATTATGGAA GGCGTGAGGG GCTCTCAGGT GTGGGTGAGA TACATAGAAA CACATTGGAT ATGAAACCAATTTA ATGGAGCGCC TACTGGTTCC CACAACTTTA ATGGGGGGC CAGTGTTCCC TACTGGTTCC TACTGGTTCC TACTGGTTCC TACTGGTTCC TACTGGTTCC TACTGGTTCC GCCGATATAT TATTTCAGAA GCAGCAAAAI TATTTCAGAA	CCTTCCCTCT GCTGCTGCTG ACAAATGCTG ACAAATGCTG 149 DNA Seid Accessiouence: 445. 11   TCACAGTGGC GTTCAGGAA TGCCCGCTCA ATCACCCGG GAGCAGCGGC GAGCAGCGGAA CTCACACA AGAGGTTTCA GAAAAACAA CGAAAGCTGC ATCCCCCA AGCACGTTCC ACTCACACA CTCACACAC ATCTCCCAATG	CCCCAGACT CTAATCTTCA CGCCCTTAAA  Quence n #: L29126 .1845 21   CAGGTCCTGT TCGAGCCGCA TCCTTGGCCCGC GGGAACCTTC CTGGCCGGG GTCGGGTGCCGC GGTGATGCGT CCTGGACTCCT TGGGCCAGC GGTGATCAT TGGGACTAAC GGCTCTTAGAGAT GACCTTAAAC GGCTCTTAGAGAT CCTCACACAC CCTCACACAC CCTCACACAC CCTTCACACAC CCTTGAAACAC CCTTCACACAC CCTTCACACAC CCTTGAAACAC CCTTCACACAC CCTTCACACAC CCTTGAAACAC CCTTCACACAC CCTTCACACAC CCTTGAAACAC CCTTCACACAC CCTTCACACAC CCTTCACACAC CCTTCACACAC CCTTGAAACAC CCTTCACACAC CCTTGAAACAC CCTTGAAACACAC CCTTGAAACACAC CCTTGAAACACAC CCTTGAAACACAC CCTTGAAACACAC CCTTGAAACACAC CCTTGAAACACAC CCTTGAAACACACAC CCTTGAAACACACAC CCTTCACACAC CCTCACACAC CCTCACAC CCTCACACAC CCTCACACAC CCTCACACAC CCTCACACAC CCTCACACAC CCTCACACAC CCTCACACAC CCCACACAC CCCACACAC CCCACACAC CCCACACAC CCCACAC	TGGTGTCCTT GGGCACTGCT ANA  1 31   GCCAGATTGT GCCACCAGCTGGT TCGATGTAGC TCTCCTTGAA AGGGGCATT TCGATGTAGC TCTCCTCCACA TATTGGAAAT TGTCCTGGAG TTCTCGGAGG TTCTCGGAGG TTCTCGGAGG TTCTCGGAGG TTCAGAAATGAAAT	41    CCCTCCACT  41    CCCTCTCAAC  TOGCAGCTCA CGCCTCAGC TOGCAAGCC TOGCAAGCTCAGC TOGCACAGGC TCATCTCACC AGCCTCAGC AGCCTCAGC AGCCTCAGC AGCCAGGATG AGCAGGATG AGCAGGATG AGCAGGATG AGCAGGATG AGCAGGATG AGCAGGATG ACTAACTTATT TCCACGACC AGAGGCTGA ACTAACTGAGG TCAAGAGC TCAAGAGC TTCAAGAGC TTCAAGAGC TTCACTGAG ATCACTGAGG TTCACTGAGG TTCACTGAGG TTCACTGAGG TTCACTGAGG TTCACTGAGG TTCACTGAGG TTCACTGAGG TTCACTGAGG TCCATGAAG	TICTAAGGCC TCTTACTGCC GTCGCTGAGG  51   CTCCAGCCGG GCCTGGTAGA AGCCAGCGCC GTATTGAGCT AGTGCCCCAG AGAGCCGAGA AGCCAGCACC CTCATCAGAGA AGCTATACAG ACACACCTT GATAACACT AGAGAGACCT AGAGAGACCT AGAGAGACCT AGAGAGACCT AGAGAGACT CAGACCT CAGACCCT AGAGAGACCAAA ACACACT CAGACCCT CAGACCCC CAGACCCC CAGACCCC CAGACCC CAGACCC CATCACACC CAGACCC CATCACACC CAGACCC CATCACCC CATCACC CATCAC C	60 120 180 240 300 360 420 480 540 660 720 780 960 1020 1140 1120 1120 1150 1150 1150
50 55 60 65 70 75	GAAGAAGGT ACCTGCTGCT AAAATAAAG Seq ID NO: Nucleic Ac Coding seq I GAATTCCGCC GCGCTGTTGG GCGTGTTGCCAG TTGGTTTGCCAG GCAGACCCA TAGGAGCCA TAGGAGCAGA GCAGACCCA TATTATGGAA GCGCTGAGG GCTCTCAGGT GTOGGTGAGA TACATAGGAA CACATTGAT ATGGAGCGC CAGGTTCCAGTT CACACTTTA ATGGAGCGC CAGGTTCCAGTT CACACTTTA ATGGAGCGC CAGGTTCCAGTT CACACTTTA ATGGAGCGC CAGGTTCCAGTT CACACTTTA ATGGAGGGC CAGGTTCCAGTT GCCCATATAGGAA CCGCATATAGGAA TACTGGGTC GCCGATATAGGAC GCCCATATAG TATTTCAGAG GCACCAAACT TATTTCAGAC CCCCCTCCTCCTCCTCCCCTCC	CCTTCCCTCT GCTGCTGCTG ACAAATGCTG ACAAATGCTG 149 DNA Seid Accessiouence: 445. 11   TCACAGTGGC CGTGAGTTGA CTTGGTGGGC GTTCCAGGAA TGCCCGCTCA ATCCACCGGG GACGAGGGGGCC GAGCAGCGGGGCC GAGCAGCGGGGCC GAGCAGCGGGGCC GAGCAGCGGGGCC GAGCAGCGGGAAAACCAA TCACCCCGG ATTCGAACCAC ATTCGGAAACAA TCACCCGG ACCTCACAAC ATCTCCAATG ACTGACACCT CGACACCT CGACACCT CGACACCT CGACACCT CGACACCT CGACACCT CGACACCT CGACACCC CGACACATG CTCCCAATG CTCCCAATG CTCCCAATG CTCCCAATG CTCCCAATG CCCCCCTTCCCAATG CCCCCCTTTCCCAATG CCCCCTTTCCCAATG CCCCCCTTTCCCAATG CCCCCCTTTCCCAATG CCCCCCTTTCCCAATG CCCCCTTTCCCAATG CCCCCCTTTCCCAATG CCCCCTTTCCCAATG CCCCTTTCCCAATG CCCCCTTTCCCAATG CCCCCTTTCCCAATG CCCCCTTTCCCAATG CCCCTTTCCCAATG CCCCCTTTCCCAATG CCCCTTTCCAATG CCCCCTTTCCCAATG CCCCCTTTCCCAATG CCCCCTTTCCCAATG CCCCCTTTCCCAATG CCCCCTTTCCCAATG CCCCCTTTCCCAATG CCCCCTTTCCCAATG CCCCTTTCCCAATG CCCCCTTTCCCAATG CCCCCTTTCCCAATG CCCCCTTTCCCAATG CCCCTTTCCCAATG CCCCTTTCCCAATG CCCCTTTTCCCAATG CCCCTTTCTCCAATG CCCCTTTTCCAATG CCCCTTTTCCCAATG CCCCTTTTCC	CCCCAGACT CTAATCTTCA GUENCE n #: L29126 .1845 21   CAGGTCCTGT TCGAGCCGCA TCCTTGGCCCGCA GGGAACCTTC CTGGCCCGCA GGGAGCCACCA GGGAACCTTC CTGGCCCGCA GGGAGCCACCA CGTGATGCGT CCTTAGAGACA CGTCATGCCC CGGGAACCATC CCTAGAGACA CGTCACACACA CGTCACACACA CGTCACACACA CGTCACACAC CGTTCAGAGAC CCTCACACACAC CGTTCCGAGGAC CCCTCCACACAC CGTTCCACACAC CCCTCCCACACAC CCCTCCCACACAC CCCTCCCACACAC CCCTCCCACACAC CCCTCCCACACAC CCCTCCCACACAC CCCTCCCACACAC CCCTCCCACACAC CCCTCCACACAC CCCTCCCACACAC CCCTCCCACACAC CCCTCCCACACAC CCCTCCCACACAC CCCCCCCACACAC CCCCCCCACACAC CCCCCC	TGGTGTCCTT GGGCACTGCT AAA  1 31   GCCAGATTGT GCCGCAGCTG GCAGCTGGT TCGATGTAGAA AGGGGCAT TGTCCTTGAA AGGGGCAT TGTCCTGGAG TGTCTCGGAG TGTCTGGAG TGAAAATGA AAAGTATCCC CAACTGGTG TGAAAAATGC AAAATGGAA GGTCACAAC CAACTGGTG TGAAAAATGC AAAATGGAAC CAACTGATC AAAATGGAAC CAACTGATC CAACTTATGAT CCACTAATG CTGGAAGCC CAACTATGAT CTGGAAGCC CAACTAATGAT CTGGAAGCC CAACTGAT CTGGAACC CAACTGAT CTGAACAACT CAACTGAT CTGGAACC CAACTGAT CTGAACT CT	41    CCCTCTCAAC    CCCTCTCAAC    CCCTCTCAAC    CCCTCTCAAC    CCCCTCCAAC    CCAGCTCAAC    CCAGCACAGAC    CAACTTATCACAC    CAACTAACCC    CAACTAACCC    CAACTAACCC    CAACTAACCC    CAACTAACCC    CAACTAACCC    CAACTAACCC    CAACTAACCC    CAACTAACCC    CCACTCAAC    CCACACAGAG    CCCACTCAAC    CCCACTCAAC    CCCACCCCAAC    CCCCCCCACCCC    CCCCCCCC	TICTAAGGCC TCTTACTGCC GTCGCTGAGG  51	60 120 180 240 300 360 420 480 540 660 720 780 1020 1140 1200 1320 1320 1340 1500 1500 1620 1620
50 55 60 65 70	GAAGAAGGGT ACCTGCTGCT AAAAATAAAG Seq ID NO: Nucleic Ac Coding seq I GAATTCCGCC GCGCTGTTGG CGTCTGCCAG TTGTTTTTGCT CCATCATCTC CCAGGAGAGA TAGGAGCCCA TAGGAGGCAC TATTATGGAA GCAGGACCA TATTATGGAA CACATTGGAT CACAACTTTA AATGAACCAA TCCCTGGTTC CACACTTTTGCT CACAACTTTTTTGCAAC TCCTGGTTCCAGGTGGGGG CTCTCAGGTGAGGG CTCTCAGGTTCAGGTTCCACGTTTCAGGTTCCAGGTTCCAGGTTCCAGGTTCCAGGTTCCAGGTTCCAGGTTCCAGGTTCCAGGTTCCAGGTTCCAGGTTCCAGGTTCCAGGTTCAGGTTCAGGTTCAGGTTCAGGTTCAGGTTCAGGTTCAGGTTCAGGTTCAGGTTCAGGTTCAGGTTCAGGTTCAGGTTCAGGTTCAGGTTCAGGTTCAGGTTCAGGTTCAGGTTCAGGTTCAGGTTCAGGTTCAGGTTCAGGTTCAGGTTCAGGTTCAGGTTCAGGTTCAGGTTCAGGTTCAGGTTCAGGTTCAGGTTCAGGTTCAGGTTCAGGTTCAGGTTCAGGTTCAGGTTCAGGTTCAGGTTCAGGTTCAGAGAGAAAAACCTGCCTCCTCTTAAAAAAAA	CCTTCCCTCT GCTGCTGCTG GCTGCTGCTG ACAAATGCTG  149 DNA Sei id Accessio uence: 445.  11  † TCACAGTGGC CGTGAGTTGA ATCCACCGG ATCCACGGC GAGGGGGCC GAGGGGGCC AGGAGTTCA AGAGGTTCA AGAGGTTCA AGAGGTTCA CTGAAGAATA CTCGTCCCAA AGAGGTTCA AGAGGTTCA AGAGGTTCA AGAGGTTCA AGAGGTTCA AGAGGTTCA AGAGGTCCACA AGAGCACCC AGGCCCCCA AGGCCCCCA AGGCCCCCCA AGGCCCCCCA AGGCCCCCCA AGGCCCCCCA AGGCCCCCCA AGGCCCCCCA AGGCCCCCCA AGCCCCCCACACCC ACCTCACACC A	CCCCAGACT CTAATCTICA GUENCE  n #: L29126 .1845 21   CAGGTCCTGT TCGAGCCGCA GCGAACCTTC GCGAACCTTC GTGGCCGGG GTGGGAGTGCT CAGGATCAT GGACCACA GGGATCATT TGGACCACA GGGATCATT TGGACCACA GGGATCATT TGGACCACA GGGATCATT TGGATCATC GAGATCATT TGGATCATC CCAGCACCT CCAGCACACA GTCCACACACA GTCCACACACAC CCTCACACACAC CCTCACACACAC TGATGACAGAC TGAAGACAGT TGAAGCAGAC TCTACAGAGA TTGAAGCAGAC TCTACACACAC CCACTCCC CAATGACTGC CAGATGACTGC CAGATGACGT CAGATGACCT CCCGTCCACT CAGATGACCCT CCCCCTCCACC CAGATGACCCT CCCGTCCACC CAGATGACCCT CCCGTCCACC CAGATGACCT CCCGTCCACC CAGATGACCC CAGATGACCT CCCGTCCACC CAGATGACCC CAGATGACCT CCCGTCCACC CAGATGACCC CAGATGACCC CAGATGACCC CAGATGACCC CAGATGACCC CAGATGACCC CAGATGACCC CAGATGACCC CAGATGACC CAGCACC CAGATGACCC CAGATGACC CAGCACC CAGATGACC CAGCACC CAGATGACC CAGCACC CAGATGACC CAGCACC CAGATGACC CAGCACC CAGCACC CAGATGACC CAGCACC CAGCACC CAGCACC CAGATGACC CAGCACC CAGCACC CAGCACC CAGATGACC CAGCACC CACCACC CACCACC CACCACC CACCACC CACCAC	TGGTGTCCTT GGGCACTGCT ANA  1  31    GCCAGATTGT GCCGCAGCTC GCAGCTGT TCGATGTAGC TCTCCTTGAA AGGGGCATT CCCCCCACCA CTCCTCTCCACA TGTCTCTGCA ATATGGAAAT TGTCCTGGAG AGCCAGCGC TCTCTGGGAGC TCTCAGAAATGG TACAGGCTCT GAAAATGGCAC GAACTGAT GGAGCACCG GGCTCACACAC GAACTGAT GGAGCACCG GCCCACCACAC GAACTGAT GAAAATGCC AGGATTAAAA AAAATGCC AAAATGCAC AAAATGCC AAAATGCAC AAAATGCC AAAATGCAC AAAATGCC AAAATGCAC AAAATGCAC AAAATGCAC AAAATGCC AAAATGCAC	41	51	2940 3000 3033 60 120 180 240 300 360 420 780 840 540 660 720 780 840 1020 1140 1200 1140 1200 1500 1560 1620 1620 1620 1620
50 55 60 65 70 75	GAAGAAGGT ACCTGCTGCT AAAATAAAG Seq ID NO: Nucleic Ac Coding seq    GAATTCCGCC GCGCTGTTGG CGTCTGCCAG TTGTTTTTGCT CCAGGGAGAAA GCAGGACCCA TAGGAGCAC TATTATGGAC GCTCTCCGATG GCAGGAGAAA CACATTGAT ATGGAGCAC TACTGGTTCCC CACAGTTTA ATGGAGCAC TACTTATGGAC TACTGGTTCCC TACTGCTCCC TACTGCTCCC TACTGGTTCCC TACTG	CCTTCCCTCT GCTGCTGCTG ACAAATGCTG ACAAATGCTG 149 DNA Seid Accessiouence: 445. 11   TCACAGTGGC CGTGAGTTGA CTTGGTGGGC GTTCCAGGAA TGCCCGCTCA ATCCACCGGG GAGCAGCGGCG GAGCAGCGGCG GAGCAGCGGCG GAGAGTTCA GAGAGTTTCA GAGAGTTTCA GAGAGTTTCA GAGAGGTTCCA AGAGGTTTCA AGAGGTTTCA AGAGGTTTCA AGAGGTTTCA AGAGGTTTCA AGAGGTTTCA AGAGGTTTCA AGAGGTTTCA AGAGGTTTCA AGAGGTTCCAA CTCACAACC ATCTCCAATGC ATTCCCAATGC CCCCTGAGGAAA TCTCCAATGC CCCCTGAGGG CCCCTGAGGC CCCCCTGAGGC CCCCCTGAGGC CCCCCTGAGGC CCCCCTGAGGC CCCCCCCCCC	CCCCAGACT CTAATCTICA GCCCTTAAA  Quence n #: L29126 .1845 21   CAGGTCCTGT TCGAGCCGCA TCCTTGGCCCGC GGGAACCTTC CTGGCCGGG GTCGGATGCCT AGGAGCCACC GGTGATGCGT AGGAGCACC GGTGATCAT CCCTTAGAGAA AGGCTTCAGAGAA AGGCTCCTAAA CGTCACACACA CGTTCCAGGGA TCGAGACTCCG CAATGACTGC CAATGACTGC CAATGACTGC ACTTGTCAAA TGAAGCAGG TTGAGAAGAG TTGAAGAAGT CCCTGTCAT CAGAATGCC CAATGACTGC AACCCTCCGC CAATGACTGC AACCCTCCACACACACC CTGACACACACCCTCCACACACACCCCCCCCCC	TGGTGTCCTT GGGCACTGCT ANA  1  31    GCCAGATTGT GCCGCAGCTC GGAGTTGT TCGATGTAGC TCTCCTTGAA AGGGGCATT TCGATGTAGC TCTCCTTGAA AGGGGCATT TCGATGTAGC TCTCCTCCA ATATGGAAAT TGTCTCTGGGG TGTCTCGGGG TGTCTGGGGG TGTCTGGGGG TGTCTGGGG TACAGGCTCT GAAGAACAC AAAAGTATCA AAAAGTATCA GAGTATCAA GGATTAAAA GGATTAAAA GGATTAAAA CAAATGG TGCTCAGAGC CAACTGGT CAAAATGG TGCTCAGAGC CAAATGGT CAACTGATG GGTCACAAGC CAACTGGT CAAAATGG GGTTAAAAGT CAACTGATGG TGCTCAAAGC CAAAATGG TACCTAATGG TGCTGGAGGC GTACCTAATGG TACCTAATGG TACCTACTG TGGGAGGC TACCTACTG TGGGAGGC TACCCTGG TACCCCTG TACCCCCTG TACCCCTG TACCCTG TACCCCTG TACCCCCTG TACCCCTG TACCCCCTG TACCCCTG TACCCCCTG TACCCCTG TACCCCCTG TACCCCTG TACCCCTG TACCCCCTG TACCCCTG TACCCCCTG TACCCCTG TACCCCTG TACCCCTG TACCCTG TACCCCTG TACCCCTG TACCCCCTG TACCCCTG TACCCCTG TACCCCTG TACCCCTG TACCCCTG TACCCCTG	41	STITATAGGCC TCTTACTGCC GTCGCTGAGG  SI CTCCAGCCGG GCCTGGTAGA AGCCAGCGCC GTATTGAGCT AGTGCCCCAG AGAGCAGAAA AGCTTACTGGA ACTACACGCTG GAAACACTTT GATAACACTG CATCTATGAA AAAGATCTCC ATGAGAAAACC ATGAGAAAACCAAAACCAAAACCAATACACCACTG	60 120 180 240 300 360 420 480 540 660 720 780 1020 1140 1200 1320 1320 1340 1500 1500 1620 1620
50 55 60 65 70 75	GAAGAAGGT ACCTGCTGCT AAAATAAAG Seq ID NO: Nucleic Ac Coding seq    GAATTCCGCC GCGCTGTTGG CGTCTGCGCG GTTGTTCGC CAGGGAGAA GCAGGACCCA TAGGAGGCGC TGCTCGCATG CAAGAGGCCA TATTATGGAA GCGCTGTAGG GCGCTGTAGG GCGCTGAGG TATTATGGAA GCCATTGGAT ATGAAGACCAA TCCCTGGTTC CACAACTTTA ATGTGGGGC CAGGGTCCAGGT TATTTCGGAA CACATTGGAT ATTTCGGAG GCAGAAAATTCCCTGGTTCC TACTGTTGCC GCCGATATAT TATTTCAGGA GCAGAAAAA CTGCCTCCTC ATGAATGAAC CTGATGAGGGC CTGATTGTGGCC CTGATGAGGGC CTGATTGTGTG	CCTTCCCTCT GCTGCTGCTG ACAAATGCTG ACAAATGCTG 149 DNA Seid Accessiouence: 445. 11   TCACAGTGGC CGTGAGTTGA CTTGGTGGGC GGTCCGGGAGCGCG GAGCAGCGGG GACGAGCGGG GAGCAGCGGA CTGAGGATTCA GGAGAGTTCA GGAGAGTTCA GGAGAGTTCA GGAGAGTTCA GGAGAGTTCA GGAGAGTTCA GGAGAGTTCA AGAGGTTCA AGAGGTTCA AGAGGTTCA AGAGGTTCA AGAGGTTCA AGAGGTTCA AGAGGTCACAAC CGAAAACAAT CTACCCAAC ATCCCAAAC ATCCCAAAC CTGCCAATGC ACTTCCAATGC ACTTCCAATGC ACTTCCAATGC ACTTCCAATGC ACTTCCAATGC CCCCTGAGG CCCCCTGAGG CCCCCTGAGG CCCCCTGAGG CCCCCTGAGG CCCCCTGAGG CCCCCTGAGG CCCAATTTTAA	CCCCAGACT CTAATCTICA GUENCE n #: L29126 .1845 21   CAGGTCCTGT TCGAGCCGCA TCCTTGGCCCGCA GTCGGAGTGCC GTGAGCCACCA GGTGATGCGT CCTGGAGTCCCT CTGGCCCGCA GGTGATGCGT CCTAGAGATCAT TGGGATCAT CCTAGAGATCAT CCTACAGAA CGTCACACAC CCTCACACAC CCTCACACAC CCTCACACAC CCTCACACAC CCTCACACAC CCTCACACAC CCTCACACAC CCTCTGCACAC CCTCACACAC CCTCACACAC CCTCCACACAC CCTCCACACAC CCTCCCACACAC CCTCCACACAC CCTCCACACAC CCTCCACACAC CCTCCACACAC CCTCCACACAC CCTCCACACAC CCTCCACACAC CCTCCACACAC CCTCACACAC CCTCACAC CCTCACACAC CCTCACACAC CCTCACACAC CCTCACACAC CCTCACACAC CCTCACAC CCTCACACAC CCTCACACAC CCTCACACAC CCTCACACAC CCTCACACAC CCTCACAC CCTCACACAC CCTCACAC CCTCACACAC CCTCACACAC CCTCACACAC CCTCACACAC CCTCACACAC CCTCACAC CCTCACACAC CCTCACACAC CCTCACACAC CCTCACACAC CCTCACACAC CCTCACACAC CCTCACAC CCTCACACAC CCTCACACAC CCTCACACAC CCTCACAC CCTCACA	TGGTGTCCTT GGGCACTGCT AAA  1  31    GCCAGATTGT GCCACAGTGTT CTGGTGTATAGAGT CTCCTTGAA AGGGGCATT TCGATGTATAGCAT TGTCCTCGGAG TGTCTCGGAGG AGCCAGGGGT TGTCCTGGAG AGCCAGGGG TGTCTGGAG AGCCAGGGG TGTCAGAAC CAACTGGTG TCAAAAATGA AAATTACAAAT AAATTAGAAAT CAACTGTGT GAGACACCTG CAACTGGTG CAACTGAT GAGATAAAAT AAAATGCA AAAATGCA AAAATGCA AAAATGCA CAACTGATG CTGGAAGGC TACCTAATG AAAATGCA AAAATGCA AAAATGCA AAAATGCA AAAATGCA CAACACTGGT CTGGAAGCC CAACCTGAT CAACACCTG CTGGAAGCC CAACCTTG CTGGAAGCC CAACCTGT CTGGAAGCC CAACCTGT CTGGAAGCC CAACCTGT CTGGAAGCC CAACCTGT CTGGAAGCC CAACCTGT CTGGAAGCC CAACCTGT CTGGAAGCC CAACTTTAA AAAATGTA CTGGAAGCC CAACCTGT CTGGAAGCC CAACTTTAA AAATGTA CTGGAAGCC CAACTTTAA AAAATGTA CTGGAAGCC CAACTTTAA AGACTTTTAA AGACTTTTAA AAAATGTAA CAACTTTAA AAAATGTAA CAACTTTAA AAAATGTAA CAACACCTG CTGGAAGCC CAACTTTAA AAAATGTAA CAACACTG CAACTTTAA AAAATGTAA AAAATGTAA CAACACTG CAACTTTAA AAAATGTAA CAACACTG CAACTTTAA AAAATGTAA AAAATGTAA CAACACTG CAACTTTAA AAAATGTAA CAACACTG CAACTTTAA AAAATGTAA AAAATGTAA CAACACTG CAACTTTAA AAAATGTAA AAAATGTAA CAACACTTAA AAAATGTAA CAACACTG CAACTTAA AAAATGTAA AAAATGTAA CAACTTAA AAAATTAAACATCAACTC CAACTTAAAAAAATCAAAAATCAAAAAAAA	41    CCCTCTCAAC   CCCTCTCAAC   CCCTCTCAAC   CTCGCAGCTCA   CTCGCAGCTCAGC   CGCAGCATGC   CGCAGCATGC   CGCAGCATGC   CGCAGCATGC   CGCAGCATGC   CGCAGCATGC   CAACTTATCCC   AGCCGGATGC   AACCAGGATG   AACCAGGATG   CAACTAACCC   AGGGGGGGGGGGGC   CAACTAACCC   CAGAGGGTGG   CACTATCAATI   CTCAGAGGC   CGGAAGGCTGA   CTCAGAGGC   CTCAGAGC   CTCAGAGGC   CTCAGAGC   CTCAGAGGC   CTCAGGC   CTCAGAGGC   CTCAGGC   CTCAGAGGC   CTCAGAGGC   CTCAGAGGC	STETAAGGCC TCTTACTGCC GTCGCTGAGG  S1   CTCCAGCCGG GCCTGGTAGA AGCCAGCGCC GTATTGAGCT AGTGCCCCAG TGAGGAGACG TCAGTTACAG CAGCACAAAA AGCACAAAAA CAGCACAAAA CAGGAAACACTT CAGTACACAAA CAGGAAAAGCC TGCCAATTTC ATGACACAAA CAGGAAAAGCC CCTTAAACACGC CCTACACAGAA CAGGAAAAGCC CCTACACAAA CAAGAAAGCC CCTAAACACT CCGTACACAAA CAAGAAAGCC CCTTAAACT CAGTACACAAA CAAGAAAAGC CCTTAAACT CAGTACACAAA CAAGAAAAGC CCTTAAACT CAGGAAAAGC CCTTAAACT CAGGAAAAGC CCTTAAACT CAGGAAAAGC CCTAAAAAGC CCTTAAACT CAGGAAAAGC CCTTAAAACG CCTTAAACT CAGGAAAAGC CCTAAAAAGC CCTTAAACT CCTACACAAAGC CCTTAAACT CCTACACAAAGC CCTTAAACT CCTACACAAAGC CCTTAAACT CCTACACAAAGC CCTTAAACT CCTACACAAAGC CCTTAAACGC CCTTAAACT CCTACACAAAGC CCTTAAACT CCTACACAAAGC CCTCAAAAGC CCTCAAAAGC CCAGGAAAATC CAGGGAAATC CAGGGAAATC	2940 3000 3033 60 120 180 240 300 360 420 780 840 600 660 720 780 840 1020 1140 1200 1320 1380 1440 1500 1560 1620 1620 1620
50 55 60 65 70 75	GAAGAAGGGT ACCTGCTGCT AAAAATAAAG Seq ID NO: Nucleic Ac Coding seq I GAATTCCGCC GCGCTGTTCG CGTCTGCCAG TTGTTTTTGCT CCATCATCTC CCAGGAAGAA GCAGGACCCA TAGGAGCCGC TATTATGGAA GCAGGACCCA TATTATGGAA CACATTGGAT AATGAACCAA TCCCTGGTTC CAAACTTTA ATGGGGGC CAGTGTTCCC TACTGTTTGC GCCATATTTC GACATTTTTTCGGAT GCCGGTTCAGCGC TATTATGGAA CCTGGTTCCC TACTGTTTCC CACACTTTTTCC GCCATATTAT	CCTTCCCTCT GCTGCTGCTG GCTGCTGCTG ACAAATGCTG 149 DNA Sei id Accessio uence: 445. 11  TCACAGTGGC CGTGAGTTGA CTTGGTGGGG GTTCCAGGAA ATCCACCGG AATCCACCGG AGGCGGCCC GAGAGATTCA CGGAGAACACA CGGAGAACACAC AGGAGTTGAAGACCA AGGGCTCCAA AGAGGTTGA AGAGGTTGA AGAGGTTGA AGAGGTCCACCC AGGAGAACACAC CTCGCCACCC AGCACCTCACAC ATCTCCACCC AGCACCTCACACC AGCACCTCACACC AGCACCTCACACC AGCACCTCACACC AGCACCTCACACC AGCACCTCACACC ACCTCACACCC AGCACCTCACACC ACCTCACACCC AGCACCTCACACCC AGCACCTCACACCC AGCACCTCACACCC AGCACCTCACACCC AGCACCTCACACCC AGCACCTCACACCC AGCACCTCACACCC AGCACCTCACACCC AGCACCTCACACCC AGCACTATGG CCCACTATGG CCCACTATGG CCCACTATGC CCCCTGAGG CCCACTTTACCCCC CACTTTACCCCC AGCACTTTACCCCC AGCACTTTACCCC AGCACTTTACCC AGCACTTTACCC AGCACTTTACCC AGCACTTACC AGCACTC AGCACTC AGCACTTACCC AGCACTTACC AGCACTC AGCACT AGCACTC AGCACT AG	CCCCAGACT CTAATCTICA GUENCE  n #: L29126 .1845 21   CAGGTCCTGT TCGAGCCCCA GCGAACCTTC GCGAACCTTC GTCGCCCGGGATCCTT CTGGCCCGGG ACGCTCCT AGAATCAT ACTCAGAGAT CCTTAGAGAT ACTCAGAGAT TCGAGTCCAC CAGGTACTCT CCTGGATCAT CCAGGTCACACA CCTCACACAC CCAGGTACAT TCGAGTCACACAC CCTCACACACAC CCTCACACACAC CCTCACACACA	TGGTGTCCTT GGGCACTGCT AAA  1  31    GCCAGATTGT GCCGCAGCTC CCGCAGCTC TCGATGTAGC TCGATGTAGC TCTCCTTGAA AGGGGCATT TGTCCTCGA ATATGGAAAT TGTCCTCGGA TGTCTCGCG TACAGGCTC CTGAAAATGG TACAGGCTC CAAACTGAT TGCCACACA GAGCACACC CAACTGAT GGAGCACAC CCACACTGG TGCTCACACC CAACTGAT GGAGCACC CCACACTGG TGCTCACACC CAACTGAT CCAAAATGGA AGGATTAAAA ATACATACT ATAAAACTGC AAAATGGCA AGGATTAAAA CAACTGAT GGAAGCCTG AGACTTATGAT CAACTTGAT CAACTGAT CAACTGAT CAACTGAT CAACTGAT CAAAACTCC AAAAATGGCA AAAATGCAA AAAAATGCAA AAAATGCAA AAAATGCAA AAAATGCAA AAAATGCAA AAAATGCAA AAAATGCAA AAAATGCAA AAAATGCAAA AAAAATGCAA AAAAATGCAA AAAAATGCAA AAAAATGCAAAAAAAATGCAAAAAAAAAA	TCCCTCCACT GCTGCCTTTA  41	51	2940 3000 3033 60 120 180 240 300 360 420 780 840 900 960 1020 1140 1200 1200 1380 1440 1560 1620 1680 1740 1890
50 55 60 65 70 75	GAAGAAGGGT ACCTGCTGCT AAAAATAAAG Seq ID NO: Nucleic Ac Coding seq I GAATTCCGCC GCGCTGTTCG CGTCTGCCAG TTGTTTTTGCT CCATCATCTC CCAGGAAGAA GCAGGACCCA TAGGAGCCGC TATTATGGAA GCAGGACCCA TATTATGGAA CACATTGGAT AATGAACCAA TCCCTGGTTC CAAACTTTA ATGGGGGC CAGTGTTCCC TACTGTTTGC GCCATATTTC GACATTTTTTCGGAT GCCGGTTCAGCGC TATTATGGAA CCTGGTTCCC TACTGTTTCC CACACTTTTTCC GCCATATTAT	CCTTCCCTCT GCTGCTGCTG GCTGCTGCTG ACAAATGCTG 149 DNA Sei id Accessio uence: 445. 11  TCACAGTGGC CGTGAGTTGA CTTGGTGGGG GTTCCAGGAA ATCCACCGG AATCCACCGG AGGCGGCCC GAGAGATTCA CGGAGAACACA CGGAGAACACAC AGGAGTTGAAGACCA AGGGCTCCAA AGAGGTTGA AGAGGTTGA AGAGGTTGA AGAGGTCCACCC AGGAGAACACAC CTCGCCACCC AGCACCTCACAC ATCTCCACCC AGCACCTCACACC AGCACCTCACACC AGCACCTCACACC AGCACCTCACACC AGCACCTCACACC AGCACCTCACACC ACCTCACACCC AGCACCTCACACC ACCTCACACCC AGCACCTCACACCC AGCACCTCACACCC AGCACCTCACACCC AGCACCTCACACCC AGCACCTCACACCC AGCACCTCACACCC AGCACCTCACACCC AGCACCTCACACCC AGCACCTCACACCC AGCACTATGG CCCACTATGG CCCACTATGG CCCACTATGC CCCCTGAGG CCCACTTTACCCCC CACTTTACCCCC AGCACTTTACCCCC AGCACTTTACCCC AGCACTTTACCC AGCACTTTACCC AGCACTTTACCC AGCACTTACC AGCACTC AGCACTC AGCACTTACCC AGCACTTACC AGCACTC AGCACT AGCACTC AGCACT AG	CCCCAGACT CTAATCTICA GUENCE  n #: L29126 .1845 21   CAGGTCCTGT TCGAGCCCCA GCGAACCTTC GCGAACCTTC GTCGCCCGGGATCCTT CTGGCCCGGG ACGCTCCT AGAATCAT ACTCAGAGAT CCTTAGAGAT ACTCAGAGAT TCGAGTCCAC CAGGTACTCT CCTGGATCAT CCAGGTCACACA CCTCACACAC CCAGGTACAT TCGAGTCACACAC CCTCACACACAC CCTCACACACAC CCTCACACACA	TGGTGTCCTT GGGCACTGCT AAA  1  31    GCCAGATTGT GCCGCAGCTC CCGCAGCTC TCGATGTAGC TCGATGTAGC TCTCCTTGAA AGGGGCATT TGTCCTCGA ATATGGAAAT TGTCCTCGGA TGTCTCGCG TACAGGCTC CTGAAAATGG TACAGGCTC CAAACTGAT TGCCACACA GAGCACACC CAACTGAT GGAGCACAC CCACACTGG TGCTCACACC CAACTGAT GGAGCACC CCACACTGG TGCTCACACC CAACTGAT CCAAAATGGA AGGATTAAAA ATACATACT ATAAAACTGC AAAATGGCA AGGATTAAAA CAACTGAT GGAAGCCTG AGACTTATGAT CAACTTGAT CAACTGAT CAACTGAT CAACTGAT CAACTGAT CAAAACTCC AAAAATGGCA AAAATGCAA AAAAATGCAA AAAATGCAA AAAATGCAA AAAATGCAA AAAATGCAA AAAATGCAA AAAATGCAA AAAATGCAA AAAATGCAAA AAAAATGCAA AAAAATGCAA AAAAATGCAA AAAAATGCAAAAAAAATGCAAAAAAAAAA	TCCCTCCACT GCTGCCTTTA  41	STETAAGGCC TCTTACTGCC GTCGCTGAGG  S1   CTCCAGCCGG GCCTGGTAGA AGCCAGCGCC GTATTGAGCT AGTGCCCCAG TGAGGAGACG TCAGTTACAG CAGCACAAAA AGCACAAAAA CAGCACAAAA CAGGAAACACTT CAGTACACAAA CAGGAAAAGCC TGCCAATTTC ATGACACAAA CAGGAAAAGCC CCTTAAACACGC CCTACACAGAA CAGGAAAAGCC CCTACACAAA CAAGAAAGCC CCTAAACACT CCGTACACAAA CAAGAAAGCC CCTTAAACT CAGTACACAAA CAAGAAAAGC CCTTAAACT CAGTACACAAA CAAGAAAAGC CCTTAAACT CAGGAAAAGC CCTTAAACT CAGGAAAAGC CCTTAAACT CAGGAAAAGC CCTAAAAAGC CCTTAAACT CAGGAAAAGC CCTTAAAACG CCTTAAACT CAGGAAAAGC CCTAAAAAGC CCTTAAACT CCTACACAAAGC CCTTAAACT CCTACACAAAGC CCTTAAACT CCTACACAAAGC CCTTAAACT CCTACACAAAGC CCTTAAACT CCTACACAAAGC CCTTAAACGC CCTTAAACT CCTACACAAAGC CCTTAAACT CCTACACAAAGC CCTCAAAAGC CCTCAAAAGC CCAGGAAAATC CAGGGAAATC CAGGGAAATC	2940 3000 3033 60 120 180 240 300 360 420 480 540 660 720 780 1020 1140 1120 1140 11500 11500 1160 11740 1160 11740 1180

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5	CCTCCCCCC	CCACCGAAGA	CAAAGCCACA CCCAGGTGGG	ACGCAAAGGG	TCCTGGGCAG	AGGAGCCGAG	1080 1140
-	CCAGTGGGGC	ACCITCION	ACCACAGGTG	CARGOGCCGG	TOTOGRAGIGO	TCATGAACCG	1200
			CTCGGGAGGC				1260
	AGGGCCCATC	CACCTGAGTG	AGGTGCGCTG	CAGGGGATAT	GAGCGGACCC	TCAGCGACTG	1320
• •	CCCTGCCCTG	GAAGGGTCCC	AGAATGGTTG	CCAACATGAG	AATGCTGCTG	CTGTCAGGTG	1380
10	CAATGTCCCT	AACATGGGCT	TTCAGAATCA	GGTGCGCTTG	GCTGGTGGGC	GTATCCCTGA	1440
			AGGTGGAGGT				1500
			CCGAAGCCAT				1560
			AAACCTGGTT				1620
15	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	CACTICCTCC	GCTCAGGCAC ACGGTGGCGG	AGAGCTGGCC	CTGCAGCAGT	CCCAGAGGCA	1680 1740
	CAGTGCACCA	GACCTGGTGA	TGAACGCCCA	GCTAGTGCAG	GAGACIGCCT	ACTTGGAGGA	1800
			ATTGTGCCCA				1860
			GATACCGCCG				1920
20	TCTGGGCCGG	ACTGACTTTC	GTCCAAAGAC	TGGACGCGAT	AGCTGGGTTT	GGCACCAGTG	1980
20			TTGAGGTCTT				2040
			ACAAGGCCAG				2100
			CATGTGCCAA				2160
			ACATTGATTG TGATTGTGAA				2220 2280
25	CTCCAACAAT	ATGCTGCAGT	GCCGCTGCAA	CTATCATCC	CACCECTCT	GGCTGCACAA	2340
	CTGCCACACA	GGGAATTCAT	ACCCAGCCAA	TGCAGAACTC	TCCCTGGAGC	AGGAACAGCG	2400
			GAAGCTGTCA				2460
			GCCATGCCCT				2520
20	CAGTGCCAAG	GGGCACCAAG	AACCTGCTCA	GGAAGCCTTT	TGATGGCAAG	ATCACCAATC	2580
30			GGATGGCTCT				2640
			GCTCAGCTGA				2700
			TCCGGGATTC GTGGTGCTTT				2760 2820
			AGTGTTAGCT				2880
35			AGAGAAGCTG				2940
	ATTTAGAACT	CACCTCTCAC	ACTCTGTTCT	TTAGTGTCCT	TACCTTTATC	TTACCACACA	3000
			TTGGAAGCAC				3060
			GAGTGCTTGA				3120
40			GCAAGAGTAG				3180
70			CCTCTGCCAA				3240
						TCAAGTCTCA	3300
		TCAACTCAAC	TTTCCATTCA	A TO A A THEORY	CCCATCCAAA	CARCATCARA	
						GAACATCAAA	3360
	CAAGCCACTC	ATCTCTACAG	AGATAAGAAA	ACAAGTTTGG	CAGAGCAAGA	GACAGAAGAC	3420
45	CAAGCCACTC CGTGGAGAAA	ATCTCTACAG TCAGAAGGGG	AGATAAGAAA GAACAGTCAG	ACAAGTTTGG TTTAGTTAAG	CAGAGCAAGA GATGGAACCT	GACAGAAGAC	
45	CAAGCCACTC CGTGGAGAAA ACCATTCCTG TCTTCTTGAC	ATCTCTACAG TCAGAAGGGG CTTGATGGGG ATGATTCTTG	AGATAAGAAA GAACAGTCAG CTCTGATTTG ATCTTTTCTC	ACAAGTTTGG TTTAGTTAAG CTCTTGCTCA CACTGAGACA	CAGAGCAAGA GATGGAACCT AGTGGAATAA CACTTAAGTG	GACAGAAGAC GGGAAAGGCC AACCCCATGG ATGATCCTTA	3420 3480
45	CAAGCCACTC CGTGGAGAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC	ATCTCTACAG TCAGAAGGGG CTTGATGGGG ATGATTCTTG	AGATAAGAAA GAACAGTCAG CTCTGATTTG ATCTTTTCTC	ACAAGTTTGG TTTAGTTAAG CTCTTGCTCA CACTGAGACA	CAGAGCAAGA GATGGAACCT AGTGGAATAA CACTTAAGTG	GACAGAAGAC GGGAAAGGCC AACCCCATGG	3420 3480 3540
45	CAAGCCACTC CGTGGAGAAA ACCATTCCTG TCTTCTTGAC	ATCTCTACAG TCAGAAGGGG CTTGATGGGG ATGATTCTTG	AGATAAGAAA GAACAGTCAG CTCTGATTTG ATCTTTTCTC	ACAAGTTTGG TTTAGTTAAG CTCTTGCTCA CACTGAGACA	CAGAGCAAGA GATGGAACCT AGTGGAATAA CACTTAAGTG	GACAGAAGAC GGGAAAGGCC AACCCCATGG ATGATCCTTA	3420 3480 3540 3600
	CAAGCCACTC CGTGGAGAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA	ATCTCTACAG TCAGAAGGGG CTTGATGGGG ATGATTCTTG ACCCTAATGC	AGATAAGAAA GAACAGTCAG CTCTGATTTG ATCTTTTCTC CAATAAAAGT	ACAAGTTTGG TTTAGTTAAG CTCTTGCTCA CACTGAGACA	CAGAGCAAGA GATGGAACCT AGTGGAATAA CACTTAAGTG	GACAGAAGAC GGGAAAGGCC AACCCCATGG ATGATCCTTA	3420 3480 3540 3600 3660
45 50	CAAGCCACTC CGTGGAGAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA Seq ID NO:	ATCTCTACAG TCAGAAGGGG CTTGATGGGG ATGATTCTTG ACCCTAATGC  175 DNA Sec	AGATAAGAAA GAACAGTCAG CTCTGATTTG ATCTTTTCTC CAATAAAAGT	ACAAGTTTGG TTTAGTTAAG CTCTTGCTCA CACTGAGACA TGCTCATTAT	CAGAGCAAGA GATGGAACCT AGTGGAATAA CACTTAAGTG	GACAGAAGAC GGGAAAGGCC AACCCCATGG ATGATCCTTA	3420 3480 3540 3600 3660
	CAAGCCACTC CGTGGAGAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA Seq ID NO: Nucleic Ac:	ATCTCTACAG TCAGAAGGGG CTTGATGGGG ATGATTCTTG ACCCTAATGC  175 DNA Sec id Accession	AGATAAGAAA GAACAGTCAG CTCTGATTTG ATCTTTTCTC CAATAAAAGT TUENCE 1 #: NM_001	ACAAGTTTGG TTTAGTTAAG CTCTTGCTCA CACTGAGACA TGCTCATTAT	CAGAGCAAGA GATGGAACCT AGTGGAATAA CACTTAAGTG	GACAGAAGAC GGGAAAGGCC AACCCCATGG ATGATCCTTA	3420 3480 3540 3600 3660
	CAAGCCACTC CGTGGAGAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA Seq ID NO: Nucleic Ac:	ATCTCTACAG TCAGAAGGGG CTTGATGGGG ATGATTCTTG ACCCTAATGC  175 DNA Sec	AGATAAGAAA GAACAGTCAG CTCTGATTTG ATCTTTTCTC CAATAAAAGT TUENCE 1 #: NM_001	ACAAGTTTGG TTTAGTTAAG CTCTTGCTCA CACTGAGACA TGCTCATTAT	CAGAGCAAGA GATGGAACCT AGTGGAATAA CACTTAAGTG	GACAGAAGAC GGGAAAGGCC AACCCCATGG ATGATCCTTA	3420 3480 3540 3600 3660
50	CAAGCCACTC CGTIGAGAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA Seq ID NO: Nucleic Ac: Coding sequil	ATCTCTACAG TCAGAAGGGG CTTGATGGGG ATGATTCTTG ACCCTAATGC  175 DNA Set Id Accession Lence: 234. 11	AGATAAGAAA GAACAGTCAG CTCTGATTTG ATCTTTTCTC CAATAAAAGT TUENCE 1 #: NM_001' 1130 21	ACAAGTTTGG TITAGTTAAG CTCTTGGTCA CACTGAGACA TGCTCATTAT	CAGAGCAAGA GATGGAACCT AGTGGAATAA CACTTAAGTG GGACTGCTAC	GACAGAAGAC GGGAAAGGCC AACCCCATGG ATGATCCTTA AAAAAAAAA 51	3420 3480 3540 3600 3660
	CAAGCCACTC CGTGGAGAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA Seq ID NO: Nucleic Ac: Coding sequ 1   GGAAGCAGGG	ATCTCTACAG TCAGAAGGGG CTTGATGGGG ATGATTCTTG ACCCTAATGC  175 DNA Set id Accession sence: 234. 11   CGGGGCCTCT	AGATAAGAAA GAACAGTCAG CTCTGATTTG ATCTTTTCTC CAATAAAAGT  Quence n #: NM_001' .1130 21   GGTGGCGGTC	ACAAGTTTGG TITAGTTAAG CTCTTGGTCA CACTGAGACA TGCTCATTAT  798.2 31   GGGAACTCGG	CAGAGCAAGA GATGGAATAA AGTGGAATAA GGACTGCTAC GGACTGCTAC	GACAGAAGAC GGGAAAGGCC AACCCCATGG ATGATCCTTA AAAAAAAAAA	3420 3480 3540 3600 3660
50	CAAGCCACTC CGTGGAGAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA Seq ID NO: Nucleic Ac: Coding sequ 1   GGAAGCAGGG TCAAGTTGGC	ATCTCTACAG TCAGAAGGGG CTTGATGGGG ATGATTCTTG ACCCTAATGC  175 DNA Sec dd Accession Lence: 234. 11   CGGGGGCCTCT CAAATTGACA	AGATAAGAAA GAACAGTCAG GATCAGTTTG ATCTTTTCTC CAATAAAAGT  Quence 1 #: NM_001' 1130 21   GGTGGGGGTC AGAGGGAGAG	ACAAGTTTGG TITAGTTAAG CACTGAGACA TGCTCATTAT  798.2  31   GGGAACTCGG GGGAACTCGG GTATACTCGG	CAGAGCAAGA GATGGAACTA AGTGGAATAA CACTTAAGTG GGACTGCTAC  41	GACAGAAGAC GGGAAAGGCC AACCCCATGG ATGATCCTTA AAAAAAAAAA	3420 3480 3540 3660 3665 665
50	CAAGCCACTC CGTIGGAGAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA Seq ID NO: Nucleic Ac: Coding sequ 1   GGAAGCAGGG TCAAGTTGGC ACCGTACTGG	ATCTCTACAG TCAGAAGGGGG ATGATTCTTG ACCCTAATGC  175 DNA Set dd Accession Lence: 234. 11   CGGGGCCTCT CAAATTGACA GCCCTGTTTC	AGATAAGAAA GAACAGTCAG CTCTGATTTG ATCTTTTCTC CAATAAAAGT TUENCE 1 #: NM_001' .1130 21   GGTGGCGGTC AGAGGGAGAG CCCCTCCTCG	ACAAGTTTGG TITAGTTAAG CTCTTGGTCA TGCTCATTAT  798.2  31   GGGAACTCGG GGTATACTCGG GCCCCCGAGA	CAGAGCAAGA GATGGAACAT AGTGGAATAA CACTTAAGTG GGACTGCTAC  41   TGGGAGGCGG TTCCATCCCG GCCAGGGTCC	GACAGAAGAC GGGAAAGGCC AACCCCATGG ATGATCCTTA AAAAAAAAA  51   CAACATTGTT ACCCGGGGCC GCCTTCTGCA	3420 3480 3540 3660 3660 3665
50	CAAGCCACTC CGTGGAGAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA  Seq ID NO: Nucleic Ac: Coding sequ 1   GGAAGCAGGG TCAAGTTGGC ACCGTACTGG GGGTTCCCAG	ATCTCTACAG TCAGAAGGGG CTTGATGGGG ATGATTCTTG ACCCTAATGC  175 DNA Set id Accession ence: 234. 11   CGGGGCCTCT CAAATTGACA GCCCTGTTTC GCCCCCCCTC	AGATAAGAAA GAACAGTCAG CTCTGATTTG ATCTTTTCTC CAATAAAAGT  TUENCE 1 #: NM_001' 1130 21   GGTGGGGGTC AGAGGGAGAG GCCCTCCTCG CAGGGCCGGG	ACAAGTTTGG TITAGTTAAG CTCTTGCTCA CACTGAGACA TGCTCATTAT  798.2  31   GGGAACTCGG GTATACTCGG GCCCCCGAGA CTGACCCGAC	CAGAGCAAGA GATGGAATAA ACACTAAGTG GGACTGCTAC  41   TGGGAGGCGG TTCCATCCCG GCCAGGGTCC TCGCTGGCGCC	GACAGAAGAC GGGAAAGGCC AACCCCATGG ATGATCCTTA AAAAAAAAA  51   CAACATTGTT ACCCGGGGCC GCCTTCTGCA TTCATCGAGA	3420 3480 3540 3600 3660 3665
50	CAAGCCACTC CGTGGAGAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA Seq ID NO: Nucleic Ac: Coding sequil GGAAGCAGGG TCAAGTTGGC ACCGTACTGG ACTCCAAAA	ATCTCTACAG TCAGAAGGGG CTTGATGGGG ATGATTCTTG ACCCTAATGC  175 DNA Set dd Accession Lence: 234. 11   CGGGGCCTCT CAAATTGACA GCCCTGTTTC GCCCCCGCTC GGTTGGAAAAG	AGATAAGAAA GAACAGTCAG CTCTGATTTG ATCTTTTCTC CAATAAAAGT  TUENCE 11130 21   GGTGGGGGTC AGAGGGAGAG CCCCTCCTCG CAGGGGCGGGATCGGAGAGGGAAGGGA	ACAAGTTTGG TITAGTTAAG CACTGAGACA TGCTCATTAT  798.2  31   GGGAACTCGG GCCCCGGGA CTGACCCGAC GCACGTACGG GCACGTACGG GCACGTACGG	CAGAGCAAGA GATGGAACTA AGTGGAATAA CACTTAAGTG GGACTGCTAC  41   TGGGAGGCGG TTCCATCCCG GCCAGGGTCC TCGCTGGCGC AGTTGTTAC	GACAGAAGAC GGGAAAGGCC AACCCCATGG ATGATCCTTA AAAAAAAAAA	3420 3480 3540 3600 3665 3665
50	CAAGCCACTC CGTGGAGAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA Seq ID NO: Nucleic Ac: Coding sequ I GGAAGCAGGG TCAAGTTGGC ACGGTACTGG GGGTTCCCAGA ACCAGTTGACAAA ACCAGTTGAC	ATCTCACAG TCAGAAGGGG ATGATTCTTG ACCCTAATGC  175 DNA Sec Ad Accession lence: 234. 11   CGGGGCCTCT CAAATTGACA GCCCTGTTTC GCCCCCCCTC GGTGGAAAAG GGGAGAAGGG	AGATAAGAAA GAACAGTCAG GAACAGTTTG ATCTTTTCTC CAATAAAAGT  Tuence 1 #: NM_001 1130 21   GGTGGGGGTC AGAGGGAGAG CCCTCCTCG CAGGGCCGGG ATCGGAGAGG GTGGCGCTTA	ACAAGTTTGG TITAGTTAAG CTCTTGATCA CACTGAGACA TGCTCATTAT  798.2  31   GGGAACTCGG GCCCCCGAGA CTGACCCGAC GCACCTACCGAC GCACGTACGG AGAAAATCCG	CAGAGCAAGA GATGGAACTA AGTGGAACTA CACTTAAGTG GGACTGCTAC  41	GACAGAAGAC GGGAAAGGCC AACCCCATGG ATGATCCTTA AAAAAAAAAA	3420 3480 3540 3660 3665 3665
50	CAAGCCACTC CGTGGAGAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA  Seq ID NO: Nucleic Ac: Coding sequ 1   GGAAGCAGGG TCAAGTTGGC ACGGTACTGG GGGTTCCCAG ACTTCCAAAA ACAAGTTGAC GTGTGCCCAG	ATCTCTACAG TCAGAAGGGG ATGATTCTTG ACCCTAATGC  175 DNA Set id Accession ence: 234. 11   CGGGGCCTCT CAAATTGACA GCCCTGTTTC GCCCCCCTC GGTGGAAAAG GGGAGAGGTG TACTGCCATC	AGATAAGAAA GAACAGTCAG CTCTGATTTG ATCTTTTCTC CAATAAAAGT  Tuence 1 #: NM_001' 1130 21   GGTGGGGGTC AGAGGAGAG CCCCTCCTCG CAGGGCOGG ATCGGAGAGAG GTGGGGGTGAAGAGAGAGAGAGAGAGAGAGA	ACAAGTTTGG TITAGTTAAG CTCTTGCTCA CACTGAGACA TGCTCATTAT  798.2  31   GGGAACTCGG GTATACTGCG GCCCCCGGGA CTGACCCGAC GCACCTACGG AGAAAATCCG CTCTGCTTAA	CAGAGCAAGA GATGGAACAA CACTTAAGTG GGACTGCTAC  41   TGGGAGGCGG TTCCATCCCG GCCAGGGTCC TCGCTGGCACAT GGAGGTTAC	GACAGAAGAC GGGAAAGGCC AACCCCATGG ATGATCCTTA AAAAAAAAA  51   CAACATTGTT ACCCGGGCC GCCTTCTGCA TTCATGGAGA AAAGCCAGAA GAGACTGAGG CATCCTAATA	3420 3480 3540 3600 3660 3665 60 120 180 240 300 360 420
50	CAAGCCACTC CGTGGAGAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA Seq ID NO: Nucleic Acc Coding sequ I   GGAAGCAGGG TCAAGTTGGC ACGGTACTGG GGGTTCCCAAA ACAAGTTGAC GTTGCCCAG TTGTCCACAG TTGCACAGGT TTGCACAGGT TTGCACAGGAGT TTGCACAGA	ATCTCACAG TCAGAAGGAG CTTGATGGGG ATGATTCTTG ACCCTAATGC  175 DNA Sec dd Accession lence: 234. 11   CGGGGGCCTCT CAAATTGACA GCCCTGTTTC GCCCCCCCTC GGTGGAAAAG GGGAGAGGTG TACTGCCATC GCTGCATCC TCTCAAGAAA	AGATAAGAAA GAACAGTCAG GAACAGTTTG ATCTTTTCTC CAATAAAAGT  TUENCE 1 #: NM_001' 1130 21   GGTGGCGGTC AGAGGAGAG CCCTCCTCG CAGGGCCGGG ATCGGAGAG GTGGCGGTTA CCAGGAGATCT TATTCACACG TTCATGGATG	ACAAGTTTGG TITAGTTAAG CTCTTGGTCA CACTGAGACA TGCTCATTAT  798.2  31   GGGAACTCGG GCCCCCGAGA CTGACCCGAC GCACCTACCG AGAAAATCCG CTCTGCTTAA AAAATAAACT CCTCTGCTCACCCCCCCCCC	CAGAGCAAGA GATGGAACTA CACTTAAGTG GGACTGCTAC  41	GACAGAAGAC GGGAAAGGCC AACCCCATGG ATGATCCTTA AAAAAAAAAA	3420 3480 3540 3660 3665 3665
50 55	CAAGCCACTC CGTGGAGAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA  Seq ID NO: Nucleic Ac: Coding sequ 1   GGAAGCAGGG TCAAGTTGGC ACGGTACTGG GGGTTCCCAG ACTTCCAAAA ACAAGTTGAC GTGTGCCCAG TTGTCAAGCT TGCACCAAGA TCATCAAGAG TCATCAAGAG	ATCTCTACAG TCAGAAGGGG ATGATTCTTG ACCCTAATGC  175 DNA Set dd Accession ence: 234. 11   CGGGGCCTCT CAAATTGACA GCCCTGTTTC GCCCCGCTC GGTGGAAAAG GGGGAAAGGTG TACTGCCATC GCTGGATTC TCTCAAGAAA CTATCTGTTC	AGATAAGAAA GAACAGTCAG CTCTGATTTG ATCTTTTCTC CAATAAAAGT  TUENCE 1 #: NM_001' 1130 21   GGTGGCGGTC AGAGGGAGAG CCCCTCCTCG CAGGGCCGGG ATCGGAGAGG ATCGGAGAGAG TTCACACAG TTCACACAG CAGCTGCTCC CAGCTGCTC ATTCACACAG CAGCTGCTCC CAGCTGCTCC CAGCTGCTCC CAGCTGCTCC CAGCTGCTCC CAGCTGCTCC CAGCTGCTCC CAGCTGCTCC	ACAAGTTTGG TITAGTTAAG CTCTTGGTAAG CACTGAGACA TGCTCATTAT  798.2  31   GGGAACTCGG GCCCCCGAGA CTGACCCGAC GCACGTACGG GCACGTACGG GCACGTACGG GCACGTACGG CTATACTCGC CTCTGCTTAA AAAATAAACT CCTCTGCTTAA AGGGCCTAGC	CAGAGCAAGA GATGGAACTA AGTGGAATAA CACTTAAGTG GGACTGCTAC  41   TGGGAGGCGG TTCCATCCCG GCCAGGGTCC TCGCTGGCAC AGTTGTTAC CTACCTGGTT CACTGGCAT CTACCTGGTT CACTGGCAT TTCTGCCAT TTCTGCCAT	GACAGAAGAC GGGAAAGGCC AACCCCATGG ATGATCCTTA AAAAAAAAA  51   CAACATTGTT ACCCGGGGCC GCCTTCTGCA TTCATGGAGA AAAGCCAGAA AGAGCCAGGAC CATCCTAATA TTTGAATTTC CCTCTTCCCC TCTCATCGGG	3420 3480 3540 3600 3660 3665 60 120 180 240 300 360 420 480
50	CAAGCCACTC CGTGGAGAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA  Seq ID NO: Nucleic Ac: Coding sequil GGAAGCAGGG TCAAGTTGGC ACGGTACTGG ACTTCCAAAA ACAAGTTGAC GTGTGCCAG TTGTCAAGCT TGCACCAAGA TCATCAAGAG TCATCAAGAG TCATCAAGAG TCATCAAGAG TCATCAAGAG TCATCAACAG TCATCAAGAG TCATCAACAG TCATCAACAG	ATCITACAG TCAGAAGGGG ATGATTCTTG ACCCTAATGC  175 DNA Set dd Accession Lence: 234. 11 CGGGGCCTCT CAAATTGACA GCCCTGTTTC GCCCCCGCTC GGTGGAAAAG GGGAGAGGTG TACTGCCATC TCTCAAGAAA CTATCTGTTC CATACTGTTC CTTACTGCTTC CTTACTGATC CTTACTGTTC CTTACTGTTC CAGACTTAAA	AGATAAGAAA GAACAGTCAG CTCTGATTTG ATCTTTTCTC CAATAAAAGT  # : NM_001' 1130 21   GGTGGGGGTC AGAGGGAGAG CCCCTCCTCG CAGGGGGGGGATCGGAGGAGGTCTAGAGAGATCT ATTCACACAG TTCATGGATG CAGGGTGCTCC CAGGATCC CAGGATCC CAGGATCC CAGGATCC CAGGATCC CCTCAGAATC	ACAGTTIGG TITAGTIANG CTCTTGCTCA CACTGAGACA TGCTCATTAT  798.2  31   GGGAACTCGG GCCCCCGAGA CTGACCCCGAGA CTGACCCCGAGA CTGACCCGTAA AAAATAACT CCTCTGCTTA AGGGCCTAGC TGCCTTATTAA	CAGAGCAAGA GATGGAACTA CACTTAAGTG GGACTGCTAC  41   TGGGAGGCGG TTCCATCCCG GCCAGGGTCC TCGCTGGCGCC AGTTGTTAC CTGGACACT CACTGGCAT CACTGGCAT TTTCTGCCAT CACAGAGGGCT CACAGAGGTCC CACAGGGTCC CACAGGGTCC CACAGGGTCC CACAGGGTCC CACAG	GACAGAAGAC GGGAAAGGCC AACCCCATGG ATGATCCTTA AAAAAAAAA  51   CAACATTGTT ACCCGGGGCC GCCTTCTGCA TTCATCGAGA AGAGCTGAGG CATCCTAATA TTTGAAATTC CCTCTTCCCC TCTCTTCCCC TCTCTTCCGG GCCATCAAGC GCCATCAAGC	3420 3480 3540 3660 3665 60 120 180 240 360 420 480 540
50 55	CAAGCCACTC CGTGGAGAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA  Seq ID NO: Nucleic Ac: Coding sequil GGAAGCAGGG TCAAGTTGGC ACCGTACTGG ACTTCCAAAA ACAAGTTGAC GTGTGCCAGG TTGTCAAGAT TGCACCAGGA TCATCAAGAGT TCATCAAGAG TCATCAAGAGT TCATCAAGAG TCATCAAGAGT TCATCAAGAGT TCATCAAGAGT TCATCAAGAGT TCATCAAGAGT TCATCAACAGT TCATCAACAGT TAGCACCACGT TAGCAGACTT	ATCTCTACAG TCAGAAGGAG CTTGATGGG ATGATTCTTG ACCCTAATGC  175 DNA Set dd Accession Lence: 234. 11   CGGGGCCTCT CAAATTGACA GCCCTGTTTC GCCCCCGCTC GCTGGAAAAG GGAGAGGTG TACTGCCATC CCTGCAGAAAA CGTGCATTC TCCAAGAAA CTACTGTTAC AGACCTTACA TGGACTTACA	AGATAAGAAA GAACAGTCAG CTCTGATTTG ATCTTTTCTC CAATAAAAGT  TUENCE 11130 21   GGTGGGGGTC AGAGGGAGAG CCCCTCTCG CAGGGCGGG ATCGGAGAGGG GTGGGGCTTA TATCACACAG TTCATGGATG CAGTGCTCC CAGGGGTTC AGAGCTTCTCAGAATC AGAGCTTTTG AGAGCTTTTT	ACAAGTTTGG TITAGTTAAG CTCTTGGTCA CACTGAGACA TGCTCATTAT  798.2  31   GGGAACTCGG GCCCCCGGGA CTGACCCGAC CTGACCCGAC GCACTTACTGCT AGAAAATCCG CTCTGCTTCA AGAAATAACT CCTCTGCTTCA AGAGCCTAGC GCCTCTGCTTCA AGAGCCTAGC TGCTTATTAA GAGTCCCTGT	CAGAGCAAGA GATGGAACTA CACTTAAGTG GGACTGCTAC  41   TGGGAGGCGG TTCCATCCCG GCCAGGGTCC TCGCTCGCGC AGTTGTTAC CTGGACACT CTACTCGGT CACTGGTT TTCTGCCAT CACAGAGGGGT CACAGAGGGT CTACCTGGT CACTGGACATT TTCTGCCAT CACAGAGGGGG CACAGAGGGG	GACAGAAGAC GGGAAAGGCC AACCCCATGG ATGATCCTTA AAAAAAAAAA	3420 3480 3540 3660 3660 3665 60 120 180 240 360 420 480 540 600 660 720
50 55	CAAGCCACTC CGTGGAGAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA  Seq ID NO: Nucleic Ac: Coding sequ I GGAAGCAGGG TCAAGTTGGC ACGGTACTGG GGGTTCCCAGG ACTTCCAAAA ACAAGTTGAC GTGTGCCAG TTGTACAGGT TGCACAGA TCATCAAGAG TCATCAAGAG TCATCAAGAG TCATCAAGAG TCATCAAGAG TCACCAAGA TCATCAAGAG TCATCAACGT TGCACCACG TAGCAGACTT TGCTGACCCT TAGCAGACTT TGGTGACCCT	ATCTCTACAG TCAGAAGGGG ATGATTCTTG ACCCTAATGC  175 DNA Sec dd Accession leince: 234. 11   CGGGGCCTCT CAAATTGACA GCCCTGTTTC GCCCCCGCTC GGTGGAAAAG GGGAGAAGGTG TACTGCCATC GCTGATGTC AGACTTAAA TGCATTACA AGACTTAAA AGACTTAAA AGGACTAACA AGGACTAACC GTGGTACCGG GTGGTACCGG GTGGTACCGG GTGGTACCGG	AGATAAGAAA GAACAGTCAG GAACAGTCAG CTCTGATTG ATCTTTTCTC CAATAAAAGT  Juence H: NM_001 1130 21   GGTGGGGGTC AGAGGAGAG CCCTCCTCG CAGGGCCGGG ATCGGAGAGG GTGGCGCTTA CCAGAGATCT ATTCACACAG TTCATGGATG CAGTGCTCC CCTCAGAATC CCTCAGAATC AGAGCTTTTTG AGAGCTTTTTG AGAGCTTTTTG AGAGGTTTTTTG AGAGGTTTTTTG AGAGGTTTTTTTT	ACAAGTTTGG TITAGTTAAG CTCTTGATCA CACTGAGACA TGCTCATTAT  798.2  31   GGGAACTCGG GCCCCCGAGA CTGACCCGAC GCACCTACCG GCACCTACCG GCACTTACTCG TCTCTCTTAA AAAATAAACT CCTCTGCTTTA AGGGCCTAGC TGCTTATTAA GAGTCCCTGG TGCTTATTAA	CAGAGCAAGA GATGGAACTA CACTTAAGTG GGACTGCTAC  41   TGGGAGGCGG TTCCATCCCG GCCAGGGTCC TCGCTGGCACC CTGCACACT CACTGGCATT TTTCTGCCAT CACTGGCATT TTTCTGCCAT CACTGGCATT TTTCTGCCAT CACTGGCATT CACTGGCATT CTCGCAATATAC CTGCAAATAT	GACAGAAGAC GGGAAAGGCC AACCCCATGG ATGATCCTTA AAAAAAAAA  51   CAACATTGTT ACCCGGGGCC GCCTTCTGCA TTCATGGAGA AAAGCCAGAA GAGACTGAGG CATCCTAATA TTTGAATTTC CCTCTTCCCC TCTCATCGGG GCCATCAAGC ACCCATGAGG TATTCCACAGG TATTCCACAGG	3420 3480 3540 3660 3665 60 120 180 240 300 360 420 480 600 660 660 780
50 55	CAAGCCACTC CGTGGAGAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA  Seq ID NO: Nucleic Ac: Coding sequi   GGAAGCAGGG TCAAGTTGGC ACGGTACTGG GGGTTCCCAG ACTTCCAAAA ACAAGTTGAC TGGACCAAGA TCATCAAGAGT TGCACCAAGA TCATCAAGAG TCATCAAGAG TCATCAAGAG TCTCCACCG TAGCAGGACTT TGGTGACCCT TGGTGACCCT TTGGTGACCT	ATCTTACAG TCAGAAGGGG ATGATTCTTG ACCCTAATGC  175 DNA Set dd Accession Lence: 234. 11   CGGGGCCTCT CAAATTGACA GCCCTGTTTC GCCCCGCTC GGTGGAAAAG GGCAGAGGTTG TCTCAAGAAA CTACTGTTC AGACTACAGCA CTACTGTTC AGACTACAGCA CTACTGTTC AGACTACAGCA CTACTGTTC AGACTACAGC CTGCATGCC CTGGAGCTACAGA CTGGAGCTACAGA CTGGAGCCTG CTGGAGCCTG CTGGAGCCTG	AGATAAGAAA GAACAGTCAG CTCTGATTTG ATCTTTTCTC CAATAAAAGT  #: NM_001' 1130 21   GGTGGGGGTC AGAGGGAGAG CCCCTCTCG ATGGGGGTTAAAAGT ATTCACACAG TTCATGATGATG CAGGTCTCC CCTCAGGATC AGAGGTTTAA GGGTTTAA GGCTCCTGAGATC AGAGGTTTTAA	ACAGTTIGE TITAGITIAGE CTCTTGETCA CACTGAGACA TGCTCATTAT  798.2  31    GGGAACTCGG GCCCCCGAGA CTGACCCCGAGA CTGACCCCGAGA CTGACCCGGA CTGACCCGGA AGAAAATCAG GCACTTATA AAAATAAACT CCTCTGCTTTA AGGGCCTAGC TGCTTATTAA GAGTCCCTGT TCCTCCTGGT TCCTCGGCT TCCTGGTTTTTAA TGCTGACTT TCCTCCTGGT TCCTCTGGCT TCCTGGCT TCCTGCTGAGAT	CAGAGCAAGA GATGGAACTA CACTTAAGTG GGACTGCTAC  41   TGGGAGGCGG TTCCATCCCG GCCAGGGTCC TCGCTGGCACACT CACTGGACACT TTTCTGCCAT CACAGAGGCCC CAGAGAGGCCC TACCTGGACACT CACAGAGGGCC CACAGAGGGCC CTACCTGGACACT CACAGAGGGGC TCGTACTTAC CTGCAAATAT	GACAGAAGAC GGGAAAGGAC AACCCCATGG ATGATCCTTA AAAAAAAAA  51   CAACATTGTT ACCCGGGGCC GCCTTCTGCA TTCATCGAGA AAAGCCAGAA GAGACTGAGG CATCCTAATA TTTGAATTTC CCTCTTCCCC TCTCTCCCC TCTCTCCCC TCTCTCCCC TCTCATCGGG GCCATCAAGC ACCCATGAGG TATTCCACAG CGGGCCCTAT	3420 3480 3540 3660 3665 3665 60 120 180 240 300 420 480 540 660 720 660 780 840
50 55	CAAGCCACTC CGTGGAGAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA  Seq ID NO: Nucleic Ac: Coding sequit GGAAGCAGGG TCAAGTTGGC ACGTACTGG ACTTCCAAAA ACAAGTTGAC GTGTGCCAG TTGTCAAGCT TGCACCAAGA TCATCAAGAG TCATCAAGAG TCATCAAGAG TCATCAAGAG TCATCAAGAG TCCTCCACCG TAGCAGACTT TGGTGACCT TTGTGAACCT TCGTGGACAT	ATCTTACAG TCAGAAGGGG ATGATTCTTG ACCCTAATGC  175 DNA Set did Accession Jence: 234.  11   CGGGGCCTCT CAAATTGACA GCCCTGTTTC GCTCGAGAAGGGTG TACTGCCATC GCTGGATGCCATC GCTGAGAAA TGACTTACA CTATCTGTTC GCTGGATACGA TGGACTAGCC GTGGTACCGA TCTGGAGCCTT TTCTGAGAT TCTGAGAT TCTGAGT	AGATAAGAAA GAACAGTCAG CTCTGATTTG ATCTTTTCTC CAATAAAAGT  "#: NM_001" 1130 21   GGTGGGGGTC AGAGGGAGAG CCCCTCCTGG ATCGAGAGATCT ATTCACACAG TTCATGGATG CAGGGTGTCC CCTCAGAATCT AGAGCTTTTG GGTGCTTTTTG GGTGCTTTTG GGTGCTTTTG GGTGCTTTTG GGTGCTTTTG GGTGCTTTTG GGTGCTTTTG GGTGCATCT AGAGCTTTTTG GGTGCATCT AGAGCTTTTTG GGTGCATCT GACCAGCTCT GACCAGCTCT GACCAGCTCT GACCAGCTCT GACCAGCTCT	ACAAGTTTGG TITAGTTAAG CTCTTGGTCA CACTGAGACA TGCTCATTAT  798.2  31   GGGAACTCGG GCCCCCGAGA CTGACCCGAC GCACCTACGG AGAAAATCCG CTCTGCTTAA AAAATAAACT CCTCTGCTTCA AGGGCCTAGG AGGACTCTG TGCTTATTAA GAGTCCCTGT TCCTCTGCT TCCTTGCT TCCTTGCAT TCCTTGCTTAT TCCTGAGAT TCCCGATCTT	CAGAGCAAGA GATGGAACTA CACTTAAGTG GGACTGCTAC  41   TGGGAGGCGG TTCCATCCCG GCCAGGGTCC TCGCTCGCCC AGTTGTGTAC CTGGACACT CACTGGACACT CACTGGACAT TTTCTGCCAT TTTCTGCCAT TTTCTGCCAT CACAGAGGGGG TCGTACTTAC CTGCAAATAT CGGTGACTCGC TCGCACATCT	GACAGAAGAC GGGAAAGGCC AACCCCATGG ATGATCCTTA AAAAAAAAA  51   CAACATTGTT ACCCGGGGCC GCCTTCTGCA ATTGATGAGA AAAGCCAGAA AGACCTGAGA AGACCTGAGA AGACCTGAGA AGACCTGAGA AGACCTGAGA ACCCATCAAC CCCTCTCCCC TCTCATCGCG ACCCATCAAGC ACCCATGAGG TATTCCACAGG CGGGCCCTAT GGGACCCCAG	3420 3480 3540 3660 3660 3665 60 120 180 240 360 420 480 540 660 720 780 840 900
50 55 60	CAAGCCACTC CGTGGAGAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA  Seq ID NO: Nucleic Acc Coding sequ I GGAAGCAGGG TCAAGTTGGC ACGGTACTGG GGTTCCCAAA ACAAGTTGAC GTGTGCCAGG TTGTACAGAT TCACCAGAGA TCATCAAGAG TCTTCAAGAG TCTTCAAGAG TCTTCAAGAG TCTTCAAGAG TCTTCAAGAG TCTTCAAGAGA TCATCAAGAG TCTTCACCTCTCACCT TGGTGACCT TTGGTGACCT TCTTGGAGAA ATCAGGTGGT	ATCTCTACAG TCAGAAGGGG ATGATTCTTG ACCCTAATGC  175 DNA Sec Ad Accession lence: 234.  11    CGGGGCCTCT CAAATTGACA GCCCTGTTTC GCCCCCCTC GGTGGAAAAG GGAGAGGT TACTGCCATC TCTCAAGAAA CTATCTGTTC AGACCTTAAA GGACCTAAAA GGAGAGCCT TCTCAAGAAA CTATCTGTTC GGGCCCTGT TCTGAGATT TGGGCCAGGA CTGGAGCCTG TTCTGAGACT TCTGAGACT GTTGGCAGGACTT GTTGGCCAGGA	AGATAAGAAA GAACAGTCAG GAACAGTTTG ATCTTTTCTC CAATAAAAGT  Illia0 21   GGTGGCGGTC AGAGGAGAG CCCTCCTCG CAGGAGGATTA ATTCACACAG TTCATGGATG CCTCTCAGAATC CAGGCTTCTC CCTCAGAATT CCAGGATC CCTCAGAATT CCAGGATC CCTCAGAATT GCTCCTGAAA GGCTGCATCT GACCAGCTTTT GCTCCTGAAA	ACAAGTTTGG TITAGTTAAG CTCTTGATCA CACTGAGACA TGCTCATTAT  798.2  31   GGGAACTCGG GCCCCCGAGA CTGACCCGAC GCCCCTATACTCGG GCACGTACCGAC CTCTGCTTAA AAAATAAACT ACAGCCTAGC TGCTTATTAA GAGTCCTGT TCCTCCTGG TTCCTCTGGATTA TCCGGATCTT TCCGGATCTT TCCGCTGATTA	CAGAGCAAGA GATGGAACTA CACTTAAGTG GGACTGCTAC  41    TGGGAGGCGG TTCCATCCCG GCCAGGGTCC TCGCTGGCGC CCTGGCACT CACTGGCATT TTTCTGCCAT CACTGGCATT TTTCTGCCAT CACTGGCATT TTCTGCCAT CACTGGCATT TCGGAAATAT GGTGACTCGC TCGGAAATAT GGTGACTCGC CAAGCCAAGT TCGGACTCTC CACAGCATCT CCGACACTCTC CACAGCACT CACAGCAAGT CCAAGCCAAG	GACAGAAGAC GGGAAAGGCC AACCCCATGG ATGATCCTTA AAAAAAAAAA	3420 3480 3540 3660 3660 3665 60 120 180 240 360 420 480 540 660 720 780 840 900 960
50 55 60	CAAGCCACTC CGTGGAGAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA  Seq ID NO: Nucleic Ac: Coding sequit GGAAGCAGGG TCAAGTTGGC ACGTACTGG ACTTCCAAAA ACAAGTTGAC GTGTGCCAG TTGTCAAGCT TGCACCAAGA TCATCAAGAG TCATCAAGAG TCCTCCACCG TAGCAGCAT TCGTGACCTT TGGTGACCT TTGTGACCT TTGTGACAT TCCTTGTGACAT TCCCTGGAGA ATCAGGGGCC ATCTGCAAAAT	ATCTCTACAG TCAGAAGGGG ATGATTCTTG ACCCTAATGC  175 DNA Set did Accession Jence: 234.  11   CGGGGCCTCT CAAATTGACA GCCCTGTTTC GCTCGAGAAAG GGGAGAGGTG TACTGCCATC GCTGGATGCCATC GCTGAGAAAG CTATCTGTTC CTCAAGAAA TGGACTAGCC GTGGTACCGA TCTGAGCCTT TCTGAGATT GTGGCCAGGA TCTGAGCCTG TCTGAGCCTG TCTGAGCCTG TCTGAGATT GTGCCAGGA AGACTTTAAA	AGATAAGAAA GAACAGTCAG CTCTGATTTG ATCTTTTCTC CAATAAAAGT  #: NM_001' 1130 21   GGTGGGGGTC AGAGGGAGAG CCCCTCTCGG ATCGAGAGAGT TACTACACAG TTCATGGATTC CAGAGGTTTCAGAGAGT TCATGGATCT AGAGCTGTTCC CCTCAGAATCT AGAGCTTTTG GCTCCTGAAA GGCTGCTTCT GACCAGCTCTT GACCAGCTCT GACCAGCACAA AAAGTTGTAC GACCCTAACAA	ACAAGTTTGG TITAGTTAAG CTCTTGGTCA CACTGAGACA TGCTCATTAT  798.2  31   GGGAACTCGG GCCCCCGAGA CTGACCCGAC CTGACCCGAC ACACTAACTCG GCCCCCGAGA CTGACCCGAC CTGACCCGAC AGAAAATACG TCCTTGACTTAA AGAGCCTAGG GCCTAGC TCCTTGCTTCA AGGGCCTAGC TCCTTCCTGGC TCCTCTCGCT TCCTGCTGT TCCTGAGAT TCCCGGATCTT TCCCGGATCTT TCCCGGATCTT TCCCTGGAAAACACACACACACACACACACACACACACAC	CAGAGCAAGA GATGGAACTA CACTTAAGTG GGACTGCTAC  41    TGGGAGGCGG TTCCATCCCG GCCAGGGTCC TCGCTCGCCC AGTTGTTAC CTTGGACACT CACTAGGTT CACTAGGTT CACTAGGTT CACTAGGTT CACTAGGTT CACTAGGTT CACTAGGTT CACTAGCT TTTCTGCCAT TTTCTGCCAT CACAGAGGGGG TCGTACTTAC CTGCAAATAT GGTGACTCTG CTGGACTCTG CAGACTCTG CAGACCAAGT CAGACCAAGGCA	GACAGAAGAC GGGAAAGGAC AACCCCATGG ATGATCCTTA AAAAAAAAA  51   CAACATTGTT ACCCGGGGCC GCCTTCTGCA ATTGATGAGA AAAGCCAGAA AGACCTGAGA AGACCTGATC CCTCTTCCCC TCTCATCGGG ACCCCATGAGG TATTCCACAGG ACCCATGAGG TATTCCACAGG TATTCCACAGG TATTCCACAGG TCCCCAAGT TCCCCAAGT TCCCCAAGT TCCCCAAGT TCCCCCAAGT TCCCCCAAGT TCCCCCAAGT TCCCCCAAGT TCCCCAAGT TCCCCCAAGT TCCCCCAAGT TCCCCCAAGT TCCCCCAAGT TCCCCCAAGT TCCCCAAGT TCCCCCAAGT TCCCCAAGT TCCCCCAAGT TCCCCCAAGT TCCCCCAAGT TCCCCCAAGT TCCCCAAGT TCCCCCAAGT TCCCCAAGT TCCCCCAAGT TCCCCAAGT TCCCCCAAGT TCCCCCAAGT TCCCCCAAGT TCCCCCAAGT TCCCCCCCAAGT TCCCCCAAGT TCCCCCAAGT TCCCCCCCCCC	3420 3480 3540 3660 3660 3665 60 120 180 240 360 420 480 540 660 720 780 840 900
50 55 60	CAAGCCACTC CGTGGAGAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA Seq ID NO: Nucleic Accoding sequence I GGAAGCAGGG TCAAGTTGGC ACCGTACTGG GGGTTCCCAAAA ACAAGTTGAC TTGTCAAAAA ACAAGTTGAC TTGTCAAGAGT TCACCAAGA TCATCAAGAGT TCACCAAGA TCATCAAGAGT TCCTCACCG TAGCAGACTT TGGTGACCAT TTGTGGACAT TCCTTGGACAT ACCCTTCTGTGAAAA ATGAGGTGGT ATGCAAAAT ACCCTTTCTT	ATCTCACAG TCAGAAGGAG CTTGATGGG ATGATTCTTG ACCCTAATGC  175 DNA Set id Accession lence: 234. 11   CGGGGCCTCT CAAATTGACA GCCCTGTTTC GGCGCCCCGCTC GGTGGAAAAG GGGAGGGT TACTGCCATC TCTCAAGAAA CTATCTGTTC GGCTGCATAGC GTGGTACGA CTGGAGCCTG TTCTGAGATT GTGGACTAGC GTGGTACCGA CTGGAGCCTG GTGGACGGA AGATTTTAGT GCTGCACTAC CCAGGATGTG CCTGCACTAC CCAGGATGTG	AGATAAGAAA GAACAGTCAG GACTAGTTTG ATCTTTTCTC CAATAAAAGT  TUENCE 1 #: NM_001' 1130 21   GGTGGGGGTC AGAGGGAGAG CCCCTCCTCG CAGGGCGGGG ATCGGAGAGG GTGCGCGTTA TCAACAAG TTCATGGATG CCCTCAGAATC AGAGCTTTTG GCTCCTGAAA GGCTGCATCT GACCAGCTGCATCT AGACTTCTTAAAGTTGTAC GACCAGCTCTAAAAAC AACCAAGCCAA	ACAGTTTGG TITAGTIANG CTCTTGCTCA CACTGAGACA TGCTCATTAT  198.2  31   GGGAACTCGG GCCCCGAGA CTGACCGAC CTGACCGAC CTGACCGAC AGAAAATCG CTCTGCTTAA AAAATAAACT CCTCTGCTTATA GGGTCTGCTGCTTATTAA GGGTCTGCTGACAT TCCCGATCT TCCCGGGTTCCCTGGGATTCCCGGATTTCCCGGATTTCCCGGATTT TCCCCTGGTATTA CTCCCCTGGATTC	CAGAGCAAGA GATGGAACTA CACTTAAGTG GGACTGCTAC  41    TGGGAGGCGG TTCCATCCCG GCAGGGTCC TCGCTGCGC CCTGGCACACT CACTGGACACT CACTGGACACT CACTGGACACT CACTGGACACT CACTGGACAT TTCTGCCAT CACAGAGGGG TCGTACTTAC CTGCAATAT CGTGACTCTGC CAGACCAAGT CAGACCAAGT TGAACTCAG CAGACCAAGT TGAACTCAG TCGACTCTGC CAGACCAAGT TGAACTCAG TCGACTCTGC CAGCCAAGCCA	GACAGAAGAC GGGAAAGGCC AACCCCATGG ATGATCCTTA AAAAAAAAA  51   CAACATTGTT ACCCGGGGCC GCCTTCTGCA TTCATGGAG AAAGCCAGAA GAGACTGAGG CATCCTAATA TTTGAATTTC CCTCTTCCC TCTCATCGGG GCCATCAAGG ACCCATGAGG TATTCCACAG GGGCCCTAT GGGACCCCAG TTCCCCAAGT TGGAACTCCTAATT TCCCCAAGT TGGAACTCTATCT TCCCCAAGT TCCCCAAGT TGGACCTCTT TCCCCAAGT TCCCCCAAGT TCCCCAAGT TCCCCAAGT TCCCCAAGT TC	3420 3480 3540 3660 3660 3665 60 120 180 240 480 600 660 720 780 840 900 960 1020
50 55 60 65 70	CAAGCCACTC CGTGGAGAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA  Seq ID NO: Nucleic Ac: Coding sequ I GGAAGCAGGG TCAAGTTGGC ACGGTACTGG GGGTTCCCAG ACTTCCAAAA ACAAGTTGAC GTGTGCCAG TTGTAAGAGT TCCTCACCG TAGCAGAAT TCCTCACCG TAGCAGACTT TCCTTGGACCT TCCTTGGACAT TCCCTGGAGA ATCAGGTGGT GGGCCCGCA TATCGCAAAA ACAGGTGGT CCTGGACAT TCCCTGGAGAT TCCCTGGAGAT TCCCTGAGAT ACCCTTTCTT GAAGCCCCCA	ATCTCTACAG TCAGAAGGGG ATGATTCTTG ACCCTAATGC  175 DNA Sec Ad Accession Leince: 234.  11    CGGGGCCTCT CAAATTGACA GCCCTGTTTC GCCCCCGCTC GGTGGAAAAG GGGAGAGGT TACTGCATC GCTGATTC AGACTTAAA CTATCTGTTC AGACTTAAA CTGGAATT TCTCAAGAA CTGGACCTG TTCTGAGATT TCTGAGATT CCTGCACTAC CCCGAGTTGG GCCCTAATCT	AGATAAGAAA GAACAGTCAG GAACAGTCAG ATCTTTTCTC CAATAAAAGT  TUENCE 1 #: NM_001* 11130 21   GGTGGGGGGTC AGAGGAGAG CCCTCCTCG CAGGGCGGGG ATCGGAGAGG GTGGCGCTTA CCAGGAGTCT ATTCACACAG TTCATGGATG CACTGCTCG CCTCAGAATC CACTGCTCT AGAGCTTTTC AGAGCTTTTC AGAGCTTTTC AGACCTGCTCAAAA GCCAGCTCT ATTCTAAAAGTTGTAC GACCCTAACAA ACCAAGCCAA	ACAAGTTTGG TITAGTTAAG CTCTTGATCA CACTGAGACA TGCTCATTAT  798.2  31   GGGAACTCGG GCCCCCGAGA CTGACCCGAC GCACCTACCGG AGAAATCCG CTCTGCTTAA AAAATAAACT TCCTCTGGTT AGGGCCTAGC TGCTGATTA TCCCGGTTTGCTGAGAT CCCCCTGGAT TCCCCCTGGAT TCCCCCTGGAT TCCCCCTGGAT TCCCCCTGGAT AGCCCCATCT TCCCAGTGTTG TCCCCCTTCG	CAGAGCAAGA GATGGAACTA CACTTAAGTG GGACTGCTAC  41    TGGGAGGCGG TTCCATCCCG GCCAGGGTCC TCGCTAGC CCTGGACACT CACTGGATTAA CACTGGAT TTTCTGCCAT CACTGGAT TTCTGCCAT CACTGGAT TTCTGCAT CACTGCAAT TTCTGCAAT CACTGCAAT TTGGAACTCTGC TCGCAAATAT GGTGACTCGC TCGAACCAGG TGAAGATGGA GCCAAGGCA GCCAAGGCA CCTGCAAGCCAGCA TGAAGATGGA GCCAAGCCA GCCAAGCCA CCTCGCAAGCCA CCTCGCAACCCAGCA CCTCTGCAACCCAGCA CCTCTGCAACCCAGCA CCTTGCAACCAGCA CCTTGCAACCACCACCACCACCACCACCACCACCACCACCACCA	GACAGAAGAC GGGAAGGCC AACCCCATGG ATGATCCTTA AAAAAAAAA  51   CAACATTGTT ACCCGGGGCC GCCTTCTGCA TTCATGGAGA AAAGCCAGAA GAGACTGAGG CCTCTTCCC TCTCATCGGG CCATCAAGC ACCCATGAGG ACCCATGAGG ACCCATGAGG TATTCCACAG GGGCCCTAT GGGACCCCAG TCCGCGCCCTCTCCACCC TCCCTCTCCCC TCTCATCGCG TCTCATCGCG TCTCCATCAGG TATTCCACAGG TATTCCACAGG TCCTCATCAGG TCCCCCAGT CGGACCTTGT GCGCTTCT TAGCCTTCT TAGCCTTCT TAGCCTTCT TAGCCTTCT TCCCCTGCCCTC TCCCCCTGCCTC TCCCTCGCCTC TCGCTCCTCT	3420 3480 3540 3660 3665 3665 60 120 180 240 420 480 600 660 780 840 900 900 1020 1080 1140 1200
50 55 60	CAAGCCACTC CGTGGAGAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA  Seq ID NO: Nucleic Ac: Coding sequil GGAAGCAGGG TCAAGTTGGC ACGTACTGG ACTTCCAAAA ACAAGTTGAC ACTTCCAAAA ACAAGTTGAC TTGCACCAGGA TCATCAGGG TCACCAGGA TCATCAGGGT TCCTCACCG TAGCAGCAT TCGCAGGACTT TGGGACCTGT TGGGCCCGGCA TATCGCAAAT ACCCTTTCTT GAAGCCCCCA GGGCTATTTG GAGCCCCCA GGGCTATTTG TCATTCTTTGAAGCCCCCA GGGCTATTTTG TCATTCTTTTT GAAGCCCCCA	ATCTTACAG TCAGAAGGGG ATGATTCTTG ACCCTAATGC  175 DNA Set dA Accession Jence: 234. 11   GGGGGCCTCT CAAATTGACA GCCTTGTTTC GCCCCCGCTC GGTGGAAAAG GGGAGAGGTG TACTGCCATC GTTGATACC GTTGATACC GTTGAGAAA CTATCTGTTC GTTGAGATACC GTGGATACCG GTGGATACCG GTGGATACCG GTGGATCCGATC GTGGACTACCT TCTGAGATT GTGCCAGGAT GTGCCAGGAT GTGCCAGGAT GTGCCAGGAT GTGCAGTTC GCTGAATTG GCTGCATTAG GCTGCATTAG GCTGCATTAG GCTGCATTAG GCTGCATTAG GCTGCATTAG GCTGCATTAG GCTGCATTAG GCCTAATCT GACTCAGGTG GCCCTAATCT GACTCAGGTG GCCTAATCT GACTCAGGTG GACTCAGGTG	AGATAAGAAA GAACAGTCAG CTCTGATTTG ATCTTTTCTC CAATAAAAGT  #: NM_001' 1130 21   GGTGGGGGTC AGAGGGAGAG CCCCTCTCG CAGGGGGGGATCGGAGAGGTCTACACAAGAGTTTTC AGAGGTTTTC AGAGGTTTTC GCTCCTGAATC AGAGCTTTTC GCTCCTGAAATC AGAGCTTTTC GCTCCTGAAATC AGAGCTTTTC GACCAGCTCT GCCCTCTCC GGCCCTCTCC	ACAAGTTIGG TITAGTIANG CTCTTGETCA CACTGAGACA TGCTCATTAT  798.2  31    GGGAACTCGG GCCCCCGAGA CTGACCCCGAGA CTGACCCCGAGA CTGACCCCGAGA CTGACCCCTACA AAAATAAACT CCTCTGCTTA AGGGCCTAGC TCGCTTATA GAGTCCCTGT TCCTGGAGAT TCCGGATCTT TGCTGAGAT TCCGGATCTT TGCCTGATTA CTCCCTGGA TTGCTGAGAT TCCGGATCTT TGCCTGATTA CTCCCCTGGA ACTGCCCTGTTT TACCGATCTT TACCCGATCTT TACCGATCTT TCCAGTGTTGG ACTTCCCTTGA	CAGAGCAAGA GATGGAACTA CACTTAAGTG GGACTGCTAC  41    TGGGAGGCGG TTCCATCCCG GCCAGGGTCC TCGGTCGCACTTAC CACAGGGTCC CACAGGGTCC TCACTGGACACT TTTCTCCAT TTTCTCCAT TTTCTCCAT CACAGAGGGG TCGTACTTAC CTGCAAATAT GGTGACTCTG CAGCCAAGG AGGCAAGGA GGCCAAGGCA GGCCAAGGCA TCGACTCTG CAGCCCATG CAGCCCTCG CAGCCCATG CAGCCCATG CAGCCCATG CACCCCTCG CACCCCTCCTC CACCCCTCC CACCCCTCCTC CACCCCTCC CACCCCTCC CACCCCTCCTC CACCCCTCC CACCCC CACCC CACC	GACAGAAGAC GGGAAAGGCC AACCCCATGG ATGATCCTTA AAAAAAAAAA	3420 3480 3540 3660 3665 3665 60 120 180 240 360 420 480 540 660 720 780 960 1020 1080 1140 1260
50 55 60 65 70	CAAGCCACTC CGTGGAGAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA  Seq ID NO: Nucleic Ac: Coding sequil GGAAGCAGGG TCAAGTTGGC ACCGTACTGG ACTTCCAAAA ACAAGTTGAC GTGTGCCCAG TTGCAAGAT TCAAGAGT TCAAGAGT TCAAGAGT TCAAGAGT TCATCAAGAG ATGAGGTGGT ACCCTTTCTT GAAGCCCCCA AGGCTATTTG GGCCAGCCAA	ATCTCACAG TCAGAAGGGG ATGATTCTTG ACCCTAATGC  175 DNA Set did Accession lence: 234. 11   CGGGGCCTCT CAAATTGACA GCCCTGTTTC GCCCCGCTC GGTGGAAAAG GGGAGGGTG TACTGCCATC TCTCAAGAAA CTATCTCTTC AGACCTTAAA GGCCTTAAA GGCCTTAAA TGGCATC CTGGAGCCTG TTCTGAGATT GTGGCAGCT GTGGTACCGA CTGGAGCTT GTGGCAGGA AGATTTTAGT GCCCAGGATTT GTGGCAGGA TCTGAGGTT CCCAGGATTT GCCTCACTATC CCCAGGATTT GCCTCACTATC CCCAGGATTT GCCCTCACTATC CCCAGGATTT GCCCTAATCT CCCCAGGATTT GCCCTAATCT CCCCAGGATTT GCCCTAATCT CCCTCAGGAT CTCTCGGGAT CTCTCGGGAT CTCTCGGGAT	AGATAAGAAA GAACAGTTAG GATCATG ATCTTTTCTC CAATAAAAGT  THENCE HENM_001* 11130 21   GGTGGGGGTC AGAGGGAGAG CCCCTCTCG CAGGGGCGGG ATCGAGAGGTTA TATCACAGG TTCATGGATG GCTCCTGAAATC AGAGCTTTTG GCTCCTGAAATC AGAGCTTTTG GCTCCTGAAATC AGAGCTTCTT GACCAGCTTCT GACCAGCTCTCT GACCAGCTCTCT AAAGTTGTAC GACCACTCTCC GACCACCCCCCCG CACCCCTCTGAAAACAACAACCAAGCCAGCCCTGAAAAACAACCAAGCCAGCC	ACAAGTTTGG TITAGTTAAG CTCTTGCTCA CACTGAGACA TGCTCATTAT  198.2  31   GGGAACTCGG GCCCCGAGA CTGACCCGAC CTGACCCGAC GCACTACGG AGAAATCCG CTCTGCTTAA AAAATAAACT CCTCTGCTTATAA GAGTCCTGT TCCTGAGAT TCCCGTGATA TCCCGTGATA TCCCGTGATA TCCCGTGATA TCCCGTGATA TCCCGTGATA TCCCCTGGATTC TCCCGTGATA TCCCCTGGATTC TCCCGTGATTA CTCCCCTGGA AGGGGATTTC TCCCCTTGAA TCCCCTTGAAAT TCCCCTTGAAAT TCCCCTTGAAAT TCCCCTTGAAAT TCCCCTTGAAAT TCCCCTTGAAAT TCCCCTTGAAAT TCCCCTTGAAAT TCCCCTTGAAAAT TCCCCTTGAAAAT TCCCCTTGAAAAAT TCCCCTTGAAAAAT TCCCCTTGAAAAAAAAAA	CAGAGCAAGA GATGGAACTA CACTTAAGTG GGACTGCTAC  41    TGGGAGGCGG TTCCATCCCG GCCAGGGTCC TCGCTGCGC CTGGCTGCTAC CTGGACACT CACTGGACACT CACTGGACACT CACTGGACACT CACTGGACACT CACTGGACACT CACAGAGGGG GGACTTAAC CTGGACATTAT CTGCAAATAT CTGCAAATAT CGGACACTCAG CAGCCAAGT CAGCCAAGT CAGCCAAGT CAGCCAAGT CACAGCCAAG CCCACTGAAAA ACACTCACC CACTGAAAAA	GACAGAAGAC GGGAAAGGCC AACCCCATGG ATGATCCTTA AAAAAAAAAA	3420 3480 3540 3660 3665 3665 60 120 180 240 360 420 780 600 660 720 780 840 900 960 1020 1140 1200 1140 1200 1320
50 55 60 65 70	CAAGCCACTC CGTGGAGAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA  Seq ID NO: Nucleic Acc Coding sequ I GGAAGCAGGG TCAAGTTGGC ACGGTACTGG GGTTCCCACA ACAAGTTGAC TTGCACAGA TCATCAAAA ACAAGTTGAC TTGCACAGA TCATCAAGAG TCCTCCACCG TAGCAGACTT TCCCTGGACAT TCCCTGAGACT TCCCTGGACAT TCCCTGAGACT TCCCTGGACAT TCCCTGAGACT TCCCTGGACAT TCCCTGAGACT TTCCCCAAGT ATCGCAAAT ACCCTTTCTT GAAGCCCCCA GGGCTATTTG GGCCAGCCCAA TTTCAGTATT	ATCTCTACAG TCAGAAGGGG ATGATTCTTG ACCCTAATGC  175 DNA Sec Ad Accession lence: 234.  11    CGGGGCCTCT CAAATTGACA GCCCGGTTTC GCCCCCCTC GGTGGAAAAG GGAGAGGT TACTGCATC CTCAAGAAA CTATCTGTTC AGACCTTACA GGCCTAATTG GTGGCAGGA GATTTTAGT GGGCCAGGA AGATTTTAGT GCTGCACTAC CCAGGATGTG GCTGCACTAC CTGCACTAC CTCTGGGATTT GCCCTAATCT GACTCAGGTA CTCTCGGGTA CTCTGGGATA AGATGCACTT	AGATAAGAAA GAACAGTCAG GAACAGTTTG ATCTTTTCTC CAATAAAAGT  ILLIAO 21   GGTGGCGGTC AGAGGAGAG CCCTCCTCG CAGGAGGTTA ATCTAGATG ATCAGAGGTGCCGGT ATTCACACAG TTCATGGATG GACTGCTCT GACCAGGTTTTG GCTCCTGAAA GGCTGCATCT GACCAGCTTTTAGACTCT GACCAGCTCTCAGAATTGACAG CACCTTACACAG CACCCTACAAA ACAGGGTGAA ACCAAGCCAG ACAGCTCTCC GGCCCTTCTCAGAATTGTAC CACCCTACAAA ACCAAGCCAG ACAGGCTGAA ACAGGGGTGA ACAGGGGTGA ACAGGGGTGA ACCAGGCTTCCC GGCCCTCTCCC GGCCCTCTCCA ACCAGGCTGAA ACAGGGGTGA ACCAGGCTGAA ACCAGGGGTGA ACCAGGCTTAGA ACCAGGGTGAA ACAGGGGTGAA ACCAGGGGTGAA ACCAGGGGTGAA ACCAGGGGTGAA ACCAGGGGTGAA ACTTAGCCTT	ACAGTTTGG TITAGTIANG CTCTTGCTCA CACTGAGACA TGCTCATTAT  798.2  31   GGGAACTCGG GCCCCCGAGA CTGACCCGAC GCCCCTATAT AAAATAAACT TCCTCTGCTTA AGGGCCTAGC TGCTTATTAA CTCCTCTGGT TCCTCTGGT TCCTCTGGAT TCCGGATCT TCCGGATCT TCCGGATCT TCCCTGGAT AGCGGACTT TCCCTGGAT AGCGCGATCT TCCCTGGAT AGCGCGATCT TCCCTTGGT TCCCTGGAT AGCGCGCTAC AGGGCGCTTC TCCAGTGTGA	CAGAGCAAGA GATGAACTA CACTTAAGTG GGACTGCTAC  41    TGGGAGGCGG TTCCATCCCG GCCAGGGTCC TCGCTAGCGC CCTGGCACT CACTGGCATT TTTCTGCCAT CACTGGCATT TTCTGCCAT CACTGGCAT TCGTACTTAC CTGCAAATAT GGTGACTCGC CAAGCCAAGT TGAAGTGGA TGAAGTGGA TGAAGTGGA TGAAGTGGA TGCGACTCTG CAAGCCAAGT TGAAGTGGA TGCAAGCCAA CCCATGACAA CCCATGACAAC TCCCCCTTC CCAGTGACAAC TTCCCCCTTC CCAGTGAAAC CCCATTCACC CCAGTGAAAA CTCCCCCTTC CCAGTGAAAA CTCCCCCTTC CCAGTGAAAA CTCCCCCTTC TCCCCTTC TTAGTGACAC CCAGTGAAAA CTCCCCCTTC TTCCCCCTTC TTCCCCCTTC TTCCCCCTTC TTCTTACCC CCAGTGAAAA CTCCCCCTTC TTCCCCCTTC TTCCCCTTC TTCCCCCTTC TTCCCCCTTC TTCCCCCTTC TTCCCCCTTC TTCCCCCTTC TTCCCCTTC TTCCCCCTTC TTCCCCTTC TTCCCTTC TTCCTTC TTCCCTTC TTCCTTC TTCCCTTC TTCCTTC TTCCTTC TTCCTTC TTCCTTC TTCCTTC TTCCTTC TTCCTTC TT	GACAGAAGAC GGGAAAGGCC AACCCCATGG ATGATCCTTA AAAAAAAAAA	3420 3480 3540 3660 3665 60 120 180 240 300 360 420 480 540 660 6720 780 840 900 900 1020 1140 1200 1240 1250 1380
50 55 60 65 70	CAAGCCACTC CGTGGAGAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA  Seq ID NO: Nucleic Ac: Coding sequil GGAAGCAGGG TCAAGTTGGC ACGTTCCAAAA ACAAGTTGAC ACTTCCAAAA ACAAGTTGAC TTGCACCAAGA TCATCAGAGT TCACCAGGA TCATCAGGGCCAG ATTGCAAAA ACAGTTGAC TTGGACATT TCGTGAACAT TCCCTGGAGA ATTGCCAAAA ACAGTTGAC TTGGACATT TCAGTATTTGAGCCCCA GGGCCAAA TTTCAGTATTT	ATCTTACAG TCAGAAGGGG ATGATTCTTG ACCCTAATGC  175 DNA Set id Accession Lence: 234. 11   CGGGGCCTCT CAAATTGACA GCCTTGTTTC GCCCCCGCTC GGTGGAAAAG GGGAGAGGTG TACTGCCATC GTTGATACC GTTGAGAAA CTATCTGTTC GTTGAGATT GTGGCCAGC TCGAGCCTTAAA TGGACTACGC TCTGAGCTTTAAA TGGACTACGA GCCTGAGTTTAGA AGACTTTAGA GGCCTGATTC GTGGGCCTG TCTGAGATT GTGCCAGGA GCCTAATCT GCCCAATCT GCCCTAATCT GCCCTAATCT GACTCAGGTT CTTGGGAT GCTCGGGTC GCTTGGGTTATAG GCCTCAATCT GCTTGGGTTATAG GCTTGGTTGT	AGATAAGAAA GAACAGTCAG CTCTGATTTG ATCTTTTCTC CAATAAAAGT  #: NM_001' 1130 21   GGTGGGGGTC AGAGGGAGAG CCCCTCTCG CAGGGGTCTACAGAATCT ACAGGAGATCT ACTCAGGATCT AGAGCTGCTCC GACCTGCTCG GACCTGCTCCT GACCTGCTCCT GACCTGCTCCT GACCTGCTCCT GACCAGCTCTTC GACCAGCTCTTC GACCAGCTCT AAAATTGTAC ACCAGCTGAT ACCAGCCTCTCC GGCCCTCTCAC ACCAGCCTCTCAC ACCAGCCTCTCAC ACCAGCCTCTCAC ACCAGCCTCTCAC ACCAGCCTCTCAC ACCAGCCTCTCAC ACCAGCCTCTCAC ACCAGCGTGA ACAGGGGTGA ACAGGGGTGA ACAGGGGTGA ACAGGGGTGA ACAGGGGTGA ACAGGGGTGA ACAGGGGTGA AAAATTAATTT	ACAAGTTIGG TITAGTIANG CTCTTGCTCA CACTGAGACA TGCTCATTAT  798.2  31    GGGAACTCGG GCCCCCGAGA CTGACCCCGAGA CTGACCCCGAGA CTGACCCCGAGA CTGACCCCTGAGA AGAAAATACG CTCTCCTTGA AGGGCCTAGC TCCCTGGAT TCCCTGGAT TCCCTGGAGAT TCCGGATCTT TGCCTGAGAT TCCGGATCTT TGCCTGATTA CTCCCCGGG AGCAGATTTC TGCCTGATTA CTCCCTGGTTTG CTCCTGGTTTG CTCCTGGTTTT ACCCCATCT TCCAGTGTTGG CACTGTTGC TCCAGTGTTGG CACTGTCCTTAAAAAGGCGGAA CCACCACCT TAAAAAAAGGC	CAGAGCAAGA GATGGAACTA AGTGGAATAA CACTTAAGTG GGACTGCTAC  41   TGGGAGGCGG TTCCATCCCG GCCAGGGTCC TCGGTCGCCA AGTTGTATA CCTGGACACT TTTCTCCAT TTTCTCCAT CACAGAGGGG TCGTACTTAC TGGCAATTAT TCGGACTCTG CAGACCAAGG AGCCAAGGA GGCCAAGGA GGCCAAGGA TCGACTCTG CAGCCAATTAT TAGACCAAG AGCCAAGCA TCGACTCTG CAGCCAAGCA TCGACTCTGA CCCAGTGACAA TTCCTACCAC CCAGTGAAAA TTCCCCCTTCACC CCAGTGAAAA TTCCCCCCTTCACC CCAGTGAAAA	GACAGAAGAC GGGAAAGGCC AACCCCATGG ATGATCCTTA AAAAAAAAA  51   CAACATTGTT ACCCGGGGCC GCCTTCTGCA TTCATCGAGA AGAGCCAGAA AGAGCCAGAA GAGACTGAGG CATCCTACTGCC TCTCATCGGG ACCCATGAGG TATTCCACAG GCGGCCCTAT GGGACCCAG TTCCCCAAGT TCCCCAAGT TCCCCAAGT TCCCCAAGT TCGAGCTTCTT GCTTGGCCTT TCTAGCTTCTT TGAAAGGAAG TCTTAGTTTT TTGAAAGGAAG TCTTAGTTTT TTGAAAGGAAG TTTAGTTTTT TTTAGATTTTT TTTAGATTTTT TTTTTTTT	3420 3480 3540 3660 3665 3665 60 120 180 360 360 420 480 540 660 720 780 840 900 91020 1080 1140 1260 1320 1320 1440
50 55 60 65 70	CAAGCCACTC CGTGGAGAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA  Seq ID NO: Nucleic Acc Coding sequ I GGAAGCAGGG TCAAGTTGGC ACCGTACTGG GGGTTCCCAGA ACTTCCAAAA ACAAGTTGAC GTGTGCCAGG TCCACCAGA TCATCAAGAG TCCTCACCG TAGCAGACTT TGCTGACCT TGGTGACCT TGGTGACCT TGGTGACCT TTGGAGAAT ACCCTTCTTT GAAGCCCCCA GGGCTATTTG GGCCAGCCAA TTTCATTT TGCTGAAAA TCCCTTTCTT TGAAGCCCCCA TGCGCCAAAT TCCCTAGTATT TGCTGAAGAC TCTTCAGACAT TTCGTAAAAT CCCTTTCTT CAAGCCCCCA CGCCTACTTTC TGAAGCCCCCA CGCCTACTTC CCAAGCCTCCT CAAGCCTCCT CAAGCCCCCT	ATCTCACAG TCAGAAGGAG ATGATTCTTG ACCCTAATGC  175 DNA Sec ACCESSION LICENSE SALA LI CAGACGAGCAT GCCCCGCTC GGGGGCCTTTC GGCGGGCCTTTC GCTGCATGC TCTCAAGAAA GGAGAGGTG TACTGGCATC CTCAAGAAA CTATCTGTTC AGACCTTAAA AGACCTTAAA AGACCTTAAA GCACTTACA GCCCTAATCT GTGGCACGA CTGCACACA AGATTTAGT GCTGCACTAC CTGCACTAC CTGCTACAGTAC CTGCACTAC GCTGCACTAC GCTGCACTAC GCTGCACTAC GCTGCACTAC GCTGCACTAC GCTGCACAA AGATGCACTT GGTGGATT GGTGCACTAC GCTGCCACAA AGATGCACTT GGTGGATT GGTGGATT GCTCTGGGAT TCTGACTAC GCTCCACACA AGATGCACCT GCTCCACACA AGATGCACCT GCTGCCACACA	AGATAAGAAA GAACAGTCAG GACCAGTTTG ATCTTTTCTC CAATAAAAGT  ILLIAO 21   GGTIGGCGGTC AGAGGAGAG CCCTCCTCG CAGGAGGTTA ATCTAGATG ATCAGAGGTTCC CCTAGGATC AGAGGTTTTG ACCAGGTTTTG GCTCCTGAAA GGCTGCATCT AGACCTTACT ACCAGGTTCT ACCAGGTTAC ACCAGGTTCT ACCAGGTT ACCAGGTT ACCAGGTT ACCAGGTT ACCAGGTT ACCAGGTT ACCAGGTT ACCAGGT	ACAAGTTIGG TITAGTIAAG CTCTTGCTCA CACTGAGACA TGCTCATTAT  198.2  31   GGGAACTCGG GCCCCGAGA CTGACCGAC GCCCCGAGA CTGACCGAC GCACTACGG GCACTACGG AGAAATCCC CTCTGCTTAA AAAATAAACT TCCGCTGATTA TCCGGATTTTACTCCGGATCTT TCCGGATTTCCGGATCT TCCGCTGATTA CTCCCTGGATA AGGCGGATCT TCCAGTGTGATA ACCCCATCT TCCAGTGTGATA ACCCCATCT TCCAGTGTGC ACTTGCCTTAA AAGGCGGATTT TCCAGTGTTG CTTCCATTACCTCTTCCATTACCTCCTTCATTACCTCTTCATTACCTCTTCATTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACTTACCTTACCTTACCTTACCTTACCTTACCTTAC	CAGAGCAAGA GATGGAACTA AGTGGAATAA CACTTAAGTG GGACTGCTAC  41     TGGGAGGCGG TTCCATCCCG GCCAGGGTCC TCGCTGGCGC CTCGCTGCGCC CACTGGACACT CACTGGATT TTCTGCCAT CACAGAGGGGG TCGAAGCTAAC CTACCTGGTT CTGCAATAT CGTGACTCTC CAGACCAAGT CAAGCCAAG CAAGCCAAG CAAGCCAAG CCAAGCCAAG CCAAGCCAAG CCACTCTAC CCCATTCACAC CCAGTGAACC CCAGTGAACC CCAGTCACAC TCGACCCATC TCCTACACG TTTCGGATT TTCCCCCTTC TTCCTACACG TTTTGGGATC TTCTGCGATC TTCTGCGACG TTTGGGATC TTCTGCACACG TTTTGGGATC TTCTGCACACG TTTTGGGATC TTCTCTACACG TTTTGGGATC TTCTTACCACG TTTTGGGATC TTCTCTACACG TTTTGGGATC TTCTTACCGGGGGCC	GACAGAAGAC GGGAAAGGCC ATGATCCTTA AAAAAAAAA  51   CAACATTGTT ACCCGGGGCC GCCTTCTGCA TTCATGAGA AAAGCCGAA GAGACTGAGG CATCCTAATA TTTACATTTC CCTCTTCCCC TCTCATCGGG TATTCCACAG GGGCCCTAT GGGACCCCAG TTCCCCAGT TCGGAGCTTGT GCTCTCTTCTC TTCTAGTTTT TCTAGTTTTT TTCTAGTTTT TTCTAGTTTT TTCTAGTTTT TTAGATTTGC ACCAGGATC TTCAGCTT TTCTAGTTTT TTAGATTTGCT TTCAAGGAAG TCTTAGTTTT TTAGATTTGCT ACCAGGATCC TAAGTTGGTG TAAGTTGGTG TAAGTTGGTG TAAGTTGGTG TAAGTTGGTG TAAGTTGGTG TAAGTTGGTG TAAGTTGGTG TTAGTTTGTT TTAGATTTGGT TAAGTTTGGTGTGTGT	3420 3480 3540 3660 3665 60 120 180 240 300 360 420 480 540 660 6720 780 840 900 900 1020 1140 1200 1240 1250 1380
50 55 60 65 70	CAAGCCACTC CGTGGAGAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA  Seq ID NO: Nucleic Ac: Coding sequil GGAAGCAGGG TCAAGTTGGC ACGGTACTGG GGGTTCCCAGG ACTTCCAAAA ACAAGTTGAC TGCACCAAGA TCATCAAGAGT TCCACCAGGACTT TGGTGACCCT TAGCAGACTT TGGTGACCCT TAGGAGGT TACCAGGAA TTCCTGGAGA TTCCTGGAGAA TTCCTGAGAA TTCGCAAAT TCCCTGGAGA TTCCTGAGAA TTCGCAAAT TCCCTGGAGA TTCGCAAT TCCCTGGAGA TTCGCAAT TCCCTGAGAA TTCAGTATT TGCTGAAGAG CGTACCAAT CCAGCCCCC CAGCCACAAT TTCAGTATT TGCTGAAGAG CCTTCTTTGAGAGAC CTTTTTGAGAAC CTTTCTGAAGAG	ATCITACAG TCAGAAGGGG ATGATTCTTG ACCCTAATGC  175 DNA Set dd Accession Lence: 234. 11   CGGGGCCTCT CAAATTGACA GCCTGTTTC GCCCCCGCTC GGTGGAAAAG GGCAGAGGTTG TCTCAAGAAA CTACTGTTC AGACTACCA CTGGAGCCTG TTCTGAGATT GCTGCACTA GCTGGAGCTT TCTGAGATT GCTGCACTA CCAGGATGTG GCTGCACTAC GCTGCACTAC GCTGCACTAC GCTGCACTAC GCTGCACTAC CCAGGATGTG GCCCCACAA CCAGGTATCT GCTCGAGCTT CCTGGAGCTT CCTGGAGTTT GCTCTGGAATT CCTCAGTT CCTCTGGAATT CCTCTGGAATT CCTCTGGAATT CCTCTGGAATT CCTCTGGAATT CCTCTGGAATT CCTCTGGAATT CCTCTGGAATT CCTCTGAATCC CCTCCCACAA CCAAGTAAAA	AGATAAGAAA GAACAGTCAG CTCTGATTTG ATCTTTTCTC CAATAAAAGT  #: NM_001' 1130 21   GGTGGGGGTC AGAGGGAGAG CCCCTCCTCG CAGGGCGGATCGAGAGAGTCT ATTCACACAG TTCATGATG CAGCTGCTCC GACGGCTCTCGAGATC AGAGCTGTTCG AGAGCTGTTTG CAGCTGCTCC CAGCTCTCTCAGATC AGAGCTTTTAGTTCTA AAAGTTTCTA AAAGTTGTAC GACCAGCCCC CACCAGCTCT AAAAGTAGTTACT CAGAGCTGTTCT AAAGGGTGATCT CACCAGCCTCTCAGAATC ACCAAGCCAG CACCCTCTCAAAAACACACCAGCCTCTCAAAAAACTACTT CCATAATTAT TCTTTATTATT CCATAATTAT TCTTTTATTAT TCTTTTATTAT CAAAACCACT	ACAGTTIGG TITAGTIANG CTCTTGETCA CACTGAGACA TGCTCATTAT  198.2  31    GGGAACTCGG GCCCCCGAGA CTGACTCAGG GCCCCCGAGA CTGACTCTAA AAAATAAACT CCTCTGCTCT AAAAATAAACT TCCTCCTGG TTCCTCTGAGA TCCTCCTGGAATATAAACT TCCTCCTGGAATT TCCTCCTGGAATT TCCTCCTGGAATT TCCTGCTTAAAAAACC TTCCAGTTGAAAAACC TTCCAGTGAATAAAAACC TTCCAGTGAATAAAAAACC TATAAAAAAACC TAAAAAAAACC TAAAAAAAA	CAGAGCAAGA GATGGAACTA AGTGGAATAA CACTTAAGTG GGACTGCTAC  41   GGACGGGGGG TTCCATCCCG GCCAGGGTCC TCGCTAGCAGA CTTCATCCCG AGTTGTTAC CCTGGACACT TCACTGGCAT TTTCTGCCAT CACAGAGGGG TCGTACTTAC CACAGAGGGG CGGACTCTG CAAGATATA GGTGACTCTG CAGCCAAGG TGGAATAT TCCTGCAATAT TCACAGGGGGGC CCAGCCCCG TCGACTCTGA CACACCCAGGT TCACTCGA TCACCCCTTC CAGCCCAGG TCACTCACC CCAGTGAAAA TTCCCCCTTC TTCCTACACG GTTGGCGAT TAGCGGGGGG TAGTTGGGAT TAGCGGGGGG TAGTTGGGAT TAGTTGGGAT TAGTTGGGATG TAGTTGGGATG TAGTTGGGATG TAGTTGGGATG TAGTTGGGGATG TAGTTGGGGATG TAGTTTAAAG	GACAGAAGAC GGGAAAGGAC AACCCCATGG ATGATCCTTA AAAAAAAAA  51   CAACATTGTT ACCCGGGGCC GCCTTCTGCA TTCATCGAGA AGAGCTGAGG CATCCTAATA TTTTGAATTTC CCTCTTCCCC TCTCTCCCC TCTCTCTCCCC TCTCTCTCTCT TCTCTCCCCAGC TCCCCAGCTCT TCGGACCCTAT TCCCCAGCTTCTT TCTAGCTTCTT TGAAAGGAAG TCTTAGTTAT TTAGATTTGC ACCAGGATCC TAAGTTGGTC AATTCGCTTCTT TCAAGTTGGTC AATTCGCTTCTT TCAAGTTGGTC AATTCGCTTCTT TAAGATTTGC ACCAGGATCC TAAGTTGGTC AATTCGGTTG AATTCGCTTCGTC AATTCGGTTG AATTCGGTTG AATTCGGTTG ACCAGGATCC TAAGTTGGTC AATTCGGTTG AAAAAAAAAA	3420 3480 3540 3660 3665 3665 60 120 180 240 480 540 600 660 720 780 840 900 1020 1020 1140 1260 1380 1440 1560 1560 1620
50 55 60 65 70	CAAGCCACTC CGTGGAGAAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA  Seq ID NO: Nucleic Ac: Coding sequil GGAAGCAGGG TCAAGTTGGC ACGTTCCAAAA ACAAGTTGAC GTGTGCCAGG ACTTCCAAAA ACAAGTTGAC GTGTGCCAGG TCATCAAGAGT TCATCAAGAGT TCCTCAACCT TGGTGACCTT CTGTGGACAT TCCTGGAGA ATCAGGTGT GGCCCGGCA ATCAGGTGT GGCCCGGCA ATTCAGATT GGCAGCAAT ACCCTTCTT TGGTAACTT TGGTAACT TTCAGTATT TGCTGAAGA TTTCAGTATT TGCTGAAGA TTTCAGTATT TGCTGAAGAC CTTCAAGAG TTTTCAGTATT TGCTGAAGAC CTTCAAGCCCCCA ATATCAGAAT CCAAGCCTCCT CAAGCCTCCT CTTTTGAGAGAC CTTTCAGTAT CAAGCCTCCT CTTTTGAGAAA AAAAAAATAGA	ATCTTACAG TCAGAAGGGG ATGATTCTTG ACCCTAATGC  175 DNA Set did Accession Jence: 234.  11   CGGGGCCTCT CAAATTGACA GCCCTGTTTC GGTTGGAAAAG GGCAGAGGTG TACTGCCATC GCTTGAATTTACA GGCTGTATTG TCTCAAGAAA TGACTAGCC TCTCAGGATGT TCTCAAGAAA CTATCTGTTC TCTCAAGAC TTCTGAGCT TCTGAGACTT TCTGAGATT TCTGAGTT TCTGAATTAC CCAGGTTTT TCTGAATTC TCTGGAATT TCTGAATCC TCTGGGATT TCTGAATCC TCTGGGATT TCTGAATCC TCTGGAATAA TCTGAATCC TCTGCACAA TCCAATCAGT TCTGAATCC TCTGCACAA	AGATAAGAAA GAACAGTCAG CTCTGATTTG ATCTTTTCTC CAATAAAAGT  TH: NM_001' 11130 21   GGTGGGGGTC AGAGCGAGAG CCCCTCTCG CAGGGCGGG ATCGGAGAGG TTGATGGATT CGAGAGATCT ATCACACAG TTCATGGATG GGTGCTCTTG AGAGTGTTC CGTGGAATC AGAGCTTTTG GGTTCTGAAA GGCTGCATCT GACAGCTCTT GACAGGTGTCT GACAGCTCT GACAGCTCT GACAGCTCT GACAGCTCT TAAAATAATTT TGTTATAAAA CAAAACCACT TTTATACCTA	ACAAGTTIGG TITAGTIANG CTCTTGCTCA CACTGAGACA TGCTCATTAT  31   GGGAACTCGG GCCCCGGAGA CTGACCCGAC GCCCCCGAGA CTGACCCGAC GCACTACGG GCACTACGG GCACTACGG GCACTACGG GCACTACGG TCCTCTGCTTAA AAAATAACT CCTCTGCTTAA TCCCTGTATA TCCCGATTAT CCCCATGT TCCTGAGAT TCCCGGATTT TCCCGGATTT TCCCGGATTT TCCCGGATTT TCCCGGATTT TCCCGGATTT TCCCGGATTT TCCCGATTA AAGGGGGAA CCACCCCT TAAAAAAGCC TAAAAAAGCC GGCCAAATGA GGCCAAATGA GGGCAAATGA GGGCAAATGA TGCGGAGGATT TTTTCCAGT TTTTTCCAGT TTTTTCCAGT TTTTTCCAGT TTTTTTCCAGT TTTTTTCAGT TTTTTTCAGT TTTTTTCAGT TTTTTTCAGT TTTTTTCAGT TTTTTTCAGT TTTTTTCAGT TTTTTTCAGT TTTTTTTCAGT TTTTTTCAGT TTTTTTTCAGT TTTTTTTCAGT TTTTTTTCAGT TTTTTTTCAGT TTTTTTTTTT	CAGAGCAAGA GATGGAACTA AGTGGAATAA CACTTAAGTG GGACTGCTAC  41    TGGGAGGCGG TTCCATCCCG GCCAGGGTCC TCGCTCGCGC AGTGTGTTAC CCTGGACACT CACAGAGGTG TCTACTCGCAT TTTCTGCCAT TTTCTGCCAT TTCGCAATAT TGGCAAGTGACTCG CAGACTCTGC CAGCCAAGG TCGACTCTGC CAGCCAAGGA TCGACTCTGC CAGCCAAGGA TCGACTCTGA CTGCAATTTT CACAGGGGG CTCACTTCACACG CACTGAAAA TTCCCCCTTC TTCCTACACG CTTTCCTACACG CTTCCTACACG CTTCCTACACG CTTCCTACACG CTTCCTACACC CTTCTACACC CTTCTTCTACACC CTTCTACACC CTTCTACACC CTTCTACC C	GACAGAAGAC GGGAAAGGCC AACCCCATGG ATGATCCTTA AAAAAAAAA  51   CAACATTGTT ACCCGGGGCC GCCTTCTGCA TTCATCGAGA AAAGCCAGAA GAGACTGAGG CATCCTAATTC CCTCTTCCCC TCTCATCGGG GCCATCAAGC ACCCATGAGG TATTCCACAG GGGACCCCAG TCCCCAAGT TCGAAGC TCGATCGGGT TCGAAGC TCTTCCCC TAGCTTCTT TGAAAGGAAG TCTTAGTTT TCTAGTTTT TCTAGTTTT TCTAGTTTT TCTAGTTTT TCTAGTTTT TCTAGTTTT TCTAGTTTGC AATTCGGTTG	3420 3480 3540 3660 3660 3665 60 120 180 240 360 420 480 540 660 720 780 960 1080 1140 1260 1320 1380 1440 1500 1500 1620 1680
50 55 60 65 70	CAAGCCACTC CGTGGAGAA ACCATTCCTG TCTTCTTGAC CAGGACTGAC AAAAA  Seq ID NO: Nucleic Accoding sequal GGAAGCAGGG TCAAGTTGGC ACCGTACTGG GGGTTCCCAGA ACTACCAGAG TTGTCCAAGA TTGCCAGG TTGTCAAGAG TTGTCAAGAG TCATCAGAG TTGTGACCTT TGGTGACCTT TGGTGACCT TTGGAGAAT ACCCTTTCTT GAAGCCCCCA GGCTATTTG GGCCAGCCAA TTTCAGTATT TGCTGAAGAG TTTCAGTATT TGCTGAAGAG CCTTACCATC CAAGCCTCCT CTTTTGAGAAA AAAAAATAGA AAAAAATAGA	ATCTCTACAG TCAGAAGGGG ATGATTCTTG ACCCTAATGC  175 DNA Set id Accession lence: 234.  11    CGGGGCCTCT CAAATTGACA GCCCTGTTTC GGTGGAAAAG GGGAGGGTG TACTGCCATC GCTGAATGC TCTCAAGAAA CTATCTGTTC GGTGGAAAAG GGGAGGGTG TCTCAAGAAA TCAATTAGT GGCTGCATC CTGAGGATTG GCTGCATAC GTGGTACCGA AGATTTAGT GCTGCATC GCTGCACTAC CCAGGATTTG GCTGCACTAC GCTGCACTAC GCTGCACTAC GCTGCACTAC GCTGCACTAC GCTGCACTAC GCTGCATTAGT GCTCCACGAT TCTGAGTTG GCTCCACATAC GCTGCACTAC CCAGGATTTG GCTCCACAA CCAGGTAAAA TCTCAGCTC GCTCCCCACAA CCAGGTAAAA TCTCAGCTC GCTCCCCACAA CCAGGTAAAA TCTCAGCCCG GCTCCCACAA CCAGGTAAAA TCCAATCAGT ACTCAGCCCG GCTCCCACAA ACCAGTAAAAA TCCAATCAGT ACTCAGCCCG GCTCCCACAA ACCAGTAAAAA TCCAATCAGT ACTCAGCCCG GCTCCCACAA	AGATAAGAAA GAACAGTCAG CTCTGATTTG ATCTTTTCTC CAATAAAAGT  #: NM_001' 1130 21   GGTGGGGGTC AGAGGGAGAG CCCCTCCTCG CAGGGCGGATCGAGAGAGTCT ATTCACACAG TTCATGATG CAGCTGCTCC GACGGCTCTCGAGATC AGAGCTGTTCG AGAGCTGTTTG CAGCTGCTCC CAGCTCTCTCAGATC AGAGCTTTTAGTTCTA AAAGTTTCTA AAAGTTGTAC GACCAGCCCC CACCAGCTCT AAAAGTAGTTACT CAGAGCTGTTCT AAAGGGTGATCT CACCAGCCTCTCAGAATC ACCAAGCCAG CACCCTCTCAAAAACACACCAGCCTCTCAAAAAACTACTT CCATAATTAT TCTTTATTATT CCATAATTAT TCTTTTATTAT TCTTTTATTAT CAAAACCACT	ACAGTTTGG TITAGTIANG CTCTTGCTCA CACTGAGACA TGCTCATTAT  198.2  31   GGGAACTCGG GCCCCGAGA CTGACCGAC CTGACCGAC CTGACCGAC AGAAAATCG CTCTGCTTAA AAAATAAACT TCCCGTGAT TCCCGGATTTC TCCCCTGGA ACTTGCCTTA AAGGGGGATTC TCCAGTGTTG ACTCCCTCT TACCCATCT TCCAGTGTTG TCCAGTGTG TATTTCCAGT TGCCCATCT TCAGTGTTG TCAGTGTTG TCAGTGTTG TCAGTGTTTT TCAGTGTTT TCAGTGTTTT TCAGTGTTTT TCAGTGTTTT TCAGTGTTT TCAGTGTT TCAGTGTT TCAGTGTT TCAGTGTT TCAGTGTT TCAGTGT TCAGTG TCAGTGT TCAGTG TCA	CAGAGCAAGA GATGGAACTA CACTTAAGTG GGACTGCTAC  41     TGGGAGGCGG TTCCATCCCG GCAGGGTCC TCGCTGCGC CCTGGCACACT CACTGGACACT CACTGGACACT CACTGGACACT CACTGGACACT CACAGAGGGG GCCAAGGTTGACTGAC TCGACTCTGACACT CAGACCAAGT TGAACTCAC CCAGTGAACA TCCCCTTC TTCTACACG GTTTGACAG GTTTGACCAG TTACCAGACT TTCCCCTTC TTCCTACACG TTTCGCAT TTCCCCTTC TTCCTACACG TTTGCGACT TTCCCCTTC TTCCTACACA TTCCCCCTTC TTCCTACACA TTCCCCCTTC TTCCTACACA TTCCCCCTTC TTCTACACC TTCCCCTTC TTCCTACACA TTCCCCCTTC TTCTACACC TTCCCCTTC TTCTACACC TTCCCCTTC TTCCTACACA TTCCCCCTTC TTCCTACACA TTCCCCCTTC TTCCTACACA TTCCCCCTTC TTCCTACACA TTCCCCCTC TACTCTCACT TTCCTCTC TTCTACACC TTCTCTACACC TTCTCTACC TTCTCTACACC TTCTCTACACC TTCTCTACACC TTCTCTACC TTCTCTACC TTCTCTACACC TTCTCTACACC TTCTCTACACC TTCTCTACACC TTCTCTACACC TTCTCTACC TTCTCTACC TTCTCTACACC TTCTCTACACC TTCTCTACC TTCTCTCTACC TTCTCTACC TTCTCTACC TTCTCTACC TTCTCTACC TTCTCTACC TTCTCTCTACC TTCTCTACC TTCTCTCTACC TTCTCTACC TTCTCTCTACC TTCTCTCTACC TTCTCTCTACC TTCTCTCTACC TTCTCTCTC	GACAGAAGAC GGGAAAGGCC AACCCCATGG ATGATCCTTA AAAAAAAAAA	3420 3480 3540 3660 3665 3665 60 120 180 240 480 540 600 660 720 780 840 900 1020 1020 1140 1260 1380 1440 1560 1560 1620

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	TOGTGTCATT G	ACATCCTGG (	GAGGTGATTT '	TGACCCCCAT	GCCTTTGCCA (	STGCCATCTT	660 720
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                                                                                                               360
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50		cession #:	NP_055059 21	31	41	51	
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75	C 10 NO	. 206 0-0	in comience				
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	1	. !	_ !			 	60
80	MGENDPPAVI	B APFSPRSLF	G LODLKISPV	A PUADAVAAQ	D GEDEABUAD D CEDEABUAD	P IIVIGIIALI V GGQNAVLQVF	
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	VTALHHSVY	V REGCASGHV	V TLQCTACGH	R RGYSSRIVG	C MMSLLSQWP	w Qaslqfqgyh	240
	LCGGSVITP	L WIITAAHCV	Y DLYLPKSWI	I OVGLVSLLD	N PAPSHLVEK	I VYHSKYKPKA G DASPVLNHAA	300
	TOWN I WINGS		- At ACREMSE				

	VPLISNKICN GIGCAEVNKP	HRDVYGGIIS GVYTRVTSFL	PSMLCAGYLT DWIHEQMERD	GGVDSCQGDS. ( LKT	GGPLVCQERR	LWKLVGATSF	420
_	Seg ID NO:	207 Protein	Sequence				
5		ession #: C	AC03433.2				
	1	11	21		41	51 1	
	1	O TOTAL LA COMPANY	PNEEQQKDVT	L DVGCDLHVG	GVMUKUVEOT	NISODWSDFA	60
	MLSSTDFTFA	SWELVVKVDH	GVQADAKLLF	TPOHKMLRLR	LPNLKMVRLR	VSFSAVVFKA	120
10	VEDICKTIMI	PRSEELSLLK	PSGDYFKKKK	KKDKNNKEPI	IEDILNLESS	PTASGSSVSP	180
10	OF VOVTWTDT	PAGTOWIGHT	STMTWFSDSP	LTEONCSILA	FSOPPOSPEA	LADMYQPRSL	240
	WINDKAKINACH	LDSSRSLMEO	GIOEDEOLLL	RFKYYSPFDL	NPKYDAVRIN	<b>OFAEGWWWT</b>	300
	TIPETIMETE	CMILERATION .	HISKLSLSAE	TODFAGESEV	DETENATION	EAT PEROVAN	360 420
1.5	SLLEDITDIP	KLADNLKLFR	PKKLLPKAFK LIPVADGMNE	OAMATAKOL2	TAIRKNEEDE	ASKGKTMADS	480
15	RGCEVVPDVN	VAGREFGIEL	ASQVASSLEN	MOMNPECEVS	PRCAKKHKSK	OLAARILEAH	540
	OVERACMED ME	ART DETOAWO	SLPEFGLTYY	LVRFKGSKKD	DILGVSYNKL	IKIDAAIGIP	600
	VTTWRFTNIK	OWNVNWETRO	VVIEFDQNVP	TAFTCLSADC	KIVHEYIGGY	IFLSTRSKDQ	660
	NETLDEDLPH	KLTGGQD					677
20			_				
	Seq ID NO:	208 Protei	n Sequence				
		cession #: 1	NP_114433.1 21	31	41	51	
	1	11	î	î	i	1	
25	MASRSMRLLL	LLSCLAKTGV	LGDI IMRPSC	APGWFYHKSN	CYGYFRKLRN	WSDAELECQS	60
	YGNGAHLASI	LSLKEASTIA	EYISGYQRSQ	PIWIGLHDPQ	KRQQWQWIDG	AMYLYRSWSG	120
	KSMGGNKHCA	<b>EMSSNNNFLT</b>	WSSNECNKRQ	HFLCKYRP			158
30	Seq ID NO:	209 Protei	n Sequence XP_051860.2				
30	Protein Ac	11	21	31	41	51	
	ï	1	1	1	1	i	
	MGAAGRODFI	FKAMLTISWL	TLTCFPGATS	TVAAGCPDQS	PELQPWNPGH	DODHHVHIGO	60
~ -	CKTLLLTSSA	TVYSTHISEC	GKLVIKDHDE	PIVLRTRHIL	IDNGGELHAG	SALCPFOGNE	120 180
35	TILLYGRADI	GIQPDPYYGL	, KYIGVGKGGA	LELHGQKKLS	MINTONCIPHE	GGMAEGGYFF	240
	ERSWGHRGV	VHVIDPKSGI	VIHSURFUTI	RSKRESERLV	SVEDHIEYHO	ILSVAVNDEG HRGSAAARVF	300
	WI POTEUCE	PATUSTISSEMA	ODVEWTEWFO	HDKVSOTKGG	; ekisdlwka:	PGKICNRPID	360
	TO A TOTAL OCT.	I LCTEUVVKKO	: ODYRFACYDR	GRACKSYRVE	FLCGKPVRP	LIVITUINVN	420
40	OTTIMIEDM	A VEMKBGULLY	/ TASTDYSMYC	) AEEFOVLPCR	R SCAPNQVKVA	GKPMYLHIGE	480
	ETOCUDADA:	C MOLLODNITI	/ MCEMEDICY P	YRNHICNFFI	) FDTFGGHIKI	ALGEKAAHLE	540 600
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45	1 CKEVNIDA	U CMVDACMITI	D NGVKTTEAS	<b>KDKRPFLSI</b>	[ SARYSPHQD	DEFKERET	780
73	TOURTAVIN	O DUCANT PCCI	D VWLDSCRFAI	O NGIGLTLASO	GTFPYDDGS	K OFIKNSPLAG	840
	COMMITTEM	M DND TWC DCC	I. DHSCRTLPIC	3 ONFPIRGIO	L YDGPINIQN	TERREVALES	900
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30	NDFPSHPLY	L EGALTRSTH	Y QQYQPVVIL	P ABLITUMDA	E OSYPGRSHY	Y WDEDSGLLFL	1140
	MI RYUNEDE	Y DARCOMKCC	E RIKTKALIP	K NAGVSDCTA'	T AYPKFTERA	A ADABMEKKTE	1200
	CCOL VTVDU	P LEVYMESSK	O HEFHLWNDE	A YIEVDGKKY	P SSEDGIQVV	V IDGNQGKVVS	1260
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55	QMAFVGFKG	S FRPIWVTLD	T EDHKAKIFQ	A ABIBAAKK	КL		1361
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	MSQVKSSYS	SY DAPSDFINE	S SLDDEGDTO	N IDSWFEEKA	N LENKLIGK	G TGGLFQGKTP	60
		T IMPOUNDED	PP VVVEXEVEN	T. VEGET DENI	C SSLEVEAAI	S KKTPADYOKK	120 180
	SLRLSAQK	OF ECKEKHHAN	M KAKRCATPV	I IDEILPSKK	M KVSNNKKKI	E EEGSAHQDTA	
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05	AGIGQPVIC	C OCKRETEUR	PT VSTVVDLAC	O VEDEHKRTE	N RYKLRSKKI	D INLLPSKSSV	360
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	KODUKPPT	EP IGFOLEIE	KR IOERESKKI	T EDEHFEFHS	SR PCPTKILEI	O AGALEKKAPL	480
	TTVPKSPA	FA LKNRIRMP	TK EDEEEDEPV	/V IKAOPVPH	(G VPFKPQIP)	EA RTVEICPFSF	540
70	DEBUKEBU	O KEKKIKELA	OK GEVPKFKAJ	P LPHFDTINI	P EKKAKNAL	<b>JI EPFCLETORK</b>	600
	GALKAOTW	KH QLEEELRQ	OK EAACFKARI	N TVISQEPIV	VE KKEKKSVA	EG LSGSLVQEPF	720
	QLATEKRA	KE KÖELEKKU	AE VEAQKAQQI BY ECTBERC	LE EARLQUEER	AV VESTAVOV	RE LVHKANPIRK	747
	AGGERKS	SD QPLTVPVS	EN FOIRFRU				'
75	Sec ID N	0: 211 Prot	ein Sequenc	<b>.</b>			
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	1	11	21	31	41	51	
	1		an an		A COLCATOR	UD CMDEVACEDE	60
80.	MSRRKQAK	PQ HINSEEDQ	GE QQPQQQTP	EF ADAAYAAY FU KKUCTYND	AN GELWAYVN DV LIMNDSFC	HP GNDEVASEDE PV PSEDFSGAVI	120
ου.	ATVKKLRR	SK DCHBENCC	SS EDMKEKPD	AE SVVYLKTE	TA LPPTPODI	SY LAKGKVANTA	180
	VTI OAT RO	TK VAVNORSA	DA LPAPVPGA	NS IPWVLEQI	TC TOOOOTOO	IQ LTEQIRIQVA	240
	MWACHALH	ISS GAGADTLK	TL GSHMSOOV	SA AVALLSQK	ag sqglslda	LK QAKLPHANII	300
	SATSSLSI	GL APPTLKPD	GT RVLPNVMS	RL PSALLPQA	PG SVLFQSPF	ST VALDTSKKGI	360

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GKPPNISAVD VKPKDEAALY KHKCKYCSKV FGTDSSLQIH LRSHTGERPP VCSVCGHRFT
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TPEPGSETLK LQQLVENIDK ATTDPNECLI CHRVLSCQSS LKMHYRTHTG ERPFQCKICG
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                                                                                                      600
         RAFSTKONLK THIGVERTNT SIKTORSCPI COKKFTNAVM LOCHIRMENG GOIPNTPLPE
NPCDPTGSEP MTVGENGSTG AICHDDVIES IDVEEVSQE APSSSSKVPT PLPSIHSASP
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         TLGPAMMASL DAPGKVGPAP FNLOROGSRE NGSVESDGLT NDSSSLMGDQ EYQSRSPDIL
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         Protein Accession #: Eos sequence
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                                                                                                       120
          ERWDAYCYNP HAKECGGVFT DPKQIFKSPG FPNEYEDNQI CYWHIRLKYG QRIHLSFLDF
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                                                                                                       120
                                                                                                       180
         DLEDDPGCLA DYVEIYDSYD DVHGFVGRYC GDELPDDIIS TGNVMTLKFL SDASVTAGGF
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RSLSSYGIDK EKTIHLTLKV VKPSDEELPL FLVESGDEAK RHLLQVRRSS SVAQVKAMIE
          TKTGIIPETQ IVTCNGKRLE DGKMMADYGI RKGNLLFLAS YCIGG
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          Seg ID NO: 216 Protein Seguence
          Protein Accession #: NP_002349.1
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          MALOLSREGG ITLRGSAEIV AEPFSFGINS ILYGRGIYPS ETPTRVQKYG LTLLVTTDLE
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          LIKYLNINVVE QLKDWLYKCS VQKLVVVISN IESGEVLERW QFDIECDKTA KDDSAPREKS
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          QKAIQDEIRS VIRQITATVT PLPLLEVSCS FDLLIYTDKD LVVPEKWEES GPOFITNSEE
                                                                                                       180
                                                                                                        205
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          Protein Accession #: NP_001889.1
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          MAQYLSTLLL LLATLAVALA WSPKEEDRII PGGIYNADLN DEWVQRALHP AISEYNKATK
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          ELYEVPWENR RSLVKSRCQE S
           Seq ID NO: 218 Protein sequence
          Protein Accession #: NP_009162.1
1 11 21
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          MDKLKCPSFF KCREKEKVSA SSENFHVGEN DENQDRGNWS KKSDYLLSMI GYAVGLGNVW
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WVLISIFVTI YYNVIIAYSL YYMFASFQSE LPWKNCSSWS DKNCSRSPIV THONVSTVNK
GIQEIIQMNK SWVDINNFTC INGSEIYQPG QLPSEQYWNK VALQRSSGMN ETGVIVWYLA
LCLLLAHLIV GAALFKGIKS SGKVVYFTAL FPYVVLLILL VRGATLEGAS KGISYYIGAQ
SNFTKLKEAE VWKDAATQIF YSLSVAWGGL VALSSYNKFK NNCFSDAIVV CLTNCLTSVF
AGFAIFSILG HWAHISGKEV SQVVKSGFDL AFIAYPEALA QLPGGPPWSI LFFFMLTLG
                                                                                                        240
75
                                                                                                        300
           LDSQFASIET ITTTIQDLFP KVMKKMRVPI TLGCCLVLFL LGLVCVTQAG IYWVHLIDHF
CACMGILIAA ILELVGIIWI YGGNRPIEDT EMMIGAKRWI FWLWWRACMF VITPILLIAI
FIWSLVQFHR PNYGAIPYPD WGVALGWCMI VFCIIWIPIM AIIKIIQAKG NIFQRLISCC
                                                                                                        480
                                                                                                        540
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           RPASNWGPYL EQHRGERYKD MVDPKKEADH EIPTVSGSRK PE
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           Protein Accession #: NP_006389.1
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21
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                  TKTGIIPETQ IVTCNGKRLE DGKMMADYGI RKGNLLFLAS YCIGG
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                  Protein Accession #: XP_094741.1
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10
                  MKANYSAEER FLLLGPSDWP SLQPVLFALV LLCYLLTLTG NSALVLLAVR DPRLHTPMYY
                 PRAMICALER FULLGESUMY SEQPENFALV LLETTLITING NSALVELAVE DEPERTMENT FLETLANDALD LANLRGPALW LPRSHCTAQL CASLALGSAE CVLLAYMALD RAAAVCRPLR YAGLVSPRLC RTLASASWIS GLTMSVAQTA LLAERPICAP RILDHFICEL PALLKHACGG DGDTTENOMF AARVVILLLP FAVILASYGA VARAVCCMRF SGGRRAVGT CGSHLTAVCL PYGSAIYTYL QPAQRYNQAR GKFVSLFYTV VTPALNPLIY TLRNKKVKGA
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CTKPSPEKKR CSDNTEVEVS NLENKQPVES TSAKSCSPSP VSPQVQPQAA DTISDSVAVP
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                   ASLLGMRRGL NSRLEATAAS SVKTRMQKLA EQRRRWDNDD MTDDIPESSL FSPMPSEEKA
                                                                                                                                                                                                 180
25
                   ASPPKPLISN ASATPVGRRG RLANLAATIC SWEDDVNNSF AKONSVQEQP GTACLSKPSS
ASGASARINS SSVKQEATFC SQRDGDASIN KALSSSADDA SLVNASISSS VKATSPVKST
TSITDAKSCE GQNPELLPKT PISPLKTGVS KPIVKSTLSQ TVPSKGELSR EICLQSQSKD
                                                                                                                                                                                                 300
                                                                                                                                                                                                 360
                   KSTTPGGTGI KPFLERFGER CQEHSKESPA RSTPHRTPII TPNTKAIQER LFKQDTSSST
THLAQQLKQE RQKELACLRG RFDKGNIWSA EKGGNSKSKQ LETKQETHCQ STPLKKHQGV
SKTQSLPVTE KVTENQIPAK NSSTEPKGFT ECEMTKSSEL KITLFLEEDK SLKVTSDPKV
                                                                                                                                                                                                  420
                                                                                                                                                                                                  480
 30
                                                                                                                                                                                                 540
                    EOKIEVIREI EMSVDDDDIN SSKVINDLFS DVLEEGELDM EKSQEEMDQA LAESSEEQED
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                    SLGSEDRDLL YSIDAYRSQR FKETERPSIK QVIVRKEDVT SKLDEKNNAF PCQVNIKQKM
QELNNEINMQ QTVIYQASQA LNCCVDEEHG KGSLEEAEAE RLLLIATGKR TLLIDELNKL
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                    KNEGPORKNK ASPQSEFMPS KGSVTLSEIR LPLKADFVCS TVQKPDANNY YYLIILKAGA
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KSKAITPKRL LTSITTKSNI HSSVMASPGG LSAVRTSNFA LVGSYTLSLS SVGNTKFVLD
                                                                                                                                                                                                  840
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KVPPLSSLEG HIYLKIKCQV NSSVEERGPL TIFEDVSGFG AWHERMCVLS GNCISYWTYP
DDEKRKMPIG RINLANCTSR QIEPANREFC ARRNTFELIT VRPQREDDRE TLVSQCRDTL
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                      VKQEMFWGSI QMDARAGETM YLVEKANTPE LKKSVSMLSL NTPNSNRKRR RLKETLAQLS
RDTDVSFPPP RKRPSAEHSL SIGSLLDISN TPESSINYGD TPKSCTKSSK SSTPVPSKQS
ARWQVAKELY QTESNYVNIL ATIIQLFQVP LEEEGQRGGP ILAPEEIKTI FGSIPDIFDV
                                                                                                                                                                                                    420
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                                                                                                                                                                                                    540
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                      HAFLKINQAK PECCROSLVE LLIRPVORLP SVALLLNDLK KHTADENPDK STLEKAIGSL
KEVMTHINED KRKTEAQKQI PDVVYEVDGC PANLLSSHRS LVQRVETISL GEHPCDRGEQ
                                                                                                                                                                                                    660
                                                                                                                                                                                                     720
                      VTLFLFNDCL EIARKRHKVI GTFRSPHGQT RPPASLKHIH LMPLSQIKKV LDIRETEDCH
                      NAFALLVRPP TEQANVLLSF QMTSDELPKE NWLKMLCRHV ANTICKADAE NLIYTADPES
FEVNTKOMDS TLSRASRAIK KTSKKVTRAF SFSKTPKRAL RRALMTSHGS VEGRSPSSND
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                                                                                                                                                                                                     120
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                        YYMSPEQMNR MSYNEKSDIW SLGCLLYELC ALMPPFTAFS QKELAGKIRE GKFRRIPYRY
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5	Protein Acc 1     RGKEHRSRMV LNNGQLLPLO EASFAQGAQA QPQQTVPRSP	225 Proteir cession #: e 11     QIFLFRSRSK LQGPLNSWIP GQVDPLQLQT QQTRQQQYEE QKEAINFRHD	OS SEQUENCE 21     IYHTKMKIII   PFSGILQQQQ   PPQTQPGPSH   QIPFYAQFGY	31     LLGFLGATLS   QAQIPGLSQP   VMPYVPSFKM   IPQLAEPAIS	SLSALDQFAG PQEQGQMFQY GGQQQLAFDP	LLPNQIPLTG YPVYMVLPWE QLGTAPEIAV	60 120 180 240 300
	LREP						304
15	Protein Acc	226 Proteir cession #: N 11	IP 003970.1 21 	31 	41 1	51 	
20	RRIMLPTOFL KLVRGRKPLS LTYVLFLMAL DDTILSSALA	NGLKSKYYRL PLLGVLGIFG LLVILGLAVG TPLMSSFTFC ANGWVFLLAY ETGDTLYAPY	LTPAPIIGLD PSLVQDVIAI GSFTGWKRHG VSPEFWLLTK	GSTGPTRPPL EYIVLTMORT AHIYLTMLLS QRNPMDYPVE	PGILPSICPS NVNVPSELSA IAIWVAWITL DAFCKPQLVK	CLLAHAVSLT PRRNEDFVLL LMLPDFDRRW KSYGVENRAY	60 120 180 240 300 357
25		227 Protein					
23	1	ession #: 1	21	31	41	51	
30	EHLRDGISAR QVINELRNTS KSLEQBLASP DLKGTVVIFD	VDFPFQPYKC KIAERAQGEL YRPKVCVLGS ILDIEDLVKS EAHNVEKMCE ELEDIAKLKM	FPDRALSSWG REQLCIHPEV GSKHRVCPYY ESASFDLTPH	NAAAAAGDPI KKQESNHLQI LSRNLKQQAD DLASGLDVID	ACYTDIPKII HLCRKKVASR IIFMPYNYLL QVLEEQTKAA	YASRTHSQLT SCHFYNNVEE DAKSRRAHNI QQGEPHPEFS	60 120 180 240 300
35	TKGCILDSLD YKVHIHPDAG TLAPVSSFAL	QIIQHLAGRA HRRTAQRSDA EMQIPFPVCL	GVFTNTAGLQ WSTTAARKRG ENPHIIDKHQ	KLADIIQIVF KVLSYWCFSP IWVGVVPRGP	SVDPSEGSPG GHSMHELVRQ DGAQLSSAFD	SPAGLGALQS GVRSLILTSG RRFSEECLSS	360 420 480 540
40	TISAYYARVA QFLDEMKGQG RAQLPSWVRP GPFFSTRKAK SEQRAGSPGE	VVPYGLLIFF APGSTGATFL GAGGQFLSGQ HVRVYDNFGH SLDLHVPSLK EQAHSCSTLS	AVCRGKASEG EWYRQQASRA VIRDVAQFFR QRSSGSPAAG LLSEKRPAEE	LDFSDTNGRG VNQAIGRVIR VAERTMPAPA DPESSLCVEY PRGGRKKIRL	VIVTGLPYPP HRQDYGAVPL PRATAPSVRG EQEPVPARQR VSHPEEPVAG	RMDPRVVLKM CDHRFAFADA EDAVSEAKSP PRGLLAALEH AQTORAKLFM	600 660 720 780 840 900
45	KQQFEEVCIQ HLNQGRPHLS AALTAYKQDD	NFATFTQALQ LTGRGCGYRP PRPPPTGDPG DLDKVLAVLA ERLAVPPVLT	EHSIPRRQRA SQPQWGSGVP ALTTAKPEDF	QPVLDPTGRT RAGKQGQHAV PLLHRFSMFV	APDPKLTVST SAYLADARRA RPHHKQRFSQ	AAAQQLDPQE LGSAGCSQLL TCTDLTGRPY	960 1020 1080 1140
50	GPSQSSGPPH DFQRCQACWQ ACPAAGAGCT	GPAASEWGEP RHLQASRMCP RSGRNTHLPL PLLQRPLRGA	HGRDIAGQQA ACHTASRKQS	TGAPGGPLSA VMQVFWPEPH	GCVCQGCGAB KDHEGAGGAR	DVVPFQCPAC PVAAVPGVGA	1200 1260 1320 1380 1400
55	Protein Acc	228 Protein cession #: 1 11	NP_057518.1 21 	31 	41 	51 	
60	EHLRDGISAR QVINELRNTS KSLEQELASP DLKGTVVIFD ADSPSPGLNM	VDFPFQPYKC KIAERAQGEL YRPKVCVLGS ILDIEDLVKS EAHNVEKMCE ELEDIAKLKM	FPDRALSSWG REQLCIHPEV GSKHRVCPYY ESASFDLTPH ILLRLEGAID	NAAAAAGDPI KKQESNHLQI LSRNLKQQAD DLASGLDVID AVELPGDDSG	ACYTDIPKII HLCRKKVASR IIFMPYNYLL QVLEEQTKAA VTKPGSYIPE	YASRTHSQLT SCHFYNNVEE DAKSRRAHNI QQGEPHPEFS LFAEAQITFQ	60 120 180 240 300 360
65	YKVHIHPDAG TLAPVSSFAL LGKALGNIAR	HRRTAQRSDA EMQIPPPVCL VVPYGLLIFF	WSTTAARKRG ENPHIIDKHQ PSYPVMEKSL	KVLSYWCFSP IWVGVVPRGP EFWRARDLAR	GHSMHELVRQ DGAQLSSAFD KMEALKPLPV	SPAGLGALQS GVRSLILTSG RRPSEECLSS EPRSKGSPSE RMDPRVVLKM	420 480 540 600 660
70	QFLDEMKGQG RAQLPSWVRP GPFFSTRKAK SEQRAGSPGE VAVKQELSQA	GAGGOFLSGQ HVRVYDNFGH SLOLHVPSLK EQAHSCSTLS NFATFTQALQ	EWYRQQASRA VIRDVAQFPR QRSSGSPAAG LLSEKRPAEE DYKGSDDFAA	VNQAIGRVIR VAERTMPAPA DPESSLCVEY PRGGRKKIRL LAACLGPLFA	HRQDYGAVFL PRATAPSVRG EQEPVPARQR VSHPEEPVAG EDPKKHNLLQ	CDHRFAFADA EDAVSEAKSP PRGLLAALEH AQTDRAKLFM GFYQFVRPHH	720 780 840 900 960
75	HLNQGRPHLS AALTAYKQDD	PRPPPTGDPG DLDKVLAVLA ERLAVPPVLT	SQPQWGSGVP ALTTAKPEDP	RAGKQGQHAV PLLHRFSMFV	SAYLADARRA RPHHKQRFSQ	AAAQQLDPQE LGSAGCSQLL TCTDLTGRPY GTVGAGGEDA	1020 1080 1140 1200 1219
80	Protein Ac	229 Protei cession #: 1		31	41	51	
•						 SPAAGDPESS RPAEEPRGGR	60 120

	KKIRLVSHPE GPLFAEDPKK PTGRTAPDPK	HNLLQGFYQF	VRPHHKQQFE LDPOEHLNOG	EVCIQLTGRG	CGYRPEHSIP	RRQRAQPVLD	240 300
	GQHAVSAYLA	DARRALGSAG	CSQLLAALTA	YKODDDLDKV	LAVLAALTTA	KPEDFPLLHR	360
5	<b>FSMFVRPHHK</b>	QRFSQTCTDL	TGRPYPGMEP	PGPQEERLAV	PPVLTHRAPQ	PGPSRSEKTG	420
	KTOSKISSFL	RQRPAGTVGA	GGEDAGPSQS	SGPPHGPAAS	EWGEPHGRDI	AGQQATGAPG	480
	GPLSAGCVCQ	GCGAEDVVPF	QCPACDFQRC	QACWQRHLQA	SRMCPACHTA	SRKQSVMQVF	540 545
	WPEPQ						313
10	Seq ID NO:						
		ession #: N		••	43	E1	
	1	11	21	31	41	51 	
	MRALEGPGLS	LLCLVLALPA	LLPVPAVRGV	AETPTYPWRD	AETGERLVCA	QCPPGTFVQR	60
15	PCRRDSPTTC	GPCPPRHYTQ	FWNYLERCRY	CNVLCGEREE	EARACHATHN	RACRCRTGFF	120
	AHAGFCLEHA	SCPPGAGVIA	PGTPSQNTQC	QPCPPGTFSA	SSSSSEQCQP	HRNCTALGLA	180 240
	CWGPTPPAGE	AMOLKLERR	LSTRVPGAEE LTELLGAQDG	ALLVRLLOAL	RVARMPGLER	SVRERFLPVH	300
•							
20		231 Protein					
	Protein Acc	cession #: 1 11	NP_110503.1	31	41	51	
	î	1	Ī	1	Ī	1	
25	MRALEGPGLS	LLCLVLALPA	LLPVPAVRGV	AETPTYPWRD	AETGERLVCA	QCPPGTFVQR	60 120
25	PCRRDSPTTC	GPCPPRHYTQ	PWNYLERCRY	OPCPPGTPSA	SSSSSEOCOP	HRNCTALGLA	180
	LNVPGSSSHD	TLCTSCTGFP	LSTRVPGAEE	CERAVIDEVA	FQDISIKRLQ	RLLQALEAPE	240
	GWGPTPRAGR	AALQLKLRRR	LTELLGAQDG	ALLVRLLQAL	RVARMPGLER	SVRERFLPVH	300
30	C ID NO.	232 Protei	n Semience				
30			NP_000584.2				
	1	11	21	31	41	51	
	1		PODDENACE	CCI CCTPOED	DADGYEGDAD	GRDRDGVRVP	60
35	MAELLASAGS	GCRCLPGASL	AWLGTVLLLL	ADWVLLRTAL	PRIFSLLVPT	ALPLLRVWAV	120
<i></i>	GLSRWAVLWL	GACGVLRATV	GSKSENAGAQ	GWLAALKPLA	AALGLALPGL	ALFRELISWG	180
	APGSADSTRL	LHWGSHPTAF	VVSYAAALPA	AALWHKLGSL	WVPGGQGGSG	NPVRRLLGCL	240
	GSETRRLSLF	LVLVVLSSLG	CEVECAULE OCCUPCAULE	DETERFOONO	TCNIMSRVTE	MSILTIASAV DTSTLSDSLS	300 360
40	ENLSLFLWYL	VRGLCLLGIM	LWGSVSLTMV	TLITLPLLFL	LPKKVGKWYQ	LLEVQVRESL	420
. •	AKSSOVAIEA	LSAMPTVRSF	ANEEGEAQKF	REKLQEIKTL	NQKEAVAYAV	NSWTTSISGM	480
	LLKVGILYIG	GOLVTSGAVS	SGNLVTFVLY	<b>QMQFTQAVEV</b>	LLSIYPRVQK	AVGSSEKIFE	540 600
	YLDRTPRCPP	SGLLTPLHLE	GLVQFQDVSF	AABNKBOAFA	VAAVGOEPOV	GEVTALVGPN FGRSLQENIA	660
45	YGLTOKPTME	EITAAAVKSG	AHSFISGLPO	GYDTEVDEAG	SQLSGGQRQA	VALARALIRK	720
	PCVLILDDAT	SALDANSQLQ	VEQLLYESPE	RYSRSVLLIT	OHLSLVEQAL	HILFLEGGAI	780
	REGGTHQQLM	EKKGCYWAM	/ QAPADAPE				808
	Sea ID NO:	233 Protei	n Sequence				
50			NP_002414.1	L			
	1	11	21	31	41	51	
	   MOI.TVI.CAVO	i TILPGSTALPI	I . POEAGGMSEI	. OWEOAODYL	RFYLYDSETI	( NANSLEAKLK	60
	EMQKFFGLPI	TGMLNSRVI	E IMQKPRCGVI	DVAEYSLEP	SPKWTSKVV	YRIVSYTRDL	120
55	PHITVDRLVS	KALNMWGKE	PLHFRKVVW	TADIMIGFA	GAHGDSYPFI	GPGNTLAHAF	180
		A HFDEDERWIT D IKGIQKLYGI		AATHELGHS	. GMGHSSDPN/	A VMYPTYGNGD	240 267
	PONT ALL ALL DE	) INGIGNATION	K KONOKIAK				
۲0			in Sequence				
60	Protein Ad	ccession #:	NP_061144 21	31	41	51	
	1	i	1	1	1	1	
	MPIEIVCKI	K PAEEDAKPK	E KEAGDEOSL	L GAVAPGAAPI	R DLATFASTS	T LHGLGRACGP	60
65	GPHGLRRTL	W ALALLTSLA	A FLYQAAGLA	R GYLTRPHLV	A MDPAAPAPV.	A GFPAVTLCNI G HQLADMLKSC	120 180
05	NESGHICSA	S NESVVYTRY	G KCYTFNADP	R SSLPSRAGG	M GSGLEIMLD	I QQEEYLPIWR	240
	ETNETSFEA	G IRVQIHSQE	E PPYIHQLGF	G VSPGFQTFV	S CQEQRLTYL	P QPWGNCRAES	300
	ELREPELQG	Y SAYSVSACR	L RCEKEAVLQ	R CHCRMVHMP	G NETICPPNI	Y IECADHTLDS	360
70						R ENFLVLDVFF W DRLKRVWRRP	420 480
,,						P GGLFEDFAC	539
•							
			in Sequence				
75	Protein A	ccession #:	21	31	41	51	
	ì	1	1	1	1	1	
						P PRSGSLALGD	
						Q EVLWTRLREL D LFLKVVHGDV	
80	TPYDLVRMS	S MQLAPQELA	R WRDQEEKRG	L NIIEQQQKE	P CRLPASKMI	H KGEVEIQRDM	240
	DOTLTLEDL	V GPQMFMDCS	P QALPIASED	T TGQHDHHFL	D PNCHICKOW	e PSNELLGSFE	300
	AAKSCGDNI	F QKALSQTPH	P APEMPKTRE	L SPTEPQDRV	P PSGLHVPAA	A SICPAKAKDV	360 420
						L PTRLEPLGGP	

5	GLEVTHSSLL GTPPPGGAWQ QHPYSVAPAG RLSSALAAPE	QSQGRGS I AP HGFGRGQHFH	RGISAWQRPP RDSCPHQALL	RGRGRLWPEP RHLESLATMS	ENWOHPGRGQ	WPPEPGLRQS	540 600 660 696
	Seq ID NO: Protein Acc	ession #: N		31	41	<b>51</b>	
10	MSKRSWWAGS LFASFYLLDF SGNHWPFGEI AFLWVVAVA LLIIRSLRQG	ILALVGNTLA ACRLTGPLPY MAPLLVSPQT	LWLFIRDHKS LNMYASIYFL VQTNHTVVCL	GTPANVFLMH TCISADRFLA QLYREKASHH	LAVADLSCVL IVHPVKSLKL ALVSLAVAPT	VLPTRLVYHF RRPLYAHLAC FPPITTVTCY	60 120 180 240 300
15	RILALANRIT LSAKSEL						360 367
	Seq ID NO: Protein Acc						
20		11	21	31	41	51	
	1	<u> </u>				1	60
	MRKTRLWGLL GEMPKTLACT						120
25	EPHMLPDRIR	LVVTKGPSGT	PGSNENSTQN	VYKIPPTTTK	ALCPLYTSPR	TVTQAPPKST	180
25	ADVSTPDSEI	NLTNVTDIIR	VPVPNIVILL	AGGFLSKSLV	PSVLFAVTLR	SFVP	234
	Seg ID NO:	238 Protein	sequence				
	Protein Acc	ession #: 1					
30	1	11	21 	31	41	51 !	
				EENANFNKIP			60
				LPFWAVDAVA			120 180
	DDRYICDREY	PNDLWVVVFO	FOHIMVGLIL	LAEKVVYVGV PGIVILSCYC	IIISKLSHSK	GHOKRKALKT	240
35	TVILILAFFA	CWLPYYIGIS	IDSFILLEII	KQGCEFENTV	HKWISITEAL	APFHCCLNPI	300
	Lyafigakek	TSAQHALTSV	SRGSSLKILS	KGKRGGHSSV	STESESSSPH	SS	352
	Sea ID NO:	239 Protein	n Secruence				
40		cession #:					
40	1	11	21	31	41	51	
	   MHPOVVILSL	ILHLADSVAG	SVKVGGEAGP	SVTLPCHYSG	AVTSMCWNRG	SCSLFTCONG	60
	IVWTNGTHVT	YRKDTRYKLL	GDLSRRDVSL	TIENTAVSDS	GVYCCRVEHR	GWFNDMKITV	120
45						TTVPTTMTVS	180 240
77						ETHPTTLQGA IYAGVCISVL	300
	VLLALLGVII	AKKYFFKKEV	QQLSVSFSSL	QIKALQNAVE	KEVQAEDNIY	IENSLYATD	359
	Sea ID NO.	240 Protei	n Semience				
50		cession #:					
	1	11	21	31	41	51	
	I MRTYRYFLLL	FWVGOPYPTI	  STPLSKRTSG	l FPAKKRALEL	I SGNSKNELNR	SKRSWMWNQF	60
	FLLEEYTGSD	YQYVGKLHSD	QDRGDGSLKY	ILSGDGAGDL	PIINENTGDI	QATKRLDREE	120
55	KPVYILRAQA	INRRTGRPVE	PESEFIIKIH	DINDNEPIPT	KEVYTATVPE	MSDVGTFVVQ QYQVVIQAKD	180 240
	MGGOMGGLSG	TTTVNITLTD	VNDNPPRFPC	STYOFKTPES	SPPGTPIGRI	KASDADVGEN	300
	AEIEYSITDG	EGLDMFDVIT	DOETQEGIII	<ul> <li>VKKLLDFEKK</li> </ul>	KVYTLKVEAS	NPYVEPRFLY	360
60	LGPFKDSATV	RIVVEDVDEP	PVFSKLAYII	. QIREDAQINT	TIGSVTAQDE	DAARNPVKYS RVPLYIKVLD	420 480
00	VNDNAPEPAE	FYETFVCEKA	KADQLIQTLE	AVDKDDPYSG	HQPSPSLAPE	AASGSNFTIQ	540
	DNKONTAGIL	TRKNGYNRHE	MSTYLLPVVI	SDNDYPVQSS	TGTVTVRVC	CDHHGNMQSC	600
	HAEALIHPTG	LSTGALVAIL	, LCIVILLVTV	VLFAALRRQR DIVPEALFLP	RKEPLIISKI RRTPTARDNI	DIRDNIVSYN DVRDFINQRL	660 720
65	KENDTDPTAP	PYDSLATYAY	EGTGSVADSI	SSLESVITDA	DODYDYLSD	GPRFKKLADM	780
	YGGVDSDKDS						790
	Seq ID NO:	241 Protei	n Sequence				
70		cession #:					
70	1	11	21	31 	41 	51 	
	   MRRLTRRLVI	, PVFGVLWIT	   LLPPWVTKR	( LEVPTGPEVO	TPKVWSLFF!	C VAGHSPHAPQ	60
	VPVSPTPPYO	RGHLPTGGHI	AVCHPPCLLO	PAQFHLQTQV	PLQVRCTLL	YCTDLPPTSI	120
75	IITFHNEARS	TLLRTIRSVI	NRTPTHLIR	IILVODFSNI	PDDCKQLIK	PKVKCLRNNE PVIDIINLDT	180 240
, ,	PTYLESASEL	RGGFDWSLHI	OWEOUSPEO	K ARRLDPTEP	RTPIIAGGL	VIDKAWFDYL	300
	GKYDMDMDIW	GGENFEISF	R VWMCGGSLE	T VPCSRVGHVI	RKKHPYVFPI	CHANTYIRNT	360
	KRTAEVWMDE	YKQYYYAARI	PEALERPPGN	V ESRLDLRKNI	RCQSFKWYL!	F YTQQILQEEL	420 480
80	CLSVITLEPC	APVVLVLCKI	GDDRQQWTK	C GSHIEHIASI	LCLDTDHFG	GTENGKEIVV	540
	NPCESSLMSC		==				557
	A ID 11A	242 Prote					

Seq ID NO: 242 Protein Sequence Protein Accession #: AAH10659

	1	11 !	21 l	31	41 	51 	
5	YLNAKKWRVG NEARSTLLRT RSRIRGADIA SASELRGGFD	PVFGVLWITV DDPYKLYAFN IRSVLNRTPT QGTTLTFLDS WSLHFQWEQL EISFRVWMCG	QRESERISSN HLIREIILVD HCEVNRDWLQ SPEQKARRLD	RAIPDTRHLR DFSNDPDDCK PLLHRVKEDY PTEPIRTPII	CTLLVYCTDL QLIKLPKVKC TRVVCPVIDI AGGLPVIDKA	PPTSIIITFH LRNNERQGLV INLOTFTYIE WFDYLGKYDM	60 120 180 240 300 360
10	VWMDEYKQYY KGNIRQRQKC	YAARPFALER LESQRQNNQE VLCKNGDDRQ	PFGNVESRLD TPNLKLSPCA	LRKNLRCQSF KVKGEDAKSQ	kwyleniype vwaftytooi	LSIPKESSIQ LQEELCLSVI	420 480 540 552
15	•	243 Protein cession #: / 11		31	41	51	
20	YLNAKKWRVG NDPDDCKQLI HRVKEDYTRV PIRTPIIAGG VFRKKHPYVF	PVFGVLWITV DDPYKLYAPN KLPKVKCLRN VCPVIDIINL LFVIDKAWPD PDGNANTYIK LENIYPELSI	QRESERISSN NERQGLVRSR DTFTYIESAS YLGKYDMDMD NTKRTAEVWM	RAIPDTRHLS IRGADIAQGT ELRGGFDWSL IWGGENFEIS DEYKRYYYAA	VLNRTPTHLI TLTFLDSHCE HFQWEQLSPE FRVWMCGGSL RPFALERPFG	REI ILVDDFS VNRDWLQPLL QKARRLDPTE EIVPCSRVGH NVESRLDLRK	60 120 180 240 300 360 420
25	GEDAKSQVWA	PTYTQQILQE GDGTENGKEI	ELCLSVITLE	PGAPVVLVLC			480 519
30	Protein Ac 1       MNGKVWSGPG	244 Protein cession #: 1 11   FGALTSPRAH LRGGFDWSLH	NP_078848.1 21     SDFLDSHCEV				60 120
35	LGKYDMDMDI TKRTAEVWMD KESSIQKGNI	WGGENFEISF EYKQYYYAAR RQRQKCLESQ GAPVVLVLCK	RVWMCGGSLE PFALERPFGN RQNNQETPNL	IVPCSRVGHV VESRLDLRKN KLSPCAKVKG	FRKKHPYVFP LRCQSFKWYL EDAKSQVWAF	DGNANTYIKN ENIYPELSIP TYTQQILQEE	180 240 300 360 378
40		245 Protei cession #: 1		31	41	51	
45	HSDILQYDAS HWGNPNDPHG PSYDKIFSHL NPVQISQEQL	LTPLEFQGYN SEHTVSGQHF	LSANKQFLLT AAELHIVHYN FVPGFNIEEL HMDDPSPREM	NNGHSVKLNL SDLYPDASTA LPERTAEYYR INNFRQVQKF	PSDMHIQGLQ SNKSEGLAVL YRGSLTTPPC DERLVYTSFS	AVLIEMGSFN NPTVLWTVFR QVQVCTAAGL	60 120 180 240 300 354
50	Seq ID NO:	246 Protei	n Sequence				
55	1     MPRRSLHAAA   HSDILQYDAS   HWGNPNDPHO   PSYDKIPSHI   NPVQISQEQI	LTPLEFQGYN SEHTVSGQHF QHVKYKGQEA LALETALYCT	21     PSSPAPVNGS   LSANKQFLLT   AAELHIVHYN   FVPGFNIEEL   HMDDPSPREM	NNGHSVKLNL SDLYPDASTA LPERTAEYYR INNFRQVQKF	PSDMHIQGLQ SNKSEGLAVL YRGSLTTPPC DERLVYTSFS	51     GGLLQSPIDL   SRYSATQLHL   AVLIEMGSFN   NPTVLWTVFR   QGIILSLALA	60 120 180 240 300
60		VSIWLPRRKS		YKPATKMETE	AHA		343
65	Protein Ad 1       MQVDETLIPE   SEVLPVDSFO	cession #: 11       KGPSLCSARY   GLSKAPKSLE	NP_006623.1 21     GIALVLHFCN   AKSSILGGQF	31     PTTIAQNVIM	ERSRLCSIAL	51     TSPQSQLNDS   SGMLLGCFTA   EYIISSLKQQ	60 120 180
70	VGSSKQPLP1 LPFIVAWVIO ALLTLSCGLS	i kamlrslpik 3 mvggyladfi	SICLGCFSHO LTKKFRLITY VLDIAPRYSS	WLVSTMVVYI RKIATILGSL PLMGASRGFS	PTYISSVYHV PSSALIVSLE SIAPVIVPTV	NIRDNGLLSA YLNSGYITAT YSGFLLSQDPE	240 300 360 401
75		: 248 Protei ccession #: 11		31	41	51	
80	LRCGWSPAEI PCRDGWVYET LTTVLINAAI YQVAYTVGLI RIIKHIAKKI	E LNYTVPGPGI I PGSSIVTEFI A GVLMAISPTY L VLAGVAYALI N GKSLPASLQI	AGEASPROCE LVCANSWMLE TWMLIFRLIC HWRWLQFTVA LRLEEETGK	RYEVDWNQST D LFQSSVNVGI D GLVSKAGWLI LPNFFFLLYY LNPSFLDLVI	FDCVDPLASI FIGSMSIGY GYILITEFVO WCIPESPRWI TPQIRKHTMI	CRSPGVAELS DTNRSRLPLG ADREGRICL RRYRRTVGIF ISQNKNAEAM LMYNWFTSSV NMVAGAACLA	60 120 180 240 300 360 420

	SALIADROM PRILISCHOM MATTERIA CRAMMERIA	480 540
	TELEATERIN TAREREMANT CARGOLANDOS ARREST TITOS CONTRACTOR CONTRACTOR	555
5	Seq ID NO: 249 Protein Sequence Protein Accession #: Eos sequence	
	1 11 21 31 41 51	
10	MOPAIOVWFG EDLPLSPRSP LTPRHGPGLA NVCQYDEWIA VRHEATLLPM QEDLSIWLSG	60 120
10	LLGIKVKAEK LLEELDNGVL LCQLIDVLQN MVKTCNSEES GNFPMRKVPC KKDAASGSFF ARDNTANFLH MCRDIGVDET YLPESEGLVL HKDPRQVYLC LLEIGRIVSR YGVEPPVLVK	180
	LEKEIELEET LLNTSGPEDS ISIPKSCCRH EELHEAVKHI AEDPPCSCSH RFSIEYLSEG RYRLGDKILF IRMLHGKHVM VRVGGGMDTL QGFLLKYDPC RILQFATLEQ KILAPQKGVS	240 300
1.5	NESVPDSPAR TPQPPEMNPL SAVNMFQKQN SKPSVPVSIP KSKEKQGRPP GALVPASSLK	360
15	GGNLGSMSVR SKLPNSPAAS SHPKLKSSKG ITKKPQAPSN NASSSLASLN PVGKNTSSPA LPRTAPCISE SPRKCISSPN TPKAKVIPAQ NSADLPESTL LPNKCSGKTQ PKYLKHNHIS	420 480
	SRDNAVSHLA AHSNSSSKCP KLPKANIPVR PKPSFQSSAK MTKTSSKTIA TGLGTQSQPS DGAPQAKPVP AQKLKSALNL NQPVSVSSVS PVKATQKSKD KNIVSATKKQ PQNKSAFQKT	540 600
20	CPSSLKSPGR TPLSIVSLPQ SSTKTQTAPK SAQTVAKSQH STKGPPRSGK TPASIRKPPS SVKDADSGDK KPTAKKKEDD DHYFVMTGSK KPRK	660 694
	Seq ID NO: 250 Protein Sequence Protein Accession #: NP 001035.1	
25	1 11 21 31 41 51	
23	MSKSKCSVGL MSSVVAPAKE PNAVGPKEVE LILVKEQNGV QLTSSTLTNP RQSPVEAQDR	60
	ETWGKKIDFL LSVIGFAVDL ANVWRFPYLC YKNGGGAFLV PYLLFMVIAG MPLFYMELAL GOFNREGAAG VWKICPILKG VGFTVILISL YVGFFYNVII AWALHYLFSS PTTELPWIHC	120 180
30	NNSWNSPNCS DAHPGDSSGD SSGLNDTFGT TPAAEYFERG VLHLHQSHGI DDLGPPRWQL TACLVLVIVL LYFSLWKGVK TSGKVVWITA TMPYVVLTAL LLRGVTLPGA IDGIRAYLSV	240 300
20	DEVELOPASV WIDAATOVOF SLGVGFGVLI AFSSYNKFTN NCYRDAIVTT SINSLTSFSS	360
	GFVVFSFLGY MAQKHSVPIG DVAKDGPGLI FIIYPEAIAT LPLSSAWAVV PFIMLLTLGI DSAMGGMESV ITGLIDEFQL LHRHRELFTL FIVLATFLLS LFCVTNGGIY VPTLLDHFAA	420 480
35	GTSILPGYLI EAIGVAMFYG VGOFSDDIQO MTGQRPSLYW RLCWKLVSPC FLLFVVVVSI VTFRPPHYGA YIFPDWANAL GWVIATSSMA MVPIYAAYKF CSLPGSFREK LAYAIAPEKD	540 600
<i>33</i>	RELVDRGEVR OFTLRHWLKV	620
	Seq ID NO: 251 Protein Sequence Protein Accession #: NP_071356.1	
40	1 11 21 31 41 51	
		60
	LAGPRAGVSK RHLRGDQITW IGGNEEGCEA ISFLLSLIDR LVLYCGSRLG KYYVKERSKA MVACYPGNGT GYVRHVDNPN GDGRCITCIY YLNKNWDAKL HGGILRIFPE GKSFIADVEP	120 180
45	IFDRLLPFWS DRRNPHEVQP SYATRYAMTV WYFDAEERAE AKKKFRNLTR KTESALTED	239
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50	1 11 21 31 41 51	
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	RTRSQLSALE RRLSACGSAC QGTEGSTDLP LAPESRVDPE VLHSLQTQLK AQNSRIQQLF HKVAQQQRHL EKQHLRIQHL QSQFGLLDHK HLDHEVAKPA RRKRLPEMAQ PVDPAHNVSR	180
55	LHRLPRDCQE LFQVGERQSG LFEIQPQGSP PFLVNCKMTS DGGWTVIQRR HDGSVDFNRP WEAYKAGFGD PKGEFWLGLE KVHSITGDRN SRLAVQLRDW DGNAELLQFS VHLGGEDTAY	240 300
55	SLQLTAPVAG QLGATTVPPS GLSVPFSTWD QDHDLRRDKN CAKSLSGGWW FGTCSHSNLN	360 406
	GQYFRSIPQQ RQKLKKGIFW KTWRGRYYPL QATTMLIQPM AAEAAS	406
60	Seq ID NO: 253 Protein Sequence Protein Accession #: NP_001207.1	
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	MAPLCPSPWL PLLIPAPAPG LTVQLLLSLL LLMPVHPQRL PRMQEDSPLG GGSSGEDDPL GEEDLPSEED SPREEDPPGE EDLPGEEDLP GEEDLPEVKP KSEEEGSLKL EDLPTVEAPG	60 120
65	DPOEPONNAH RDKEGDDQSH WRYGGDPPWP RVSPACAGRP QSPVDIRPQL AAFCPALRPL	180
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	EEGSETQVPG LDISALLPSD FSRYFQYEGS LTTPPCAQGV IWTVFNQTVM LSAKQLHTLS DTLWGPGDSR LQLNPRATQP LNGRVIEASF PAGVDSSPRA AEPVQLNSCL AAGDILALVF	360 420
70	GLIFAVTSVA FLYQMRRQHR RGTKGGVSYR PAEVAETGA	459
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	FMEDPPUTLL WSVTVSMFPP GGFIGSLLVG PLVNKFGRKG ALLFNNIFSI VPAILMGCSR VATSFELIII SRLLVGICAG VSSNVVPMYL GELAPKNLRG ALGVVPQLPI TVGILVAQIP	120 180
	CLENILAND GWPILLGUTG VPARLOLLLL PPFPESPRYL LIOKKDEAAA KKALOTLRGW	240
80	DSVDREVAEI RQEDEAEKAA GFISVLKLFR MRSLRWQLLS IIVLMGGQQL SGVNAIYYYA DQIYLSAGVP EEHVQYVTAG TGAVNVVMTF CAVPVVELLG RRLLLLLGFS ICLIACCVLT	300 360
	AALALODTVS WMPYISIVCV ISYVIGHALG PSPIPALLIT EIFLQSSRPS AFMVGGSVHW	420 480 ·
	LSMTTVGLIP PFIQEGLGPY SFIVFAVICL LTTIYIFLIV PETKAKTFIE INQIFTKMNK VSEVYPEKEE LKELPPVTSE Q	501

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5	 MPEEGSGCSV QLNHTGPQQD SRHHPTTLAV TDETFFGVQW	PRLYWQGGPA GICSPASRSI	LGRSFLHGPE	LDKGQLRIHR	DGIYMVHIQV	TLAICSSTTA	60 120 180 193
10	Seq ID NO: Protein Acc			31	41	51	
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20	Seq ID NO: Protein Acc		-	9 31 	41 	51 	
25	HELQSVLAMQ DIKTRLEVEI	SSPEGTLADT ETYHRLLGGE	EAGYVAQLSE GGSEAREAES	LQTQISTDAE IKMYISILEE KG			60 120 152
		258 Protein ession #: 1					
30	1	11	21	31	41	51 I	
35	nqlrrlpaan PCTNLTELHL NKIQALKSEE LCLELANTSI	PTRYSQLTSL MSNSIQKIKN LDIFANSSLK RNLSLSNSQL	DVGFNTISKL NPFVKQKNLI KLELSSNQIK STTSNTTFLG	LKWTNLTMLD	LKVLNLQHNE STKLGTQVQL GRLFGLFLNN LSYNNLNVVG	LSQLSDKTFA ENLQELLLSN VQLGPSLTEK NDSFAWLPQL	60 120 180 240 300
40	NMEDNDIPGI KIESDAFSWL SLQRLMLRRV NLARLWKHAN	KSNMFTGLIN GHLEVLDLGL ALKNVDSSPS PGGPIYFLKG	LKYLSLSNSF NEIGQELTGQ PFQPLRNLTI LSHLHILNLE	EWRGLENIFE LDLSNNNIAN SNGFDEIPVE	FVSLAHSPLH IYLSYNKYLQ INDDMLEGLE VFKDLFELKI	ILNLTKNKIS LTRNSFALVP KLEILDLQHN IDLGLNNLNT	360 420 480 540 600
45	INETHTNIPE LLIHFEGWRI DQSLKFCLEE	LSSHYLCNTP SPYWNVSVHR RDFEAGVFEL	PHYHGFPVRL VLGFKEIDRQ EAIVNSIKRS	FDTSSCKDSA TEQFEYAAYI RKIIFVITHH	PFELFFMINT IHAYKDKDWV LLKDPLCKRF	CESIAWFVNW SILLIFIFIV WEHPSSMEKE KVHHAVQQAI HKLQVALGSK	660 720 780 840 900 904
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55	LKSMTDIYLL LLTIDRYLAV HPPYSQYQFW MIVYFLFWAP	NLAISDLFFL VHAVFALKAR KNFQTLKIVI VNIVLLLNTF	LTVPFWAHYA TVTPGVVTSV LGLVLPLLVN QEFFGLNNCS	AAQWDFGNTM ITWVVAVFAS VICYSGILKI	CQLLTGLYF1 LPG11PTRSC LLRCRNEKG VTETLGMTHC	VILILINCKR GFFSGIFFII KEGLHYTCSS HRAVRLIFTI CINPILYAFV	60 120 180 240 300 352
60		260 Protei				r	
		cession #:		e 31	41	51	
65	ADGLKGEKGE GERGPSGLPG	SASDSLQESI	AQLIVEPGPI PGTKGEKGRI	GPPGPPGPMC GEPGLDGFPC	LQGIQGPKG	A GEMGLSGLPG L DGAKGEKGAS E RGEKGERGVP	60 120 180 216
70		261 Protei		•			
	1	11 	2Î 	31 	41 	51 	
75	AVIRANGSAG FARSLVQDYF VPLTWKLSAG EVERRFHLVI NMLDSHLYRI	ECOPRRNIVE PGACFNIICE DKLTEFLQDE LQEYFDESL' FNASFWRKVI	F LKTHKTASS N HMRFHYDEVI P DRYYDPNGFI V LLKDLLCWE E AFGRERMAR	I LLNILFRFG R GLVPTNAIF: N AHYLRNLLF: L EDVLYFKLN. E VAALRHANE:	Q KHRLKFAFP I TVLRDPARL P DLGYDNSLD A RRDSPVPRL R MRTICIDGG	A SCSPPALEPE N GRNDFDYPTF P ESSFHYFGPV P SSPQVQEHIL S GELYGRATAW H AVDAAAIQDE	60 120 180 240 300 360
80	amqpwqplgi Lrw	r KSILGYNLKI	K SIGQRHAQL	C RRMLTPEIQ	Y LMDLGANLW	V TKLWKFIRDF	420 423
		: 262 Prote: ccession #: 11			41	51	

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SNSGGLDETQ LLSSENNPLV QPKEGGDKSP SPSAADTTAT PASYSSIVSP PWEKPTTLTA
NNECFQATRE TVTIATEVHP AKYLAVSIPE DKHAGGTEER FPRASHEKVS QPPSQVQVDH
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ESPFEGRIMA LFEEEMDSNP MYSSLLINKLA NYTNLSQGVV EHEEDEESRR REAKAPRMGT
FIGVYLPCLQ NILGVILPLR LTNIVGVAGV LESFLIVAMC CTCTMLTAIS MSAIATNGVV
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NGVIHYIDEL LIPDSAKTLP ELAAESDVST AIDLPRQAGL GNHLSGSERL TLLAPLNSVF
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	1     Makksaen(	1	1	1	ı	  P PRETWIRQMD	60
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	Protein Acc	ession #: f 11	genes predi 21	iction 31	41	51	
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	EGAHRD						546
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					SVFDYVHPGD		180
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23					ASATAALAPV		720
					LQRLQAGNVV FVDVNSPGFG		780 840
					LPFPVYSNGI		900
	D	0.1000	0019				901
30							
		312 Protein					
		cession #: 1					
	1	11	21	31	41	51	
35	MUCUVET ACT	PRESERVAT	PI.DADCVGGG	CSAPTCCTVS	SSTPSDCPPE	I.CAPI.PGAMG	60
55					MTEPELQQLR		120
					MLTNSLEEMK		180
					ILPPAAAAAA		240
40	ASLPGSGLPS	VGSIRPPHGL	LKSPSAAAAA	PLGGGGGGSG	ASGGFQHWGG	MPCPCSMCQV	300
40	PPPHHHVSAM	GAGSLPRLTS	DAK				323
	G 10 VO	313 December					
		313 Protei: cession #: :					
		ccssion w.	W01312				
	1	11	21	31	41	51	
45	i	11	21 	31 	41 	51	
45	MTVLEESSIS	 LMSSVVADFS	 EFEEDPQVFN	 TLFPSRPIVP	 LSSRSMEISE	 TSVGISAEVD	60
45	MTVLEESSIS MSSVTTTQVP	 LMSSVVADFS PAHGRLSVPA	 EFEEDPQVFN SLDPTAGSLS	i TLFPSRPIVP VAETQVTPSS	 LSSRSMEISE VTTAFFSVIT	 TSVGISAEVD SILLDSSFSV	120
45	MTVLEESSIS MSSVTTTQVP IANKNTPSLA	 LMSSVVADFS PAHGRLSVPA VRDPSVFTPY	 EFEEDPQVFN SLDPTAGSLS SLVPSVESSL	 TLFPSRPIVP VAETQVTPSS FSDQERSSFS	 LSSRSMEISE VTTAPFSVIT EHKPRGALDF	TSVGISAEVD SILLDSSFSV ASSFFSTPPL	120 180
	MTVLEESSIS MSSVTTTQVP IANKNTPSLA ELSGSISSPS	 LMSSVVADFS PAHGRLSVPA VRDPSVFTPY EAPASLSLMP	 EFEEDPQVFN SLDPTAGSLS SLVPSVESSL SDLSPFTSQS	 TLFPSRPIVP VAETQVTPSS FSDQERSSFS PSPLVETFTL	LSSRSMEISE VTTAFFSVIT EHKPRGALDF FDSSDLQSSQ	TSVGISAEVD SILLDSSFSV ASSPFSTPPL LSLPSSTNLE	120 180 240
<ul><li>45</li><li>50</li></ul>	MTVLEESSIS MSSVTTTQVP IANKNTPSLA ELSGSISSPS FSQLQPSSEL	 LMSSVVADFS PAHGRLSVPA VRDPSVFTPY EAPASLSLMP PLNTIMLLPS	EFEEDPQVFN SLDPTAGSLS SLVPSVESSL SDLSPFTSQS RSEVSPWSSF	† TLFPSRPIVP VAETQVTPSS FSDQERSSFS FSPLVETFTL PSDSLEFVEA	LSSRSMEISE VTTAFFSVIT EHKPRGALDF FDSSDLQSSQ STVSLTDSEA	TSVGISAEVD SILLDSSFSV ASSPFSTPPL LSLPSSTNLE HPTSAFIETT	120 180 240 300
	MTVLEESSIS MSSVTTTQVP IANKNTPSLA ELSGSISSPS FSQLQPSSEL SYLESSLISH	 LMSSVVADFS PAHGRLSVPA VRDPSVFTPY EAPASLSLMP PLNTIMLLPS ESAVTALVPP	EFEEDPQVFN SLDPTAGSLS SLVPSVESSL SDLSPFTSQS RSEVSPWSSF GSESFDILTA	 TLFPSRPIVP VAETQVTPSS FSDQERSSFS FSPLVETFTL PSDSLEFVEA GIQATSPLTT	LSSRSMEISE VTTAFFSVIT EHKPRGALDF FDSSDLQSSQ STVSLTDSEA VHTTPILTES	TSVGISAEVD SILLDSSFSV ASSFFSTPPL LSLPSSTNLE HPTSAFIETT SLFSTLTPPD	120 180 240 300 360
	MTVLEESSIS MSSVTTTQVP IANKNTPSLA ELSGSISSPS FSQLQPSSEL SYLESSLISH DQISALDCHV	IMSSVVADFS PAHGRLSVPA VRDPSVFTPY EAPASLSLMP PLNTIMLLPS ESAVTALVPP SVLASFSKAI	EFEEDPQVFN SLDPTAGSLS SLVPSVESSL SDLSPFTSQS RSEVSPWSSP GSESFDILTA PTGTVLITDA	TLFPSRPIVP VAETQVTPSS FSDQERSSFS FSPLVETFTL PSDSLEFVEA GIQATSPLTT YLPSGSSFVS	LSSRSMEISE VTTAFFSVIT EHKPRGALDF FDSSDLQSSQ STVSLTDSEA	TSVGI SAEVD SILLDSSFSV ASSFFSTPPL LSLPSSTNLE HPTSAFIETT SLFSTLTPPD LTVVGPSLTP	120 180 240 300
50	MTVLEESSIS MSSVTTTQVP IANKNTPSLA ELSGSISSPS FSQLQPSSEL SYLESSLISH DQISALDGHV TEVPLNTSTE VDTPTLATAK	IMSSVVADFS PAHGRLSVPS PAHGRLSVPS EAPASLSIMP PLNTIMLLPS ESAVTALVPP SVLASFSKAI VSTTSTGAAT PPYVCDITVP	EFEEDPQVFN SLDPTAGSLS SLVPSVESSL SDLSPFTSQS RSEVSPWSSF GSESFDILTA PTGTVLITDA GGPLDSTLMG DAYLITTVLA	TLFPSRPIVP VAETQVTPSS FSDQERSSFS FSPLVETFTL PSDSLEFVEA GIQATSPLTT YLPSGSSFVS DAASQSPPES RRAVQEYIIT	LSSRSMEISE VTTAFFSVIT EHKPRGALDF FDSSDLQSSQ STVSLTDSEA VHTTPILTES EATPFPLPTE SAAPPLPSLR AIKEVLRIHF	TSVGISAEVD SILLDSSFSV ASSFPSTPPL LSLPSSTNLE HPTSAFIETT SLFSTLTPPD LTVVGPSLTP PVTAFTLEAT NRAVELKVYE	120 180 240 300 360 420 480 540
	MTVLEESSIS MSSVTTTQVP IANKNTPSLA ELSGSISSPS FSQLQPSSEL SYLESSLISH DQISALDGHV TEVPLNTSTE VDTPTLATAK LFTDPTFLVT	LMSSVVADFS PAHGRLSVPA VRDPSVFTPY EAPASLSLMP PLNTIMLLPS ESAVTALVPP SVLASFSKAI VSTTSTGAAT PPYVCDITVP SGPFVYTAIS	EFEEDPQVFN SLDPTAGSLS SLVPSVESSL SDLSPFTSQS RSEVSPWSSF GSESFDILTA PTGTVLITDA GGPLDSTLMG DAYLITTVIA VINVLINSKL	I TLFPSRPIVP VAETQVTPSS FSDQERSSFS FSPLVETFTL PSDSLEFVEA GIQATSPLTT YLPSCSSFVS DAASQSPPES RRAVQEYIIT VRDQTPLILS	LSSRSMEISE VTTAFFSVIT EHKPRGALDF FDSSDLQSSQ STVSLTDSEA VHTTPILTES EATFFPLPTE SAAPPLPSLE AIKEVLRIHF VKPSFLVPES	TSVGISAEVD SILLDSSPSV ASSPFSTPPL LSLPSSTNLE HPTSAFIETT SLFSTLTPPD LTVVGPSLTP PVTAFTLEAT NRAVELEVYE RFQVQTVLQF	120 180 240 300 360 420 480 540
50	MTVLEESSIS MSSVTTTQVP IANKNTPSLA ELSGSISSPS FSQLQPSSEL SYLESSLISH DQISALDGHV TEVPLNTSTE VDTPTLATAK LFTDFTFLVT VPPSVDTGFC	IMSSVVADFS PAHGRLSVPA VRDPSVFTPY EAPASLSLMP PINTIMLLPS SSAVTALVPP SVLASFSKAI VSTTSTGAAT PPYVCDITVP SGPFVYTAIS NFTQRIEKGL	EFEEDPQVFN SLDPTAGSLS SLVPSVESSL SDLSPFTSQS RSEVSPWSSF GSESFDILTA PTGTVLITDA GGPLDSTLMG DAYLITTVLA VINVLINSKL MTALFEVRKH	TLFPSRPIVP VAETQVTPSS FSDQERSSFS FSPLVETFTL PSDSLEFVEA GIQATSPLTT YLPSCSSFVS DAASQSPPES RRAVQEYIIT VRDQTPLILS HQGTYNLTVQ	LSSRSMEISE VTTAFFSVIT EHKPRGALDF FDSSDLQSSQ STVSLTDSEA VHTTPILTES EATPPLPTE SAAPPLPSLR AIKEVLRIHF VKPSFLVPES ILNITISSSR	TSVGI SAEVD TSVGI SAEVD SILLDSSFSV ASSFFSTPPL LSLPSSTNLE HPTSAFIETT SLFSTLTPPD LTVVGPSLTP PVTAFTLEAT NRAVELKYJE RFQVGTVLOF VTPRRGPVNI	120 180 240 300 360 420 480 540 600 660
50	MTVLEESSIS MSSVTTTQVP IANKNTPSLA ELSGSISSPS FSQLQPSSEL SYLESSLISH DQISALDGHV TEVPLNTSTE VDTPTLATAK LFTDFTFLVT VPPSVDTGPC IFAVKSTQGF	IMSSVVADFS PAHGRLSVPA VRDPSVFTPY EAPASLSLMP PLNTIMLLPS ESAVTALVPS SVLASFSKAI VSTTSTGAAT PPYVCDITVP SGPFVYTAIS NFTORIEKGL LNGSEVSELL	EFEEDPQVFN SLDPTAGSLS SLVPSVESSL SDLSPFTSQS RSEVSPWSSF GSESFDILTA PTGTVLITDA GGPLDSTLMG DAYLITTVLA VINVLINSKL WTALFEVRKH RNLSVVEFSF	TLFPSRPIVP VAETQVTPSS FSDQERSSFS FSPLVETFTL PSDSLEFVEA GIQATSPLTT YLPSGSSFVS DAASQSPPES RRAVQEYIIT VRDQTTPLILS YCGYPVLQIA	LSSRSMEISE VTTAFFSVIT EHKPRGALDF FDSSDLQSSQ STVSLTDSEA VHTTPILTES EATPFPLPTE SAAPPLPSLR AIKEVLRIHF VKPSFLVPES ILNITISSSR EPFQYPQLNL	TSVGISAEVD SILLDSSFSV ASSPFSTPPL LSLPSSTNLE HPTSAFIETT SLFSTLTPPD LTVVGPSLTP PVTAFTLEAT NRAVELKYYE RFQVQTVLQF VTPRRGPVNI SQLLKSSWVR	120 180 240 300 360 420 480 540 600 660 720
50	MTVLEESSIS MSSVTTTQVP IANKNTPSLA ELSGSISSPS FSQLQPSSEISH DQISALDGHV TEVPLNTSTE VDTPTLATAK LFTDFTFLVT VPPSVDTGFC IFAVKSTQGF	IMSSVVADFS PAHGRLSVPA VRDPSVFTPY EAPASLSIMP PLNTIMLLPS ESAVTALVPP SVLASFSKAI VSTTSTGAAT VSTTSTGAAT VSTTSTGAT SGPFVYTAIS NFTQRIEKGL LINGSEVSELL LQNEVFQAEM	EFEEDPQVFN SLDPTAGSLS SLUPSVESSL SDLSPFTSQS RSEVSPWSSF GSESFDILTA PTGTVLITDA GGPLDSTLMG DAYLITTVIA VINVLINSKL MTALFEVKHH RNLSVVEPSF ERKLAQLLSE	TLFPSRPIVP VABTQVTPSS FSDQERSSFS FSPLVETFTL PSDSLEFVEA GIQATSPLTT YLPSGSSFVS DAASQSPPES RRAVQEYIIT VRDQTPLILS HQGTVNLTVQ VLGYPVLQIA VSTRRRMMRR	LSSRSMEISE VTTAFFSVIT EHKPRGALDF FDSSDLQSSQ STVSLTDSEA VHTTPILTES EATPFPLPTE SAAPPLPSLE AIKEVLRIHF VKPSFLVPES ILNITISSSR EPFQYPQLNL ATVAAGNSVV	TSVGISAEVD SILLDSSFSV ASSPFSTPPL LSLPSSTNLE HPTSAFIETT SLFSTLTPPD LTVVGPSLTP PVTAFTLEAT NRAVELKYYE RFQVQTVLQF VTPRRGPVNI SQLLKSSKVR QVVNVSRLEG	120 180 240 300 360 420 480 540 600 660 720 780
50	MTVLEESIS MSSVTTTQVP IANKNTPSLA ELSGSISSPS FSQLQPSSEL DQISALDGHV TEVPLNTSTE VDTPTLATA LFTDPTFLVT VPPSVDTGPC IFAVKSTQGF TVLLGVMEKQ DDNPVQLIYF	IMSSVVADFS PAHGRLSVPA VRDPSVFTPY EAPASLSLMP PLATIMLLPS ESAVTALVPP SVLASFSKAI VSTTSTGAAT PPYVCDITVP SGPFVYTAIS NFTQRIEKGL LNGSEVSELL LQNEVFÇAE VEDQUGERLS	FFEEDPQVFN SLDPTAGSLS SLVPSVESSL SDLSPFTSQS RSEVSPWSSF GSESFDILTA PTGTVLITDA GGPLDSTLMG DAYLITTVLA VINVLINSKL MTALFEVRKH RNLSVVEFSF ERKLAQLLSE AVKSSDLINK	TLFPSRPIVP VAETQVTPSS FSDQERSSFS FSPLVETFTL PSDSLEFVEA GIQATSPLTT YLPSCSSFVS DASGSPPES RRAVQEYIIT VRDQTPLILS HQGTYNLTVQ YLGYEVLOIA VSTRRMMRR MDLQRAAIIL	LSSRSMEISE VTTAFFSVIT EHKPRGALDF FDSSDLQSSQ STVSLTDSEA VHTTPILTES EATPFPLPTE SAAPPLPSLR AIKEVLRIHF VKPSFLVPES ILNITISSSR EPFQYPQLINL ATVAAGNSVV GYRIQGVIAQ	TSVGISAEVD TSVGISAEVD SILLDSSFSV ASSPFSTPPL LSLPSSTNLE HPTSAFIET SLFSTLTPPD LTVVGPSLTP PVTAFTLEAT NRAVELKVYE RFQVQTVLQF VTPRRGPVNI SQLLKSSWVR QVVNVSRLEG PVDRVKRPSP	120 180 240 300 360 420 480 540 600 720 780 840
50 55	MTVLEESSIS MSSVTTTQVP IANKNTPSLA ELSGSISSPS FSQLQPSSEL SYLESSLISH DQISALDGHV TEVPLNTSTE VDTPTLATAK LFTDFTFLVT VPPSVDTGFC IFAVKSTQGF TVLLGYMEKQ DDNPVQLIYP ESQSNNLWVI	IMSSVVADFS PAHGRLSVPA VRDPSVFTPY EAPASLSLMP PINTIMLLPS SSAVTALVPP SVLASFSKAI VSTTSTGAAT PPYVCDITVP SGPFVYTAIS NFTQRIEKGL LNGSEVSELL LQNEVFQAE VEDQDGERLS VGVVIPVLVV	EFEEDPQVFN SLDPTAGSLS SLVPSVESSL SDLSPFTSQS RSEVSPWSSF GSESFDILTA PTGTVLITDA GGPLDSTLMG DAYLITTVLA WINVLINSKL MTALPEVRKH RNLSVVEFSF ERKLAQLLSE AVKSSDLINK MVIVVILYWK	TLFPSRPIVP VAETQVTPSS FSDQERSSFS FSPLVETFTL PSDSLEFVEA GIQATSPLTT YLPSGSSFVS DAASQSPPES RRAVQEYIIT VRDQTPLILS HQGTVNLTVQ YLGYPVLQIA VSTRRMMRR MDLQRRAIIL LCRTDKLDFQ	LSSRSMEISE VTTAFFSVIT EHKPRGALDF FDSSDLQSSQ STVSLTDSEA VHTTPILTES EATPFPLPTE SAAPPLPSLE AIKEVLRIHF VKPSFLVPES ILNITISSSR EPFQYPQLNL ATVAAGNSVV	TSVGISAEVD TSVGISAEVD SILLDSSFSV ASSFFSTPPL LSLPSSTNLE HPTSAFIETT SLFSTLTPPD LTVVGPSLTP PVTAFTLEAT NRAVELKYYE RFOVOTVLOF VTPRRGPVNI SQLLKSSWVR QVVNVSRLEG PVDRVKRPSP QKLQIPSVKG	120 180 240 300 360 420 480 540 600 660 720 780
50 55	MTVLEESSIS MSSVTTTQVP IANKNTPSLA ELSGSISSPS FSQLQPSSEL DQISALDGHV TEVPLNTSTE VDTPTLATSTE VDTPTLATSTE VPFSVDTGPC IFAVKSTQGF TVLLGYMEKQ DDNPVQLIYP ESQSNNLWVI FDFAKQHLGQ PSDADSTVSE	IMSSVVADFS PAHGRLSVPA VRDPSVFTPY EAPASLSLMP PLNTIMLLPS ESAVTALVPP SVLASFSKAI VSTTSTGAAT PPYVCDITVP SGPFVYTAIS NFTQRIEKGL LNGSEVSELL LQNEVFQAEM VEDQDGERLS VGVVIPVLVV HNKDDILIIH ESSERDAGDX	FEEDPQVFN SLDPTAGSLS SLVPSVESSL SDLSPFTSQS RSEVSPWSSF GSESFDILTA PTGTVLITDA GGPLDSTLMG DAYLITTVLA VINVLINSKL MTALFEVRSH RNLSVVEFSF ERKLAQLLSE AVKSSDLINK MVIVVILYWK EPAPLPGPLK TPGAVMDGRS	TLFPSRPIVP VAETQVTPSS FSDQERSSFS FSPLVETFTL PSDSLEFVEA GIQATSPLTT YLPSGSSFVS DASGSPES RRAVQEYIIT VRDQTPLILS HQGTVNLTVQ YLGYPLQIA VSTRRMMER MDLQRAAIIL LCRTDKLDPQ DHTTPSENGD HRAPQSGPPL	LSSRSMEISE LSSRSMEISE VTTAFFSVIT EHKPRGALDF FDSSDLQSSQ STVSLTDSSE AVHTTPILTES EATPFPLPTE SAAPPLPSLR AIKEVLRIHF VKPSFLVPES ILNITISSSR EPFQYPQLM GYRIQGVIAQ PDTVANIQOR PDTVANIQOR PSSKSKIPS PSSGREQHSS	TSVGI SAEVD TSVGI SAEVD SILLDSSFSV ASSPFSTPPL LSLPSSTNLE HPTSAFIETT SLFSTLTPPD LTVVGPSLTP PVTAFTLEAT NRAVELKVYE RFQVQTVLQF VTPRRGPVNI SQLLKSSWVR QVVNVSRLEG PVDRVKRPSP QKLQI PSVKG KNVRHRGRVS ASI FEHVDRI	120 180 240 300 360 420 480 540 600 660 720 780 840 900
50 55	MTVLEESIS MSSVTTTQVP IANKNTPSLA ELSGSISSPS FSQLQPSSEL BQISALDGHV TEVPLNTSTE VDTPTLATX LFTDPTFLVT VPPSVDTGPC IFAVKSTQGF TVLLGVMEX DDNPVQLIYP ESQSNNLWVI FDFAKQRLGQ SPSDADSTVSE SRPPEASRRV	IMSSVVADFS PAHGRLSVPA VRDPSVFTPY EAPASLSLMP PINTIMLLPS ESAVTALVPP SVLASFSKAI VSTTSTGAAT PPYVCDITVP SGPFYYTAIS NFTQRIEKGL LNGSEVSELL LQNEVFQALM VEDQDGERLS VGVVIPULVV HKDDILIIH ESSERDAGDK PSKIQLIAMO	FFEEDPQVFN SLDPTAGSLS SLVPSVESSL SDLSPFTSQS RSEVSPWSST GSESFDILTA PTGTVLITDA GGPLDSTLMG DAYLITTVLA WINVLINSKL MTALFEVRKH RNLSVVEFSF ERKLAQLLSE AVKSSDLINK MVIVVILYMK EPAPLPGPLK TPGAVMOGRS PIPAPPVQRP	TLFPSRPIVP VAETQVTPSS FSDQERSSFS FSPLVETFTL PSDSLEFVEA GIQATSPLTT YLPSGSSFVS DAASGSPPES RRAVQEYIIT RRDYPLLIS HQGTYNLTVQ YLGYPVLQIA VSTRRMWRR MDLQRAAIIL LCRTDKLDFQ DHTTPSEMGD HRAPQSGPPL SPADRVAESN	LSSRSMEISE LSSRSMEISE VTTAFFSVIT EHKPRGALDF FDSSDLQSSQ STVSLTDSEA VHTTPILTES EATPFPLPTE SAAPPLPSLR AIKEVLRIHF VKPSFLVPES ILNITISSSR EPFGYPQLINL ATVAAGNSVV GYRIQGVIAQ PDTVANIQQR VPSPKSKIPS PSSGNECHSS KINKEIQTAL	TSVGISAEVD TSVGISAEVD SILLDSSFSV ASSFFSTPPL LSLPSSTNLE HPTSAFIETT SLFSTLTPPD LTVVGPSLTP PVTAFTLEAT NRAVELKVYE RFQVQTVLOF VTPRRGPVNI SQLLKSSWVR QVVNVSRLEG PVDRVKRPSP QKLQIPSVKG KNVRHRGRVS ASIFEHVDRI RHKSEIEHHR	120 180 240 300 420 480 540 660 720 780 840 900 960 1020 1080
50 55 60	MTVLEESSIS MSSVTTTQVP IANKNTPSLA ELSGSISSPS FSQLQPSSEL SYLESSLISH DQISALDGHV TEVPLNTSTE VDTPTLATAK LFTDPTFLVT VPPSVDTGFC IFAVKSTQGF TVLLGVMEKQ DDNPVQLIYP FSQSNILMVI FDFAKQHLGQ PSDADSTVSE SRPPEASRN NKIRLRAKRR	IMSSVVADFS PAHGRLSVPA VRDPSVFTPY EAPASLSIMP PLNTIMLLPS ESAVTALVPP SVLASFSKAI VSTTSTGAAT PPYVCDITVP SGPFVYTAIS NFTQRIEKGL LQNEVFQAEM VEDQDGERLSS VGVVIPULVV HNKDDILIIH ESSERDAGDK PSKIQLIAMQ GHYEFPVVDD	FEEDPQVFN SLDPTAGSLS SLDPTAGSLS SLDSPTSQS RSEVSPWSSF GSESFDILTA PTGTVLITDA GGPLDSTLMG DAYLITTVLA VINVLINSKL MTALPEVRKH MTALPEVRKH MTALPEVRKH MTALPEVRKH MTAUFURFSF ERKLAQLLSE AVKSSDLINK MYLVVILYMK EPAPLPGPLK TPGAVMDGRS PIPAPPVQRP LSSGDTKERH	TLFPSRPIVP VAETQVTPSS FSDQERSSFS FSDQERSSFS FSDLVETFTL PSDSLEFVEA GIQATSPLTT VLPSGSSFVS DAASQSPPES RRAVQEYIIT VRDQTPLILS HQGTVNLTVQ VLGYPVLOIA VSTRRMWRR MDLQRAAIIL LCRTDKLDFQ DHTTPSENGD HRAPQSGPPL SPADRVAESN RVYRRAQMQI	LSSRSMEISE LSSRSMEISE VTTAFFSVIT EHKPRGALDF FDSSDLQSSQ STVSLTDSEA VHTTPILTES EATPFPLPTE SAAPPLPPSLR AIKEVLRIHF VKPSFLVPES ILNITISSSR EPFGVPQLNL ATVAAGNSVV GYRIQGVIAQ PDTVANIQOR VPSPKSKIPS PSSGNEQHSS KINKEIQTAL DKILDPTASV	TSVGISAEVD SILLDSSFSV ASSPFSTPPL LSLPSSTNLE HPTSAFIETT SLFSTLTPPD LTVVGPSLTP PVTAFTLEAT NRAVELKYYE RFQVQTVLQF VTPRRGFVNI SQLLKSSKVR QVVNVSRLEG PVDRVKRPSP QKLQIPSVKG KNVRHRGRVS ASIFEHVDRI RHKKEIEHHR RSVFIEPRKS	120 180 240 300 360 420 480 540 660 720 780 900 960 1020 1140
50 55	MTVLEESSIS MSSVTTTQVP IANKNTPSLA ELSGSISSPS FSQLQPSSEL SYLESSLISH DQISALDGHV TEVPLNTSTE VDTPTLATAK LFTDFTFLVT VPPSVDTGPC IFAVKSTQGP TVLLGYMEKQ DDNPVQLIYP ESQSNNLWVI FDFAKORHGQ PSDADSTVSE SRPPEASRRV NKIRLRAKRR SRIKRSPKPR	IMSSVVADFS PAHGRLSVPA VRDPSVFTPY EAPASLSLMP PLNTIMLLPS ESAVTALVPP SVLASFSKAI VSTTSTGAAT PPYVCDITVP SGPFVYTAIS NFTQRIEKGL LNGSEVSELL LQNEVFQAEM VEDQDGERLS VGVVIFVLV HNKDDILIH ESSERDAGDK PSKIQLIAMQ GHYEFPVVDD RKHQVNGCPA	FEEDPQVFN SLDPTAGSLS SLDSPTSQS RSEVSPWSSF GSESFDILTA PTGTVLITDA GGPLDSTLMG GDAYLITTVLA VINVLINSKL MTALFEVRKH MTALFEVRKH MTVVILYWK ENALPEGPLK TPGAVNDGRS PIPAPPVQRR LSSGDTKERH DAEKORLITT	TLFPSRPIVP VAETQVTPSS FSDQERSSFS FSPLVETFTL PSDSLEFVEA GIQATSPLTT YLPSGSSFVS DASGSPES RRAVQEYIIT VRDQTPLILS HQGTVNLTVQ YLGYPVLQIA VSTRRRWER MDLQRAAIIL LCRTDKLDFQ DHTTPSENGD HRAPQSGPPL SPADRVAESN RVYRRAQMQI DSDGTYRRP	LSSRSMEISE LSSRSMEISE VTTAFFSVIT EHKPRGALDF FDSSDLQSSQ STVSLTDSEA VHTTPILTES EATPFPLPTE SAAPPLPSLR AIKEVLRIHF VKPSFLVPES ILNITISSSR EPFQYPQLNL ATVAAGNSVV GYRIQGVIAQ PDTVANIQGV VPSPKSKIPS PSSGNEQHSS KINKEIQTALL DKILDPTASV	TSVGISAEVD TSVGISAEVD SILLDSSPSV ASSPFSTPPL LSLPSSTNLE HPTSAFIETT SLFSTLTPPD LTVVGPSLTP PVTAFTLEAT NRAVELKYVE RFQVQTVLQF VTPRGFVNI SQLLKSSWVR QVVNVSKLEG PVDRVKRPSP QKLQIPSVKG RNVRHRGRVS ASIFEHVDRI RHKSEIEHHR PSVPIEPRKS PSDPDLPADV	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020 1080 1140 1200
50 55 60	MTVLEESSIS MSSVTTTQVP IANKNTPSLA ELSGSISSPS FSQLQPSSEL DQISALDGHV TEVPLNTSTE VDTPTLATA LFTDPTFLVT VPPSVDTGPC IFAVKSTQGF TVLLGVMEKQ DDNPVQLIYP ESQSNNLWVI FDFAKQHLGQ PSDADSTVSE SRPPEASRRV NKIRLRAKRR SRIKRSPKPR	IMSSVVADFS PAHGRLSVPA VRDPSVFTPY EAPASLSLMP PLATIMLLPS ESAVTALVPP SVLASFSKAI VSTTSTGAAT PPYVCDITVP SGPFVYTAIS NFTQRIEKGL LNGSEVSELL LQNEVFQAEM VEDQDGERLS VGVVIPVLVV HNKDDILIIH ESSERDAGDK PSKIQLIAMQ GHYEFPVASG RKHQVNGCPA	FFEEDPQVFN SLDPTAGSLS SLVPSVESSL SDLSPFTSQS RSEVSPWSST GSESFDILTA PTGTVLITDA GGPLDSTLMG DAYLITTVLA VINVLINSKL MTALFEVRKH RNLSVVEFSP ERKLAQLLSE AVKSSDLINK MVIVVILYWK EPAPLPGPLK TPGAVMDGRS PIPAPPVQRP LSSGDTKERH DAEKORLITT YIPPQPSIEE	TLFPSRPIVP VAETQVTPSS FSDQERSSFS FSPLVETFTL PSDSLEFVEA GIQATSPLTT YLPSCSSFVS DASGSPPES RRAVQEYIIT VRDQTPLILS HQGTYNLTVQ YLGYEVLQIA VSTRRMMRR MDLQRAAILL LCRTDKLDFQ DHTTPSENGD DHTPSENGD RYYRRAQMQI DSDGTYRRPP DSDGTYRRPP DSDGTYRRPG DSDGTYRRPG	LSSRSMEISE LSSRSMEISE VTTAFFSVIT EHKPRGALDF FDSSDLQSSQ STVSLTDSEA AVHTTPILTES EATPFPLPTE SAAPPLPSLR AIKEVLRIHF VKPSFLVPES ILNITISSSR EPFQYPQLNL ATVAAGASVV GYRIGGVIAQ PDTVANIQOR PPSFKSKIPS PSSGNEQHSS KINKEIQTAL DKILDPTASV GVHNSAYIGG DAFALVAPSS	TSVGISAEVD TSVGISAEVD SILLDSSFSV ASSPFSTPPL LSLPSSTNLE HPTSAFIETT SLFSTLTPPD LTVVGPSLTP PVTAFTLEAT NRAVELKVYE RFQVQTVLQF VTPRGPVNI SQLLKSSWVR QVVNVSRLEG PVDRVKRPSP QKLQIPSVKG KNVRHRGRVS ASIFEHVDRI RHKSEIEHHR PSVFIEPRKS PSDPDLPADV QPASTAGVGP	120 180 240 300 360 420 480 600 660 720 780 840 900 1020 1080 1140 1200 1260
50 55 60	MTVLEESSIS MSSVTTTQVP IANKNTPSLA ELSGSISSPS FSQLQPSSEL SYLESSLISH DQISALDGHV TEVPLNTSTE VDTPTLATAK LFTDFTFLVT VPPSVDTGF IFAVKSTQGF TVLLGVMEKQ DDNPVQLIY FDFAKQHLGQ PSDADSTVSE SRPPEASREV NKIRLRAKRR SRIKRSPKR QTPSSVELGR	IMSSVVADFS PAHGRLSVPA VRDPSVFTPY EAPASLSIMP PLNTIMLLPS ESAVTALVPP SVLASFSKAI VSTTSTGAAT PPYVCDITVP SGPFVYTAIS NFTQRIEKGL LQNEVFQAEM VEDQUEERLS VGVVIPULVV HNKDDILIIH ESSERDAGDU PSKIQLIAMQ GHYEFPVVDD RKHQVNGCPA TPSQEERRAT	FEEDPQVFN SLDPTAGSLS SLVPSVESSL SDLSPFTSQS RSEVSPWSSF GSESFDILTA PTGTVLITDA DAYLITTVLA VINVLINSKL MTALFEVRKH MTAVLFEVRKH MYLVVLIYWK EPAPLPGPLK TPGAVMDGRS PIPAPPVQRP LSSGDTKERH DAEKORLITT YIPPQPSIEE QWGSFYSPAQ	I TLFPSRPIVP VAETQVTPSS FSDQERSSFS FSDQERSSFS FSDQERSSFS FSDQERSFET LAW TURN FOR THE TOTAL TO THE TOTAL THE TOTAL TO THE TOTAL THE TOTAL TO THE TOTA	LSSRSMEISE VTTAFFSVIT EHKPRGALDF FDSSDLQSSQ STVSLTDSEA VHTTPILTES EATPFPLPTE SAAPPLPSLR AIKEVLRIHF VKPSFLVPES ILNITISSS EPFGYPQLNL ATVAAGNSVV GYRIGGVJAN VPSPKSKIPS PSSGNEQHSS KINKEIQTAL DKILDPTASV GVHNSAYIGG DAFALVAPSS DYGMTPPTGF	TSVGISAEVD SILLDSSFSV ASSPFSTPPL LSLPSSTNLE HPTSAFIETT SLFSTLTPPD LTVVGPSLTP PVTAFTLEAT NRAVELKYYE REQVQTVLOF VTPRRGPVNI SQLLKSSWVR QVVNVSRLEG PVDRVKRPSP OKLQIPSVKG KNVRHRGRVS ASIFEHVDRI RHKSEIEHRR PSVFIEPRKS PSDPDLPADV LPPRFGFGGL	120 180 240 300 360 420 540 660 720 780 840 900 960 1020 1140 1200 1200 1320
50 55 60 65	MTVLEESSIS MSSVTTTQVP IANKNTPSLA ELSGSISSPS FSQLQPSSEL SYLESSLISH DQISALDGHV TEVPLNTSTE VDTPTLATAK LFTDPTFLVT VPPSVDTGFC IFAVKSTQGF TVLLGYMEKQ DDNPVQLIYP ESQSNNLWU PSDADSTVSE SRPPEASRY NKIRLRAKRR SRIKRSPKPR GVPPGLPANS LQSTELVPPD	IMSSVVADFS PAHGRLSVPA VRDPSVFTPY EAPASLSIMP PLNTIMLLPS ESAVTALVPP SVLASFSKAI VSTTSTGAT PPYVCDITVP SGPFVYTAIS NFTQRIEKGL LUNGSEVSELL LUNGSEVSELL LUNGVEQAEM VEDQDGERLS VGVVIPVLVV HNKDDILIIH ESSERDAGDK PSKIQLIAMQ GHYEFPVVDD RKHQVNGCPA YPALPPPASQ TPSQEERRAT PQQPQASAEA	EFEEDPQVFN SLDPTAGSLS SLDFPTSQS RSEVSPWSSF GSESFDILTA PTGTVLITDA GGPLDSTLMG DAYLITVLA VINVLINSKL MTALFEVKHH RNLSVVEPSP ERKLAQLLSE AVKSSDLINK MVIVVLLYM TPGAVNDGRS PIPAPPVRGR PIPAPPVRGH DAEKDRLITT YIPPQFSIEG QWGSFYSPA PFAARGIYSE	TLFPSRPIVP VAETQVTPSS FSDQERSSFS FSDLEFFUA GIQATSPLTT YLPSGSSFVS DAASQSPPES RAVQEYIIT VRDQTPLILS HQGTVNLTVQ YLGYPVLQIA VSTRRRWRR MDLQRAAIIL LCRTDKATA DHTTPSENGD HRAPQSGPPL SPADRVAESN RVYRRAQMQI DSDGTYRPP ARQTHISLLD TANNPCSRYE EMPSVARPRE	LSSRSMEISE LSSRSMEISE VTTAFFSVIT EHKPRGALDF FDSSDLQSSQ STVSLTDSEA VHTTPILTES EATPFPLPTE SAAPPLPSLR AIKEVLRIHF VKPSFLVPES ILNITISSSR EPFGYPQLNL ATVAAGNSVV GYRIQGYIAQ PDTVANIQQR PDTVANIQQR PDTVANIQQR PSSSREQHSS KINKEIQTAL DKILDPTASV GVHNSAYIGG DAFALVAPSS DYGMTPPTGP VGGTTGSQIQ	TSVGISAEVD TSVGISAEVD SILLDSSFSV ASSPFSTPPL LSLPSSTNLE HPTSAFIETT SLFSTLTPPD LTVVGPSLTP PVTAFTLEAT NRAVELKYYE RFQVQTVLQF VTPRGFVNI SQLLKSSWVR QVNNVSRLEG PVDRVKRPSP QKLQIPSVKG KNVRHRGRVS ASIFEHVDRI RHKSEIEHHR SPVFIEPRKS PSUPLEPRKS PSUPLPADV QPASTAGYGP LPRFGFGPGL HLTQVGIASR	120 180 240 300 360 420 600 660 720 780 840 900 960 1020 1140 1200 1260 1320
50 55 60	MTVLEESSIS MSSVTTTQVP IANKNTPSLA ELSGSISSPS FSQLQPSSEL SYLESSLISH DQISALDGHV TEVPLNTSTE VDTPTLATX VPPSVDTGPC IFAVKSTOGP TVLLGYMEKQ DDNPVQLIYP ESQSNNLMVI FDFAKQHLGQ PSDADSTVSE SRPPEASRRV NKIRLRAKRS SRIKRSPKPR QTPSSVELGR GVPPGLPANS LQSTELVPPD IGAQPVEIPP	IMSSVVADFS PAHGRLSVPA VRDPSVFTPY EAPASLSLMP PLNTIMLLPS ESAVTALVPP SVLASFSKAI VSTTSTGAAT PSTYCDITVP SGPFVYTAIS NFTQRIEKGL LMGSEVSELL LQNEVFQAEM VEDQDGERLS VGVVIPVLVV HNKDDILIIH ESSERDAGDK PSKIQLIAMQ GRYEFPVVDI RKHQVNGCPA YPALPPPASQ TPSQEERRAT PQQPQASAEA SRGSQYGGPG	EFEEDPQVFN SLDPTAGSLS SLDFPTSQS RSEVSPWSSF GSESFDILTA PTGTVLITDA GGPLDSTLMG DAYLITVLA VINVLINSKL MTALFEVKHH RNLSVVEPSP ERKLAQLLSE AVKSSDLINK MVIVVLLYM TPGAVNDGRS PIPAPPVRGR PIPAPPVRGH DAEKDRLITT YIPPQFSIEG QWGSFYSPA PFAARGIYSE	I TLFPSRPIVP VAETQVTPSS FSDQERSSFS FSPLVETFTL PSDSLEFVEA GIQATSPLTT YLPSGSSFVS DASGSPES FRAVQEYIIT VRDQTPLILS HQGTYNLTVQ YLGYPLQIA VSTRRMMER MDLQRAAIIL LCRTDKLDPQ DHTPSENGD HTAPCSGPPL SPADRVAESN RVYRRAQMQI DSDGTYRRP ARQTMHSLLD TANNECSRVE EMPSVARPRE RREAVPRTSG	LSSRSMEISE LSSRSMEISE VTTAFFSVIT EHKPRGALDF FDSSDLQSSQ STVSLTDSSE AVHTTPILTES EATPFPLPTE SAAPPLPSLR AIKEVLRIHF VKPSFLVPES ILNITISSSR EPFQYPQLM GYRIQGVIAQ PDTVANIQOR PDTVANIQOR PDTVANIQOR PSSKSKIPS PSSGNEQHSS KINKEIQTAL DKILDPTASS GVHNSAYIGG DAFALVAPSS DYGMTPPTGP VGGTTGSGIG REPSAPSGNL	TSVGISAEVD SILLDSSFSV ASSPFSTPPL LSLPSSTNLE HPTSAFIETT SLFSTLTPPD LTVVGPSLTP PVTAFTLEAT NRAVELKYYE REQVQTVLOF VTPRRGPVNI SQLLKSSWVR QVVNVSRLEG PVDRVKRPSP OKLQIPSVKG KNVRHRGRVS ASIFEHVDRI RHKSEIEHRR PSVFIEPRKS PSDPDLPADV LPPRFGFGGL	120 180 240 300 360 420 540 660 720 780 840 900 960 1020 1140 1200 1200 1320
50 55 60 65	MTVLEESSIS MSSVTTTQVP IANKNTPSLA ELSGSISSPS FSQLQPSSEL SYLESSLISH DQISALDGHV TEVPLNTSTE VDTPTLATAK LFTDPTFLVT VPPSVDTGFC IFAVKSTQGF TVLLGVMEKQ DDNPVQLIYP ESQSNNLWVI FDFAKQHLGQ PSDADSTVSE SRPPEASRY SRIKRSPKPR QTPSSVELGR GVPPGLPANS LQSTELVPPD IGAQPVEIPP GYPTSSTEDL	IMSSVVADFS PAHGRLSVPA VRDPSVFTPY EAPASLSIMP PLNTIMLIPS ESAVTALVPP SVLASFSKAI VSTTSTGAAT VSTTSTGAAT VSTTSTGAAT VSTTSTGALE LUNGSEVSELL LUNGSEVSELL LUNGSEVSELL LUNGVPQAEM VEDQDGERLS VGVVIPULVV HNKDDILIIH ESSERDAGDK PSKIQLIAMQ GHYEFPVVDD GHYEFPVVDD TPSQEERRAT PQQPQASAEA SRGSQYGGPG QPGHSSASLI	FEEDPQVFN SLDPTAGSLS SLDPFTSQS RSEVSPWSSF GSESFDILTA PTGTVLITDA GGPLDSTLMG DAYLITTVLA VINVLINSKL MTALPEVKHH KNLSVVEPSF ERKLAQLLSE AVKSSDLINK MVIVVILYMK EPAPLPGPLK TPGAVNDGRS PIPAPPVQRS PIPAPPVQRS DAEKORLITT YIPPQFSIEE QMGSFYSPAQ PFAARGIYSE WPSYGEDEAG KAIREELLRL	I TLFPSRPIVP VAETQVTPSS FSDQERSSFS FSPLVETFTL PSDSLEFVEA GIQATSPLTT YLPSGSSFVS DASGSPES FRAVQEYIIT VRDQTPLILS HQGTYNLTVQ YLGYPLQIA VSTRRMMER MDLQRAAIIL LCRTDKLDPQ DHTPSENGD HTAPCSGPPL SPADRVAESN RVYRRAQMQI DSDGTYRRP ARQTMHSLLD TANNESRYE EMPSVARPRE RREAVPRTSG	LSSRSMEISE LSSRSMEISE VTTAFFSVIT EHKPRGALDF FDSSDLQSSQ STVSLTDSSE AVHTTPILTES EATPFPLPTE SAAPPLPSLR AIKEVLRIHF VKPSFLVPES ILNITISSSR EPFQYPQLM GYRIQGVIAQ PDTVANIQOR PDTVANIQOR PDTVANIQOR PSSKSKIPS PSSGNEQHSS KINKEIQTAL DKILDPTASS GVHNSAYIGG DAFALVAPSS DYGMTPPTGP VGGTTGSGIG REPSAPSGNL	TSVGISAEVD TSVGISAEVD SILLDSSFSV ASSPFSTPPL LSLPSSTNLE HPTSAFIETT SLFSTLTPPD LTVVGPSLTP PVTAFTLEAT NRAVELKYYE RFQVQTVLQF VTPRGFVNI SQLLKSSWVR QVNNVSRLEG PVDRVKRPSP QKLQIPSVKG KNVRHRGRVS ASIFEHVDRI RHKSEIEHHR SPVFIEPRKS PSUPLEPRKS PSUPLPADV QPASTAGYGP LPRFGFGPGL HLTQVGIASR	120 180 240 300 360 420 600 660 720 780 900 960 1020 1080 1140 1200 1260 1320 1380
50 55 60 65	MTVLEESSIS MSSVTTTQVP IANKNTPSLA ELSGSISSPS FSQLQPSSEL SYLESSLISH DQISALDGHV TEVPLNTSTE VDTPTLATAK LFTDFTFLVT VPPSVDTGPC IFAVKSTQGP TVLLGYMEKQ DDNPVQLIYP ESQSNNLWVI FDFAKORHGQ PSDADSTVSE SRPPEASRRV NKIRLRAKRR SRIKRSPKPR QTPSSVELGR GVPPGLPND IGAQPVEIPP GYPTSSTEDL Seq ID NO:	IMSSVVADFS PAHGRLSVPA VRDPSVFTPY EAPASLSLMP PLNTIMLLPS ESAVTALVPP SVLASFSKAI VSTTSTGAAT PPYVCDITVP SGPFVYTAIS NFTQRIEKGL LNGSEVSELL LQNEVFQAEM VEDQDGERLS VGVVIPVLVM HNKDDILIH ESSERDAGDK PSKIQLIAMQ GHYEFPVVDD RKHQVNGCPA YPALPFPASQ TPSQEERAS POQPQASAEA SRGSQYGGPG QPGHSSASLI 314 Protei	FFEEDPQVFN SLDPTAGSLS SLDSPTSQS RSEVSPWSSL SDLSPTSQS RSEVSPWSSP GSESFDILTA PTGTVLITDA GGPLDSTLMG GDAYLITTVLA VINVLINSKL MTALFEVRKH MTALFEVRKH KNLSVVEPSP ERKLAQLLSE AVKSSDLINK MVIVVILYWK EPAPLPGPLK TPGAVNDGRS PIPAPPVQRP LSSGDTKERH DAEKORLITT YIPPQPSIEE QWGSFYSPAG WPSYGEDEAG KAIREELLRL  N Sequence	I TLFPSRPIVP VAETQVTPSS FSDQERSSFS FSPLVETFTL PSDSLEFVEA GIQATSPLTT YLPSGSSFVS DASGSPES FRAVQEYIIT VRDQTPLILS HQGTYNLTVQ YLGYPLQIA VSTRRMMER MDLQRAAIIL LCRTDKLDPQ DHTPSENGD HTAPCSGPPL SPADRVAESN RVYRRAQMQI DSDGTYRRP ARQTMHSLLD TANNESRYE EMPSVARPRE RREAVPRTSG	LSSRSMEISE LSSRSMEISE VTTAFFSVIT EHKPRGALDF FDSSDLQSSQ STVSLTDSSE AVHTTPILTES EATPFPLPTE SAAPPLPSLR AIKEVLRIHF VKPSFLVPES ILNITISSSR EPFQYPQLM GYRIQGVIAQ PDTVANIQOR PDTVANIQOR PDTVANIQOR PSSKSKIPS PSSGNEQHSS KINKEIQTAL DKILDPTASS GVHNSAYIGG DAFALVAPSS DYGMTPPTGP VGGTTGSGIG REPSAPSGNL	TSVGISAEVD TSVGISAEVD SILLDSSFSV ASSPFSTPPL LSLPSSTNLE HPTSAFIETT SLFSTLTPPD LTVVGPSLTP PVTAFTLEAT NRAVELKYYE RFQVQTVLQF VTPRGFVNI SQLLKSSWVR QVNNVSRLEG PVDRVKRPSP QKLQIPSVKG KNVRHRGRVS ASIFEHVDRI RHKSEIEHHR SPVFIEPRKS PSUPLEPRKS PSUPLPADV QPASTAGYGP LPRFGFGPGL HLTQVGIASR	120 180 240 300 360 420 600 660 720 780 900 960 1020 1080 1140 1200 1260 1320 1380
50 55 60 65	MTVLEESSIS MSSVTTTQVP IANKNTPSLA ELSGSISSPS FSQLQPSSELS DQISALDGHV TEVPLNTSTE VDTPTLATX VPPSVDTGPC IFAVKSTQGP TVLLGVMEKQ DDNPVQLIYP ESQSNNLWVI FDFAKQHLGQ PSDADSTVSE SRPPEASRRV NKIRLRAKRR QTPSSVELGR GVPPGLPANS LQSTELVPPI GYPTSSTEDL Seq ID NO: Protein Ac	IMSSVVADFS PAHGRLSVPA VRDPSVFTPY EAPASLSLMP PLNTIMLLPS ESAVTALVPP SVLASFSKAI VSTTSTGAAT VSTTSTGAAT PPYVCDITVP SGPFVYTAIS INFTORIEKGL LUNGSEVSELL VEDQDGERLS VGVVIPVLVV HNKDDILIIH ESSERDAGDK PSKIQLIAMQ GRYFFPVUDIS RKHQVNGCPA YPALPPPASQ TPSQEERRAT PQQPQASASLI 314 Protein cession #:	FEEDPQVFN SLDPTAGSLS SLVPSVESSL SDLSPFTSQS RSEVSPWSSF GSESFDILTA PTGTVLITDA GGPLDSTLMG DAYLITTVLA VINVLINSKL MTALFEVRKH RNLSVVEFSS ERKLAQLLSE AVKSSDLINK MVIVVILYWK EPAPLPGPLK TPGAVMDGRS PIPAPPVQRP LSSGDTKEH VIPPQPSIEE QWGSFYSPAQ GWGSFYSPAQ EWPSYGEDEAG KAIREELLRL  n Sequence BAC04820.1	TLFPSRPIVP VAETQVTPSS FSDQERSSFS FSDLEFFUE FSDSLEFVEE GIQATSPLIT YLPSGSSFVS DASGSPES RRAVQEYIIT VRQTPLILS HQGTVNLTVQ YLGYFVLQIA VSTRRMMER MDLQRAAIIL LCRTDKLDFQ DHTTPSENGD DHTTPSENGD DHTPSENGD TRAPQSGPL SPADRVAESN RVYRRAQMGI TANNPCSRVE EMPSVARPRE EMPSVARPRE EMPSVARPRE RREAVPRTSG SQKQSTVQNF	LSSRSMEISE LSSRSMEISE VTTAFFSVIT EHKPRGALDF FDSSDLQSSQ STVSLTDSSE AVHTTPILTES EATPFPLPTE SAAPPLPSLR AIKEVLRIHF VKPSFLVPES ILNITISSSR EPFQYPQLMA GYRIQGVIAQ PDTVANIQOR PDTVANIQOR VPSPKSKIPS PSSGNEQHSS KINKEIQTAL DKILDPTASV GVHSNAYIGC DAFALVAPSS DYGMTPFTGF VGGTTGSQIL REPSAPSGNL	TSVGI SAEVD TSVGI SAEVD SILLDSSFSV ASSPFSTPPL LSLPSSTNLE HPTSAFIETT SLFSTLTPPD LTVVGPSLTP PVTAFTLEAT NRAVELKVYE RFQVQTVLQF VTPRRGPVNI SQLLKSSWVI QVVNVSKLEG PVDRVKRPSP QKLQI PSVKG KNVRHRGRVS ASI FEHVDRI RHKSEI EIHR PSVFI EPRKS PSDPDLPADV QPASTAGVGP LPRPGFGGCL HLTQVGI ASR PHRGLQGPGL	120 180 240 300 360 420 650 720 780 900 960 1020 1080 1140 1200 1260 1320 1380
50 55 60 65 70	MTVLEESSIS MSSVTTTQVP IANKNTPSLA ELSGSISSPS FSQLQPSSEISH DQISALDGHV TEVPLNTSTE VDTPTLATAK LFTDPTFLVT VPPSVDTGFG TVLLGVMEKQ DDNPVQLIYE ESQSNNLWVI FDFAKQHLGQ PSDADSTVSE SRPPEASRN QTPSSVELGR GVPPGLPANS LQSTELVPPD IGAQPVEIPP GYPTSSTEDL Seq ID NO: Protein Act	IMSSVVADFS PAHGRLSVPA VRDPSVFTPY EAPASLSLMP PLNTIMLLPS ESAVTALVPP SVLASFSKAI VSTTSTGAAT PPYVCDITVP SGPFVYTAIS NFTQRIEKGL LNGSEVSELL LQNEVFQAEM VEDQDGERLS VGVVIPVLVM HNKDDILIH ESSERDAGDK PSKIQLIAMQ GHYEFPVVDD RKHQVNGCPA YPALPFPASQ TPSQEERAS POQPGASAEA SRGSQYGGPG QPGHSSASLI 314 Protei	FFEEDPQVFN SLDPTAGSLS SLDSPTSQS RSEVSPWSSL SDLSPTSQS RSEVSPWSSP GSESFDILTA PTGTVLITDA GGPLDSTLMG GDAYLITTVLA VINVLINSKL MTALFEVRKH MTALFEVRKH KNLSVVEPSP ERKLAQLLSE AVKSSDLINK MVIVVILYWK EPAPLPGPLK TPGAVNDGRS PIPAPPVQRP LSSGDTKERH DAEKORLITT YIPPQPSIEE QWGSFYSPAG WPSYGEDEAG KAIREELLRL  N Sequence	I TLFPSRPIVP VAETQVTPSS FSDQERSSFS FSPLVETFTL PSDSLEFVEA GIQATSPLTT YLPSGSSFVS DASGSPES FRAVQEYIIT VRDQTPLILS HQGTYNLTVQ YLGYPLQIA VSTRRMMER MDLQRAAIIL LCRTDKLDPQ DHTPSENGD HTAPCSGPPL SPADRVAESN RVYRRAQMQI DSDGTYRRP ARQTMHSLLD TANNESRYE EMPSVARPRE RREAVPRTSG	LSSRSMEISE LSSRSMEISE VTTAFFSVIT EHKPRGALDF FDSSDLQSSQ STVSLTDSSE AVHTTPILTES EATPFPLPTE SAAPPLPSLR AIKEVLRIHF VKPSFLVPES ILNITISSSR EPFQYPQLM GYRIQGVIAQ PDTVANIQOR PDTVANIQOR PDTVANIQOR PSSKSKIPS PSSGNEQHSS KINKEIQTAL DKILDPTASS GVHNSAYIGG DAFALVAPSS DYGMTPPTGP VGGTTGSGIG REPSAPSGNL	TSVGISAEVD TSVGISAEVD SILLDSSFSV ASSPFSTPPL LSLPSSTNLE HPTSAFIETT SLFSTLTPPD LTVVGPSLTP PVTAFTLEAT NRAVELKYYE RFQVQTVLQF VTPRGFVNI SQLLKSSWVR QVNNVSRLEG PVDRVKRPSP QKLQIPSVKG KNVRHRGRVS ASIFEHVDRI RHKSEIEHHR SPVFIEPRKS PSUPLEPRKS PSUPLPADV QPASTAGYGP LPRFGFGPGL HLTQVGIASR	120 180 240 300 360 420 650 720 780 900 960 1020 1080 1140 1200 1260 1320 1380
50 55 60 65	MTVLEESSIS MSSVTTTQVP IANKNTPSLA ELSGSISSPS FSQLQPSSEL SYLESSLISH DQISALDGHV TEVPLNTSTE VDTPTLATAK LFTDFTFLVT VPPSVDTGPC IFAVKSTQGF TVLLGYMEKQ DDNPVQLIYP ESQSNNLWVI FDFAKORHGQ PSDADSTVSE SRPPEASRVR KIRLRAKRVR SRIKRSPKPR GVPPGLPANS LQSTELVPPD IGAQPVEIPP GYPTSSTEDL Seq ID NO: Protein Ac	IMSSVVADFS PAHGRLSVPA VRDPSVFTPY EAPASLSIMP PLNTIMLLPS ESAVTALVPP SVLASFSKAI VSTTSTGAAT PPYVCDITVP SGPFVYTAIS NFTQRIEKGL LUNGSEVSELL LUNGSEVSELL LUNGSEVSELL LUNGVEQAEM VEDQDGERLS VGVVIPVLVV HNKDDILIH ESSERDAGDK PSKIQLIAMQ GHYEFPVVDD RKHQVNGCPA YPALPPPASQ TPSQEERRAT PQOPQASAEA SRGSQYGGG QPGHSSASLI 314 Protei cession #: 11	FEEDPQVFN SLDPTAGSLS SLDSPTSQS RSEVSPWSSL SDLSPTSQS RSEVSPWSSF GSESFDILTA PTGTVLITDA GGPLDSTLMG GDAYLITTVLA VINVLINSKL MTALFEVKH RNLSVVEPSP ERKLAQLLSE AVKSSDLINK MVIVILYWL TPGAVNDGRS PIPAPPVRGR LSAGDTKEH DAEKDRLITT YIPPOPSIEE QWGSFYSPAG WPSYGEDEAG KAIREELLRL  N SEQUENCE BACO4820.1 21	TLFPSRPIVP TLFPSRPIVP VAETQVTPSS FSDQERSSFS FSPLVETFTL PSDSLEFVEA GIQATSPLTT YLPSGSSFVS DAASQSPPES RAVQEYIIT VRDQTPLILS HQGTYNLTVQ YLGYPVLQIA VSTRRRWAR MDLQRAAIIL LCRTDKLDFQ DHTTPSENGD HRAPQSGPPL SPADRVAESN RVYRRAQMQI DSDGTYRPP ARQTHISLLD TANNPCSRVE EMPSVARPAE RREAVPRTSG SQKQSTVQNF	LSSRSMEISE LSSRSMEISE VTTAFFSVIT EHKPRGALDF FDSSDLQSSQ STVSLTDSEA VHTTPILTES EATPFPLPTE SAAPPLPSLR AIKEVLRIHF VKPSFLVPES ILNITISSSR EPFQYPQLNL ATVAAGNSVV GYRIQGVIAQ PDTVANIQGVIAQ PDTVANIQGVIAQ PDTVANIQGVIAQ PDTVANIQGVIAQ PDTVANIQGVIAQ PDTVANIQGVIAQ PDTVANIQGVIAQ VSSPKSKIPS PSSGNEQHSS KINKEIQTALL DKILDPTASV GVHNSAYIGC DAFALVAPSS DYGMTPPTGIQ VGGTTGSQIQ REPSAPSGNL	TSVGISAEVD TSVGISAEVD TSVGISAEVD ASSPFSTPPL LSLPSSTNLE HPTSAFIETT SLFSTLTPPD LTVVGPSLTP PVTAFTLEAT NRAVELKYYE RFQVQTVLQF VTPRRGFVNI SQLLKSSWVR QVVNVSRLEG PVDRVKRPSP QKLQIPSVKG KNVRHRGRVS ASIFEHVDRI RHKSEIEHHR PSVFIEPRKS PSUFIEPRKS PHRGLQGPGL	120 180 240 300 360 420 600 660 720 780 840 900 960 1020 1140 1200 1260 1320 1440 1482
50 55 60 65 70	MTVLEESSIS MSSVTTTQVP IANKNTPSLA ELSGSISSPS FSQLQPSSELS DQISALDGHV TEVPLNTSTE VDTPTLATX VPPSVDTGPC IFAVKSTQGP TVLLGWEKQ DDNPVQLIYP ESQSNNLWVI FDFAKQHLGQ PSDADSTVSE SRPPEASRRV NKIRLRAKRS SRIKRSPKPR QTPSSVELGR GVPPGLPANS LQSTELVPPI GYPTSSTEDL Seq ID NO: Protein Ac 1   MAPRPLGPLV	I LMSSVVADFS PAHGRLSVPA VRDPSVFTPY EAPASLSIMP PLNTIMLPS ESAVTALVPP SVLASFSKAI PPYVCDITVP SGPFVYTAIS NFTQRIEKGL LNGSEVSELL LQNEVFQAEM VEDQDGERLS VGVVIEVLVV HNKDDILIIH ESSERDAGDK PSKIQLIAMQ GHYEFPVVDD RKHQVNGCPA TPSQEERRAT PQQPQASAEA SGRGQYGGPG QPGHSSASLI 314 Protei Cession #: 11	FEEDPQVFN SLDPTAGSLS SLDYPSVESSL SDLSPFTSQS RSEVSPWSSF GSESFDILTA PTGTVLITDA GGPLDSTLMG DAYLITTVLA VINVLINSKL MTALFEVRKH RNLSVVEFSS ERKLAQLLSE AVKSSDLINK MVIVVILYWK EPAPLPGPLK TPGAVMDGRS PIPAPPVQRP LSSGDTKEM VIPQPSIEE QWGSFYSPAQ WGSFYSPAQ WGSFYSPAG WFSYGEDEAG KAIREELLRL  1 Sequence BAC04820.1 21   GSVLFILMKT	TLFPSRPIVP TLFPSRPIVP VAETQVTPSS FSDQERSSFS FSDQERSSFS FSDLVETFUL FSDSLEFVEA GIQATSPLTT VLPSGSSFVS DAASQSPPES RAVQEYIIT VRDQTPLLLS HQGTYNLTVQ LGYPVLQIA VSTRRMMER MDLQRAMILL LCRTDKLDFQ DHTTPSENGD HRAPQSGPPLL SPADRVAESN RVYRRAQMQI DSDGTYRRPE EMPSVARPRE EMPSVARPRE REAVPRTSG SQKQSTVQNE	LSSRSMEISE LSSRSMEISE VTTAFFSVIT EHKPRGALDF FDSSDLQSSQ STVSLTDSSE AVHTTPILTES EATPFPLPTE SAAPPLPSLR AIKEVLRIHF VKPSFLVPES ILNITISSSR EPFQYPQLINA GYRIQGVIAQ PDTVANIQOR VPSPKSKIPS PSSGNECHSS KINKEIQTAL DKILDPTASV GVHSAXIGC DAFALVAPSS DYGMTPFTGP VGCTTGSQIL HS	TSVGISAEVD TSVGISAEVD SILLDSSFSV ASSPFSTPPL LSLPSSTNLE HPTSAFIETT SLFSTLTPPD LTVVGPSLTP PVTAFTLEAT NRAVELKVYE RFQVQTVLQF VTPRGEPVNI SQLLKSSWVI QVVNVSKLEG PVDRVKRPSP QKLQIPSVKG KNVRHRGRVS ASIFEHVDRI RHKSEIEHR PSVFIEPRKS PSDPDLPADV QPASTAGVGP LPRPGFGFGL HLTQVGIASP PHRGLQGPGL	120 180 240 300 360 420 650 720 780 900 960 1020 1080 1140 1200 1260 1320 1380
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50 55 60 65 70	MTVLEESSIS MSSVTTTQVP IANKNTPSLA ELSGSISSPS FSQLQPSSEL SYLESSLISH DQISALDGHV TEVPLNTSTE VDTPTLATA VPPSVDTGPC IFAVKSTQG DDNPVQLIYP ESQSNNLMVI FDFAKQNLGQ PSDADSTVSE SRPPEASRRV NKIRLRAKRR SRIKRSPKPR QTPSSVELGR GVPPGLPND IGAQPVEIPP GYPTSSTEDL Seq ID NO: Protein AC 1   MAPRPLGPLV DPEDEEDEESE DPEVDLLEIG VVVANKQDLS	IMSSVVADFS PAHGRLSVPA VRDPSVFTPY EAPASLSIMP PLNTIMLLPS ESAVTALVPP SVLASFSKAI VSTTSTGAT PPYVCDITVP SGPFVYTAIS NFTQRIEKGL LUNGSEVSELL SGSCRUGGERA PSKIQLIAMQ GHYEFPVVDD RKHQVNGCPA YPALPPPASQ TPSQEERRAT PQQPGASASAI OPGHSSASLI 314 Protei CCESSION #: 11   LALGGAAAVI ALEGLEQREV GSQNLRFYM	FEEDPQVFN SLDPTAGSLS SLDSPTSQS RSEVSPWSSS RSEVSPWSSF GSESFDILTA PTGTVLITDA GGPLDSTLMG DAYLITVILA VINVLINSKL MTALFEVKH MTALFEVKH MTALFEVKH MTALFEVKH MVIVILYW EPAPLPGPLK TPGAVNDGRS PIPAPPVRGR PIPAPPVRGR DAEKDRLITT YIPPOFSIEE QWGSFYSPA WPSYGEDEAG KAIREELLRL  SEQUENCE BACO4820.1 21   GSVLFILMKT LVLGLDGAGK EFVSEVDVLA	TLFPSRPIVP TLFPSRPIVP VAETQVTPSS FSDQERSSFS FSDLEFFUA GIQATSPLTT YLPSGSSFVS DAASQSPPES RRAVQEYIIT VRDQTPLILS HQGTVNLTVQ YLGYPVLQIA VSTRRRWRR MDLQRAAIIL LCRTDKIDFO HRAPQSGPPL SPADRVAESN RVYRRAQMQI DSDGTYRPP ARQTHISLLD TANNPCSRYE EMPSVARPR REAVPRTSG SQKQSTVQNF	LSSRSMEISE LSSRSMEISE VTTAFFSVIT EHKPRGALDF FDSSDLQSSQ STVSLTDSEA VHTTPILTES EATPFPLPTE SAAPPLPSLR AIKEVLRIHF VKPSFLVPES ILNITISSSR EPFQYPQLNL ATVAAGNSVV GYRIQGVIAQ PDTVANIQGVIAQ PDTVANIQGVIAQ PDTVANIQGVIAQ PDTVANIQGVIAQ PDTVANIGGVIAG VSPSRSKIPS PSSGNEQHSS KINKEIQTALL DKILDPTASV GVHNSAYIGC DAFALVAPSS DYGMTPPTGP VGGTTGSQIQ REPSAPSGNL HS	TSVGISAEVD TSVGISAEVD SILLDSSFSV ASSPFSTPPL LSLPSSTNLE HPTSAFIETT SLFSTLTPPD LTVVGPSLTP PVTAFTLEAT NRAVELKYYE RFQVQTVLQF VTPRGFVNI SQLLKSSNVR QVVNVSRLEG PVDRVKRPSP QKLQIPSVKG KNVHRGRVS ASIFEHVDRI RKKSEIEHR PSVFIEPRKS PSDPDLPADV QPASTAGVGP LPRPGFGGGL HLTQVGIASR PHRGLQGPGL	120 180 240 300 360 480 540 660 720 780 900 960 1020 1140 1200 1320 1320 1440 1482
50 55 60 65 70	MTVLEESSIS MSSVTTTQVP IANKNTPSLA ELSGSISSPS FSQLQPSSEL SYLESSLISH DQISALDGHV TEVPLNTSTE VDTPTLATAK LFTDPTFLVT VPPSVDTGFC IFAVKSTQGF TVLLGYMEKQ DDNPVQLIYP ESQSNNLWVI RFDFAKOHLGQ PSDADSTVSE SRPPEASRVR KIRLRAKRR SRIKRSPKPR GVPPGLPANS LQSTELVPPD IGAQPVEIPP GYPTSSTEDL Seq ID NO: Protein Ac 1   MAPRPLGPLV DPEDEEDEEF DFEVDLLEIG	IMSSVVADFS PAHGRLSVPA VRDPSVFTPY EAPASLSIMP PLNTIMLLPS ESAVTALVPP SVLASFSKAI VSTTSTGAT PPYVCDITVP SGPFVYTAIS NFTQRIEKGL LUNGSEVSELL SGSCRUGGERA PSKIQLIAMQ GHYEFPVVDD RKHQVNGCPA YPALPPPASQ TPSQEERRAT PQQPGASASAI OPGHSSASLI 314 Protei CCESSION #: 11   LALGGAAAVI ALEGLEQREV GSQNLRFYM	FEEDPQVFN SLDPTAGSLS SLDSPTSQS RSEVSPWSSS RSEVSPWSSF GSESFDILTA PTGTVLITDA GGPLDSTLMG DAYLITVILA VINVLINSKL MTALFEVKH MTALFEVKH MTALFEVKH MTALFEVKH MVIVILYW EPAPLPGPLK TPGAVNDGRS PIPAPPVRGR PIPAPPVRG LSGDTKERH DAEKDRLITT YIPPOFSIEE QWGSFYSPA WPSYGEDEAG KAIREELLRL  SEQUENCE BACO4820.1 21   GSVLFILMKT LVLGLDGAGK EFVSEVDVLA	TLFPSRPIVP TLFPSRPIVP VAETQVTPSS FSDQERSSFS FSDLEFFUA GIQATSPLTT YLPSGSSFVS DAASQSPPES RRAVQEYIIT VRDQTPLILS HQGTVNLTVQ YLGYPVLQIA VSTRRRWRR MDLQRAAIIL LCRTDKIDFO HRAPQSGPPL SPADRVAESN RVYRRAQMQI DSDGTYRPP ARQTHISLLD TANNPCSRYE EMPSVARPR REAVPRTSG SQKQSTVQNF	LSSRSMEISE LSSRSMEISE VTTAFFSVIT EHKPRGALDF FDSSDLQSSQ STVSLTDSEA VHTTPILTES EATPFPLPTE SAAPPLPSLR AIKEVLRIHF VKPSFLVPES ILNITISSSR EPFQYPQLNL ATVAAGNSVV GYRIQGVIAQ PDTVANIQGVIAQ PDTVANIQGVIAQ PDTVANIQGVIAQ PDTVANIQGVIAQ PDTVANIGGVIAG VSPSRSKIPS PSSGNEQHSS KINKEIQTALL DKILDPTASV GVHNSAYIGC DAFALVAPSS DYGMTPPTGP VGGTTGSQIQ REPSAPSGNL HS	TSVGISAEVD TSVGISAEVD SILLDSSFSV ASSPFSTPPL LSLPSSTNLE HPTSAFIETT SLFSTLTPPD LTVVGPSLTP PVTAFTLEAT NRAVELKYYE RFQVQTVLQF VTPRGFVNI SQLLKSSWVR QVNNVSRLEG PVDRVKRPSP QKLQIPSVKG RNVRHRGRVS ASIFEHVDRI RHKSEIEHHR PSVFIEPRKS PSUFIEPRKS PSUFIERR SYFIEPRKS PSUFIERR PHRGLQGPGL	120 180 240 300 360 420 600 660 660 720 780 840 1020 1080 1140 1200 1320 1340 1440 1482
50 55 60 65 70	MTVLEESSIS MSSVTTTQVP IANKNTPSLA ELSGSISSPS FSQLQPSSEL SYLESSLISH DQISALDGHV TEVPLHTSTE UTPTLATAK LFTDFTFLVT VPPSVDTGFC IFAVKSTQGF TVLLGYMEKQ DDNPVQLIYF ESQSNNLWVI FDFAKQHLGQ PSDADSTVSE SRPPEASRN VKIRLRAKRR SRIKRSPKPR QTPSSVELGR GVPPGLPANS LQSTELVPPD IGAQPVEIPF GYPTSSTEDL Seq ID NO: Protein Ac 1   MAPRPLGPLV DPEDEEDEEF DPEVDLLEIG VVVANKQDLS ELLS	IMSSVVADFS PAHGRLSVPA VRDPSVFTPY EAPASLSIMP PLNTIMLLPS ESAVTALVPP SVLASFSKAI VSTTSTGAAT SGPFVYTAIS NFTQRIEKGL LQNEVFQAEM VEDQDGERLS VGVVIPVLVV HNKDDILIIH ESSERDAGDK PSKIQLIAMQ GHYEFPVVDD RKHQVNGCPA YPALPFPASQ TPSQEERRAT PQQPQASAEA SRGSQYGGPG QPGHSSASI 11   CLALGGAAAVI LALGGAAAVI CALEGELEQREV GSQNLRPYWS EAMSMGELQE	FEEDPQVFN SLDPTAGSLS SLDPFTAGSLS SLDSPFTSQS RSEVSPWSSF GSESFDILTA PTGTVLITDA GPIDSTLMG DAYLITTVLA VINVLINSKL MTALFEVRKH MTALFEVRKH MVIVVLLYBK ERKLAQLLSE AVKSSDLINK MVIVVILYBK EPAPLPGPLK TPGAVNDGRS PIPAPPVQRB LSSGDTKERH DAEKDRLITT YIPPOPSIEE QWGSFYSPAQ PFAARGIYSE WPSYGEDEAG KAIREELLRL  1 SEQUENCE BACO4820.1 21   GSVLFILWKT LVIGLDGAGK EFVSEVDVLX LELGLQAIDNO	TLFPSRPIVP TLFPSRPIVP VAETQVTPSS FSDQERSSFS FSDLEFFUA GIQATSPLTT YLPSGSSFVS DAASQSPPES RRAVQEYIIT VRDQTPLILS HQGTVNLTVQ YLGYPVLQIA VSTRRRWRR MDLQRAAIIL LCRTDKIDFO HRAPQSGPPL SPADRVAESN RVYRRAQMQI DSDGTYRPP ARQTHISLLD TANNPCSRYE EMPSVARPR REAVPRTSG SQKQSTVQNF	LSSRSMEISE LSSRSMEISE VTTAFFSVIT EHKPRGALDF FDSSDLQSSQ STVSLTDSEA VHTTPILTES EATPFPLPTE SAAPPLPSLR AIKEVLRIHF VKPSFLVPES ILNITISSSR EPFQYPQLNL ATVAAGNSVV GYRIQGVIAQ PDTVANIQGVIAQ PDTVANIQGVIAQ PDTVANIQGVIAQ PDTVANIQGVIAQ PDTVANIGGVIAG VSPSRSKIPS PSSGNEQHSS KINKEIQTALL DKILDPTASV GVHNSAYIGC DAFALVAPSS DYGMTPPTGP VGGTTGSQIQ REPSAPSGNL HS	TSVGISAEVD TSVGISAEVD SILLDSSFSV ASSPFSTPPL LSLPSSTNLE HPTSAFIETT SLFSTLTPPD LTVVGPSLTP PVTAFTLEAT NRAVELKYYE RFQVQTVLQF VTPRGFVNI SQLLKSSWVR QVNNVSRLEG PVDRVKRPSP QKLQIPSVKG RNVRHRGRVS ASIFEHVDRI RHKSEIEHHR PSVFIEPRKS PSUFIEPRKS PSUFIERR SYFIEPRKS PSUFIERR PHRGLQGPGL	120 180 240 300 360 480 540 660 720 780 900 960 1020 1140 1200 1320 1320 1440 1482
50 55 60 65 70	MTVLEESSIS MSSVTTTQVP IANKNTPSLA ELSGSISSPS FSQLQPSSEL SYLESSLISH DQISALDGHV TEVPLNTSTE VDTPTLATS VPDTPTLATV VPPSVDTGPC IFAVKSTQGP TVLLGYMEKQ DDNPVQLIYP ESQSNNLMVI FDFAKQNLGQ PSDADSTVSE SRPPEASRRV NKIRLRAKRR SRIKRSPKPR QTPSSVELGR GVPPGLPND IGAQPVEIPP GYPTSSTEDL Seq ID NO: PTOTEIN AC 1 MAPRPLGPLW DPEDEEDEEF DPEVDLLEIG VVVANKQDLS ELLS Seq ID NO:	IMSSVVADFS PAHGRLSVPA VRDPSVFTPY EAPASLSLMP PLNTIMLLPS ESAVTALVPP SVLASFSKAI VSTTSTGAAT PSYVCDITVP SGPFVYTAIS NFTQRIEKGL LNGSEVSELL LQNEVFQAEM VEDQDGERLS VGVVIFVLVM HNKDDILIH ESSERDAGDK PSKIQLIAMQ GHYEFPVVDD RKHQVNGCPA SYPALPFPASQ TPSQEERAT PQQPQASAEA SRGSQYGGPG QPGHSSASLI 314 Protei CCESSION #: 11     LALGGAAAVI   ALEELEQREV G GSQNLRFYWS G GSQNLRFYWS G EAMSMGELQF	FFEEDPQVFN SLDPTAGSLS SLDSPTSQS RSEVSPWSSL SDLSPTSQS RSEVSPWSSP GSESFDILTA PTGTVLITDA GGPLDSTLMG GDAYLITTVLA VINVLINSKL WINVLINSKL WINVLINSKL WINVLINSKL PRIPEGPLK TPGAVNDGRS PIPAPPVQRP LSSGDTKERH DAEKORLITT YIPPOPSIEE QWGSFYSPA WPSYGEDEAG KAIREELLRL  N Sequence BACO4820.1 21   GSVLFILMKT LVIGLDCAGK EFVSEVDVLA ELGLQAIDNO IN Sequence	TLFPSRPIVP TLFPSRPIVP VAETQVIPSS FSDQERSSFS FSPLVETFIL PSDSLEFVEA GIQATSPLTT YLPSGSSFVS DAASQSPES RAVQEYIIT VRDQTPLILS HQGTVNLTVQ YLGYPVLQIA VSTRRRMRR MDLQRAAIIL LCRTDKLDFQ DHTTPSENGD HRAPQSGPPL SPADRVAESN RVYRRAQMQII DSDGTYRRP ARQTHISLLD TANNPCSRYE EMPSVARPRE RREAVPRTSG SQKQSTVQNE  31   YFGRGGRERR STFLRVLSGM FVYDSADRLE REVFLLAASI	LSSRSMEISE LSSRSMEISE VTTAFFSVIT EHKPRGALDF FDSSDLQSSQ STVSLTDSEA VHTTPILTES EATPFPLPTE SAAPPLPSLR AIKEVLRIHF VKPSFLVPES ILNITISSSR EPFQYPQLNL ATVAAGNSVV GYRIQGVIAQ PDTVANIQGVIAQ PDTVANIQGVIAQ PDTVANIQGVIAQ PDTVANIQGVIAQ PDTVANIGGVIAG VSPSRSKIPS PSSGNEQHSS KINKEIQTALL DKILDPTASV GVHNSAYIGC DAFALVAPSS DYGMTPPTGP VGGTTGSQIQ REPSAPSGNL HS	TSVGISAEVD TSVGISAEVD SILLDSSFSV ASSPFSTPPL LSLPSSTNLE HPTSAFIETT SLFSTLTPPD LTVVGPSLTP PVTAFTLEAT NRAVELKYYE RFQVQTVLQF VTPRGFVNI SQLLKSSWVR QVNNVSRLEG PVDRVKRPSP QKLQIPSVKG RNVRHRGRVS ASIFEHVDRI RHKSEIEHHR PSVFIEPRKS PSUFIEPRKS PSUFIERR SYFIEPRKS PSUFIERR PHRGLQGPGL	120 180 240 300 360 480 540 660 720 780 900 960 1020 1140 1200 1320 1320 1440 1482
50 55 60 65 70	MTVLEESSIS MSSVTTTQVP IANKNTPSLA ELSGSISSPS FSQLQPSSEL SYLESSLISH DQISALDGHV TEVPLNTSTE VDTPTLATS VPDTPTLATV VPPSVDTGPC IFAVKSTQGP TVLLGYMEKQ DDNPVQLIYP ESQSNNLMVI FDFAKQNLGQ PSDADSTVSE SRPPEASRRV NKIRLRAKRR SRIKRSPKPR QTPSSVELGR GVPPGLPND IGAQPVEIPP GYPTSSTEDL Seq ID NO: PTOTEIN AC 1 MAPRPLGPLW DPEDEEDEEF DPEVDLLEIG VVVANKQDLS ELLS Seq ID NO:	IMSSVVADFS PAHGRLSVPA VRDPSVFTPY EAPASLSLMP PLNTIMLLPS ESAVTALVPP SVLASFSKAI VSTTSTGAAT PSYVCDITVP SGPFVYTAIS NFTQRIEKGL LNGSEVSELL LQNEVFQAEM VEDQDGERLS VGVVIFVLVM HNKDDILIH ESSERDAGDK PSKIQLIAMQ GHYEFPVVDD RKHQVNGCPA SYPALPFPASQ TPSQEERAT PQQPQASAEA SRGSQYGGPG QPGHSSASLI 314 Protei CCESSION #: 11     LALGGAAAVI   ALEELEQREV G GSQNLRFYWS G GSQNLRFYWS G EAMSMGELQF	FEEDPQVFN SLDPTAGSLS SLDPFTAGSLS SLDSPFTSQS RSEVSPWSSF GSESFDILTA PTGTVLITDA GPIDSTLMG DAYLITTVLA VINVLINSKL MTALFEVRKH MTALFEVRKH MVIVVLLYBK ERKLAQLLSE AVKSSDLINK MVIVVILYBK EPAPLPGPLK TPGAVNDGRS PIPAPPVQRB LSSGDTKERH DAEKDRLITT YIPPOPSIEE QWGSFYSPAQ PFAARGIYSE WPSYGEDEAG KAIREELLRL  1 SEQUENCE BACO4820.1 21   GSVLFILWKT LVIGLDGAGK EFVSEVDVLX LELGLQAIDNO	TLFPSRPIVP TLFPSRPIVP VAETQVIPSS FSDQERSSFS FSPLVETFIL PSDSLEFVEA GIQATSPLTT YLPSGSSFVS DAASQSPES RAVQEYIIT VRDQTPLILS HQGTVNLTVQ YLGYPVLQIA VSTRRRMRR MDLQRAAIIL LCRTDKLDFQ DHTTPSENGD HRAPQSGPPL SPADRVAESN RVYRRAQMQII DSDGTYRRP ARQTHISLLD TANNPCSRYE EMPSVARPRE RREAVPRTSG SQKQSTVQNE  31   YFGRGGRERR STFLRVLSGM FVYDSADRLE REVFLLAASI	LSSRSMEISE LSSRSMEISE VTTAFFSVIT EHKPRGALDF FDSSDLQSSQ STVSLTDSEA VHTTPILTES EATPFPLPTE SAAPPLPSLR AIKEVLRIHF VKPSFLVPES ILNITISSSR EPFQYPQLNL ATVAAGNSVV GYRIQGVIAQ PDTVANIQGVIAQ PDTVANIQGVIAQ PDTVANIQGVIAQ PDTVANIQGVIAQ PDTVANIGGVIAG VSPSRSKIPS PSSGNEQHSS KINKEIQTALL DKILDPTASV GVHNSAYIGC DAFALVAPSS DYGMTPPTGP VGGTTGSQIQ REPSAPSGNL HS	TSVGISAEVD TSVGISAEVD SILLDSSFSV ASSPFSTPPL LSLPSSTNLE HPTSAFIETT SLFSTLTPPD LTVVGPSLTP PVTAFTLEAT NRAVELKYYE RFQVQTVLQF VTPRGFVNI SQLLKSSWVR QVNNVSRLEG PVDRVKRPSP QKLQIPSVKG RNVRHRGRVS ASIFEHVDRI RHKSEIEHHR PSVFIEPRKS PSUFIEPRKS PSUFIERR SYFIEPRKS PSUFIERR PHRGLQGPGL	120 180 240 300 360 480 540 660 720 780 900 960 1020 1140 1200 1320 1320 1440 1482

	   MARRAGGARM	j PGSLLLPALL	 AAGVAPLSHD	   LPEPRSRASK	   IRVHSRGNLW	 ATGHFMGKKS	60
5	LEPSSPSHWG K	QLPTPPLRDQ	REQUISHDEEG	ILLERRALGV	SLSRPAPQIQ	AKKPPAĞIPĞ	120
J	Seq ID NO: Protein Acc			31	41	<b>51</b>	
10	RELRLRLDQL LARLDLERKI	AEMMELNDRP TANSARLEVE ESLEEEIRFL	 MVGGLAPGRR ASYIEKVRFL RDNLAQDLAT RKIHEEEVRE FADLTDAAAR	EQQNKALAAE VRQKLQDETN LQEQLARQQV	lnqlrakept Lrleaennla Hveldvakpd	KLADVYQAEL AYRQEADEAT LTAALKEIRT	60 120 180 240 300
15	GTNESLEROM	REQEERHVRE EGEENRITIP	AASYQEALAR VQTFSNLQIR	LEEEGQSLKD	<b>EMARHLQEYQ</b>	DLLNVKLALD	360 420 432
20	Seq ID NO: Protein Acc	317 Proteir ession #: F 11		31 	41 	51 	
25	I I SREQADEL IHDLVTDGLI THEEHTAVEK VRCSDCGLNV ARGLKSEGLY	LGGVEGAYIL TLYIETKAAE ISSLVRRAAL HKQCSKHVPN RVSGFTEHIE	PPIWKSYLYQ RESQRQPGCY YISKMTTNPI THNDNHFNYE DCQPDLKRIK DVKMAPDRDG ERLEAVHEVL	TLALRFGNOT YEHIGYATLL KTHNPKVHTP KVYCCDLTTL EKADISANVY	LNYRLFHDGK REKVSRRLSR RGPHWCEYCA VKAHNTQRPM PDINIITGAL	HFVGEKRFES SKNEPRKTNV NFMNGLIAQG VVDICIREIE KLYFRDLPIP	60 120 180 240 300 360 420
30			TLTTLHDMRY	ÖKTIAĞIFIE	NEDVLF		466
35		318 Protein cession #: 3 11		31	41	51	
	RRDRINNSLS DYRSLGFREC	ELRRLVPSAP LAEVARYLSI	VEKESADENG EKQGSAKLEK I EGLDASDPL HGNAGTTASP	AEILQMTVDH RVRLVSHLNN	LKMLHTAGGK YASQREAASG	Gyfdahalam Ahaglghipw	60 120 180 240
40	LPVVTSASKL IGAF	SPPLLSSVAS	LSAPPFSFGS				300 304
45	Protein Ac		NP_001927.2	•		<b></b>	
43			21     LVGSNPPQRN   IHDPEAKWIS			51   SVILLTPAED NTSTVLIEGK	60 120
50	QYAGWGPKGQ AHWWSPDGTR GPTHDLEMMP EDESEAWLHR	QLIFIFENNI LAYAAINDSR PDDPRMREYY QNEEPVFSKD	ITMVKWATST GRKFFFIRAI	IRVVSTGKEG GSIYPTVKPY KVAVTWLNRA PQGGRGKFYH	VIYNGLSDWL HYPKAGSENP QNVSILTLCD ITVSSSQPNS	YEEEILKTHI SISLHVIGLN ATTGVCTKKH SNDNIQSITS	180 240 300 360 420 480
55	PSHSMDPFLL DYNLPMQILK RGSGFQGTKL PAKGENQGQT	KCEGPGVPMV PATFTDTTHY LHEVRRRLGL PTCGSALSPI	TVHNTTDKKK PLLLVVDGTP LEEKDQMEAV TDFKLYASAF	MPDLETNEHV GSQSVAEKFE RTMLKEQYID SERYLGLHGL	KKAINDROMF VSWETVMVSS RTRVAVFGKE DNRAYEMTKV	VENCTYFSAS KVEYRDIEID HGAVVVKCDG YGGYLSTYIL AHRVSALEEQ QHLYRSIINF	540 600 660 720 780
60	PVECFRIQDK	LPTVTAKEDE	EED	MISDVIIFUE	311113331	. Qubicolini	803
			XP_087461.1	31	41	51	
65	ARARRRRRR	   AACPLPPVRG   RRLCNISVQF	 GAADAPGLLO QMLSSLLVRW	   VPSNASVNAS   GRPRGPQCDL	LLPSTNAHGE	   WPRRPPGPPS   APFAAAFHRV   GAPTALPAYP	60 120 180
70	AAEPPGPLWL	QGEPLHFCCI		: PGWRLNRKPI	ESTLVACEM	LVIVVWSVAA	240 299
		: 321 Protest cession #:	in Sequence NP_036393.1 21	31	41	51	
75	   MDLQGRGVPS   EFAAKFIVP	   IDRLRVLLMI   DVWASNYVDI	 L PHTMAQIMAI L ITEQADIAL	   QEVENLSGLS   RGAEVKGRCC	   TNPEKDIPV   HSQSELQVP	   RENGTTCLMA   VDRAYALKML   ALVTPAGKSY	60 120 180
80	ECQAQQTIS	L ASSDPQKTV		POIISDFVF	S EEHKCPVDE	REQLEETLPLI	240 280
		: 322 Protes ccession #: 11		31	41	51	

	   MWVLGIAATF   QSAGIMYRKS   LRPGLRTTIL	CASSAACLIA	SAGYQSFCSP				60 120 141
	Seq ID NO: Protein Acc	ession #: N		31	41	51	
	IGIISGLGYC YSLLFVGLLQ	VFVLTFSAPL PSFLPTVTIL LNIVIFGALL	ATVLSNRFGH SQYFGKRRSI RPIIIRGPAS	RLVVMLGGLL VTAVASTGEC PKIVIQENRK	vstgmvaasf Favfafapai Eaqymlenek	SQEVSHMYVA MALKERIGWR TRTSIDSIDS	60 120 180 240
	AAGVYIFIQS	PSLYIIPLGI VSLPAFTFAT IAGLAGPPLA	SLGIDQDRAA EFWGLMSCSI GLLVDQSKIY		VFGRIGAGFV GLTFHCLLKM MALAAVCLAL	LNREPIRKIY MSWALQKMSS	300 360 420 480 523
20		324 Protein ession #: N					
	1	11	21 	31 	41 	51 	
25	AVMKTIRIFQ QRAAPKVSPH VATEKEFFFV NIIRKAGETP	KLNYMLLAKR VKPEQKQMVA KVFNTLLKDK KINTLQTQPL	LQEEKEKVDK QQESIREGFQ FIPKRIIIIA GTIVNGLFVV	DEFNIATGKL QYKSVTKPKP KRCLPVMVLK RYYRHSGFLB QKVTEKKKNI HSTIKVIKAK	LSQAEMSPAA AKKPFTFETQ VNSASRVLDA LFDLSDNTGK	SAAIRNDVAK EGKQEMFHAT ESDQKVNVPL	60 120 180 240 300 343
30		325 Protein					
		ession #: 1		31	41	51	
35		 AVILCATVVQ GQRCLNPKSK		LCIGPGVKAV RKNF	   KVADIEKASI	Madenucoki 	60 94
	•	326 Protein	-				
40	1	11	21	31	41	51	
45	VHTKVKGIAE EYPTRRTLCS	VKEEIVENGV SDRGCKKGWM	KKLVHSVFDT DPQSKGIQTG	WFFHVIIFSY ADYTFPLQGN RCVVHEGNQK GLNITCTFHK	SFFVMTNFLK TCEVSAWCPI	TEGQEQRLCP EAVEEAPRPA	60 120 180 240
	NFSDVAIQGG ENNVEKRTLI NCCRSHIYPW	IMGIEIYWDC KVFGIRFDIL CKCCQPCVVN	NLDRWFHHCH VPGTGGKFDI EYYYRKKCES	PKYSFRRLDD IQLVVYIGST IVEPKPTLKY PIPGQPEEIQ	KTTNVSLYPG LSYFGLAAVF VSPVDESHIR	Ynpryakyyk Idplidtyss Mvnqqllgrs	300 360 420 480
50	SCLPSQLPES TNSRLRHCAY	HRCLEELCCR RCYATWRFGS	KKPGACITTS QDMADFAILP	ELFRKLVLSR SCCRWRIRKE	HVLQFLLLYQ	EPLLALDVDS	540 595
55	-	327 Protein cession #: 1	NP_001784.2				
33						51   LGKVFMGCPG VAPISVPENG	60 120
60	YELFGHAVSE DEDDAIYTYN	NGASVEDPMN GVVAYSIHSQ	ISI IVTDQND EPKDPHDLMF	DSPPEGVFAV HKPKFTQDTF TIHRSTGTIS QKYEAHVPEN	RGSVLEGVLP VISSGLDREK	VPEYTLŤIQA	180 240 300 360
65	PTSTATIVVH	VEDVNEAPVP	VPPSKVVEVQ	EGIPTGEPVC	VYTAEDPDKE	TNEAPFVLKL NQKISYRILR TGTLLLTLID	420 480 540
	TVVLSLKKFL GAVLALLFLL	KODTYDVHLS LVLLLLVRKK	LSDHGNKEQL RKIKEPLLLP	TVIRATVCDC EDDTRDNVFY	HGHVETCPGP YGEEGGGEED	WTAEVNEEGD WKGGFILPVL QDYDITQLHR	600 660 720
70				PDEIGNFIIE EWGSRFKKLA		APPYDTLLVF	780 829
		328 Protei					
75	1	cession #:	NP_002562.1	31	41	51	
75	WENNSCVEKK	VLGEKTGNPK	KFKINYTVAN		NFLFLCLQDT	EDNLEIVLHR TTPIQSMHCQ	60 120 162
80		329 Protei					
	1	11 	21 	31 	41 	51 	
		STGDADGPGG	PGIPDGPGGN	AGGPGEAGAT	GGRGPRGAGA	ARASGPGGGA	60

VYQETDDAC IPPOGROES GSMSQKSSPV VVMKTMQNM QVLGGPVSLG SIGTGRAMLG  THTMEVTYH RRGSRSYVPL ABSSSRPII DOVPSVSNS QLALDGGK HELRORDLIF ALQLEDSSY LARDLESTY DORSCTILL GSSPVROIT DGRRFARAP HTDGGVFT FRALLYTHY LERGPVTAQV VLQAAIDLTS 300 CSSPVROIT DGRRFARAP HTDGGVFT FRALLYSIVUL SGTTAAQVTT TAVVOMPTAE STORTPERVY PSEMOTIAL BMTPEATOM TPAEVSIVUL SGTTAAQVTT 420 CSSPVROIT DGRRFARAP HTDGGVFTAQVTT 420 CSSPVROIT ALSELTARAV STOLLARD BELLDVALV SGTTAAQVTT 420 CSSPVROIT ASSISTANT ALSELTARAV STOLLARD BELLDVALV SGTTAAQVTT 420 CSSPVROIT ASSISTANT ALPRANCAP HTDGGVFTAQVTT AND ALPRANCAP HTDGGVFTAQVTT ALPRANCAP HTDGGGVFTAQVT ALPRANCAP HTDGGGVFTAQVT ALPRANCAP HTDGGGVFT		PRGPHGGAAS VLLKEFTVSG	GLNGCCRCGA NILTIRLTAA	RGPESRLLEP DHRQLQLSIS	ylanppatpm Sclqqlsllm	EAELARRSLA WITQCFLPVF	QDAPPLPVPG LAQPPSGQRR	120 180
1 11 21 31 41 51	5				EK6			
PROPRIGADAS AGOGREPOSA REPOSILLOF RITAADRIQU GLSISSCLOQ LSLLAMITOC 1105  Seq ID NO: 331 Protein Sequence Protein Accession 8: NP.008859.1  15	_	1			31	41	51	
PROPRIGADAS AGOGREPOSA REPOSILLOF RITAADRIQU GLSISSCLOQ LSLLAMITOC 1105  Seq ID NO: 331 Protein Sequence Protein Accession 8: NP.008859.1  15		1	1	]	1 CONCRECET	CCBCBBCACA	ADACCDDCCA	60
Protein Accession #: NP_008859.1  11 21 31 41 51    MOLVLERCLL HLAVIGALLA VGATKYPENQ DMLGVSRQLE TRAMBRQLYP EMTEAGRIDG   MRGGGVSLEV SMCDPTLICA NASFSIALBP PGSQRVLEDG QVIMNSTII MGSVMGGDP   VYRQETDAC IPPOGCOPE GSMSRASRPY YVMKTMOMY QVLGGSVGLGS GSTGRANGG   VYRQETDAC IPPOGCOPE GSMSRASRPY YVMKTMOMY QVLGGSVGLGS GSTGRANGG   AQLIBDSOY LAEADLSTN POGDSSGRY VYMKTMOMY QVLGGSVGLGS GSTGRANGG   COSSPVGTT DGHRPTARAP MTTMGQVFTT EVVGTTFGQA PTARESGRITS VQVPTTEVIS   COSSPVGTT DGHRPTARAP MTTMGQVFT EVVGTTFGQA PTARESGRITS VQVPTTEVIS     COSSPVGTT DGHRPTARAP MTTMGQVFT EVVGTTFGQA PTARESGRITS VQVPTTEVIS     COSSPVGTT DGHRPTARAP MTTMGQVFT EVVGTTFGQA PTARESGRITS VQVPTTEVIS     COSSPVGTT DGHRPTARAP MTTMGQVFT EVVGTTFGQA PTARESGRITS VQVPTTEVIS     COSSPVGTT DGHRPTARAP MTTMGQVFT EVVGTTFGQA PTARESGRITS VQVPTTARAP MTTMGQA PTARESGRITS VQVPTTARAP MTTMGQA PTARESGRITS VQVPTTARAP MTTMGQA PTARESGRITS VQVPTTARAP MTTMGQA PTARESGRITS VQVPTTARAP VQVPTTARAP MTTMGQA PTARESGRITS VQVPTTARAP VQVPTTARAP MTTMGQA PTARESGRITS VQVPTTARAP VQVPTTARAP VQVPTTARAP MTTMGQA PTARESGRITA PTARESG	10	PRGPHGGAAS	AQDGRCPCGA	PGI PDGPGGN RRPDSRLLQF	RLTAADHRQL	QLSISSCLQQ	LSLLMWITQC	120
MOUNTAINCELL HLAVIGALIA VORTKVPRNO DIMGVSRQIR TKANNRQLYP ENTEAGRIDG   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100			cession #: 1	NP_008859.1	••	43	<b>5</b> 1	
MOLVILIGACIA HLAVIGALIA VGATIVIPRO) DMIGVSRQUE TRAMBIQLIP ENTENGRICO MORGOVISKY SINGEPTIJOR ANSFILAND PROSVUPED QUIVENNII INSONMOGOP VPQETDACI IPPOGGCES GSMSQKSEVY VWKTMOGYM QVLGGVSVA SIGTGRAMUS THREVTVIN ROSSSEVPL AMSSEVIL DEGOSTALI GRALVVIHTY LEGGVTAOV VLQALIDIS GSSEVPROTT DGRIFFLADA NITAGOVPTE VVGTTROOQ TARGESTIS VQVPTEVIS TAPVQMPTAS STCMTPEKDY VSEVACTILA BASTEATO TARVSIVVL SGITAQVIT TEWVETTARE LPIPEPEPED ASSINTESI TSICAPILLO TARLEURRO VPLOVINTY GSSEVTLDIV GGISSAELIQ AVPSGEDDAP ELIVSCQGGI PKEACHSISS PROGPAQRI CGSPVTLDIV GGISSAELIQ AVPSGEDDAP ELIVSCQGGI PKEACHSISS PROGPAQRI CGLIVLAAVV LASLIYRREL MKQDFSVPOL PHSSSHMLEL PRIPCSCPIG EMSPLLSQQ  Seq ID NO: 332 Protein Sequence Protein Accession 8: NP_001913.2  1 11 21  MSPLMMGFLL SCLGCKILPG AQGGFPRVCH TVDSLVNKEC CPRIGAESAN VCGSQQGRQQ CTEVRADTRE WSGPYLLEND DDRELMPEKF FIRTHCKTEN FACHACOBER FGRTGPACES KKPPVTRONI HISSISPERED FLAGALDLAKK RWHEDVITT GHALGLER FGRTGPACES ALPYMRATA RIBECTUCTO LEGGAREDDE TLISRNSEFS SMSTUCOSIA DYMITTLEN ALPYMRATO RIBECTUCTO LEGGAREDDE TLISRNSEFS SMSTUCOSIA DYMITTLEN TYDEFVRILLY SVAUDTLIGF GREVARIDES GGGRAVTHE RYBLICLERD LQALIGRESFY VALMOGLYPLL ARTICHENTA DATABANDH IPVVALMSFTD ALTDRAMPY INVEPEPRUT MEELFLITSD LGYSYAIDLE VSVEETPCHP TILLVANGT  Seq ID NO: 333 Protein Sequence Protein Accession 8: XP_059422-1  1 11 21  MMMHLPLFLL ASVTLPSICS HENPLSLEEL GSNTGIQVFN QIVKSSPIDEN IVISPHGIAS SEQ ID NO: 333 Protein Sequence Protein Accession 8: XP_059422-1  MMMHLPLFLL ASVTLPSICS HENPLSLEEL GSNTGIQVFN QIVKSSPIDEN IVISPHGIAS DILVANAVYK GUMKSRFOPE NIKKRTVAA DOKSTQVPNL AGLSCOST STABADHYNA THE PROTECTION OF THE PROTECTION	15	1	11	21	31 1	7*	ï	
WRGGGVSLKV SINGETLIGA NASFSIALNF PGSQNVLPDG QVIGNOVAL INGSOVAGOFO THIMEVTVIK RGSRSYVPL ABSSAFILI DQVPFSVSVS QLRALDGGK HPLRRQPLFF ALGEBRANG THIMEVTVIK RGSRSYVPL ABSSAFILI DQVPFSVSVS QLRALDGGK HPLRRQPLFF CASSAVEL ABSSAVEL ABSSAFILI AVSGAVEL ABSSAVEL ABSAVEL ABSSAVEL ABSSA	13	MULVI KRCIA	HLAVIGALLA	VGATKVPRNO	DWLGVSROLR	TKAWNRQLYP	EWTEAQRLDC	60
VYPOGTODAC IPPOGGCES GSHSQKSSPY VWKTNOGYM QVLGGDYSGL SIGTGRANLG THMENTVIN ROSSSTYPL ABSABITI DOYPSSVS QLALLDGGK HELROPLIF ALQLEDPSGY LABALISTIN DPGDSSTLL BRALVYHTY LEGGVTAGV VLQALTELTS GSSPYRDTT DGRIPFARAP MITAGRYFT EVGTTOQA PTABESGTTS VQPTTEVIS TAPVOMPTAS STOMTPEKUP VSEVAGTILA BMSTPEATOM TPABESTVIL SGTTAAQVTT TEWVETTARE LPIPEPEGPD ASSINESSI TSGLOPLIGO TALLUNGQ VLQUVLHYY GSPSYTLDIV GGISSAELIQ AVPSGEGDAP ELTVSCQGGL PKEACMEISS PGCOPPAQRI CSSPSYTLDIV GGISSAELIQ AVPSGEGDAP ELTVSCQGGL PKEACMEISS PGCOPPAQRI GSPSYTLDIV GGISSAELIQ AVPSGEGDAP ELTVSCQGGL PKEACMEISS PGCOPPAQRI THE STOMTPEKUP VSEVAGTILAS BMSTPEATOM TPABESTVIL SGTTAAQVTT GSPSYTLDIV GGISSAELIQ AVPSGEGDAP ELTVSCQGGL PKEACMEISS PGCOPPAQRI THE STOMTPEKUP VSEVAGTILAS BMSTPEATOM TPABESTVILLS GSPSYLLDSQQ  Seq ID NO: 332 Protein Sequence Protein Accession 8: NP_001913.2  1		WRGGOVSLKV	SNDGPTLIGA	NASFSIALNF	PGSQKVLPDG	QVIWVNNTII	NGSQVWGGQP	120
ALQUINDESTY LAEADLSYTM DEGOSSTILI SEALVATHITY LERGEPTIAQV VLQAAIPLES  GISPYDGTT DORPHTAEAP NITAGOVETT EVVCTTPOQA PLAEPSGITS QUVOTTEVIS  TAPVQMPTAE STGMIPEKVP VSEVMGTILA EMSTPEATCH TPARVSIVVL SCITAQVITT  TRAVETTARE LEIPEREGED ASISMISTESI TSSIGUILDG TALRILVERQ VULCULTRY  GSFSVTLDIV QGISABEILQ AVPSGEDDAP ELTVSCQGGL PKEACHEISS PGCOPPAQRL  GOPLPSPAC QULVINGILKG GSGTYCLINNS LAUTSILAVY STQLINGVGE AGLQVPLIV  VLOVUPSPAC QULVINGILKG GSGTYCLINNS LAUTSILAVY STQLINGVGE AGLQVPLIV  SEQ ID NO: 332 Protein Sequence  Protein Accession 8: NP_001913.2  1		VYPOETDDAC	IPPDGGPCPS	GSWSOKRSFV	YVWKTWGQYW	QVLGGPVSGL	SIGTGRAMLG	
CGSSPVETT DORRPTAEAB NTTAGOVET EVYCTTROQA PTARSSISTS VOVPTEVIS TAPOVETA TAPOVETAE LPIREPEGED ASSINSTES! TOSLOPLOG APPRAISE THANDER THE METATAE LPIREPEGED ASSINSTES! TOSLOPLOG ATTAINTY TEMVETTAE LPIREPEGED ASSINSTES! TOSLOPLOG ATTAINTY TEMVETTAE LPIREPEGED ASSINSTES! TOSLOPLOG ATTAINTY STOLING COPPAGE.  25 COPPLEYBRA COLUMBILED GESTYCLING LADTISLAVY STOLINGOG ACCOPPAGE.  30 POTOLINAV LASLIYRREL MKODFSVPOL PHSSSMURL PRIFCSCPIG EMSPLLSOQO  31 PROTEIN ACCESSION #: NP. 001913.2  1 1 21  1 1 21  1 1 1 51  1 1 1 1 51  1 1 1 51  1 1 1 51  1 1 1 51  1 1 1 51  1 1 1 51  1 1 1 51  2 1 1 1 51  3 1 1 51  3 1 1 51  3 1 1 51  3 1 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4 1 51  4	20	THIMEVIVYH	RRGSRSYVPL	AHSSSAFTIT	DOVPFSVSVS	QURALIXGONK	HYLKNOPLTF	
TAPUQNPTIAE STGMTPEKUP VSENGTILA EMSTERATGY TRANSLIVE STTMAQUTT TENVETTARE LIPEPEGGD ASSINSTEST ISSIGNILOS TATLELUKRO, VPLOCULRY, GSPSYTIDIV QGIESABELIQ AVPSGEGDAP ELTVSCQGCL PKEACHEISS PGCQPPAQRL GSPSYTIDIV QGIESABELIQ AVPSGEGDAP ELTVSCQGCL PKEACHEISS PGCQPPAQRL GILLVLMAVV LASLIYRRIL MKQDFSVPQL PHSSSMURL PRIFCSCPIG EMSPLLSQQQ  Seq ID NO: 312 Protein Sequence Protein Accession #: NP_001913.2  1	20	ALQLHDPSGY	LAEADLSYTW	DFGDSSGTLI	ENGTTPGOA	PTARPSGTTS	VOVPTTEVIS	
25 GSPSYTIDIV QGIESAREIQ ANY SEGGEDAP ELTVISOGGE PERCOLESS PECOPPAÇAE  GULVIMAVV LASLIYRRE MKODFSVPQL PHSSSHMERL PRIFCSCPIG EMSPLLSQQ  OT POTEIN ACCESSION 8: NP.001913:2  30 Protein Accession 8: NP.001913:2  31 11 21 31 41 51  11 27 31 41 51  11 27 31 41 51  11 27 31 41 51  11 27 31 41 51  11 27 31 41 51  11 27 31 41 51  12 31 41 51  13 41 51  14 51  15 51 51  16 51 51  17 6 51 51  18 6 51 51  19 6 661  35 KKPPVIRONI HELSPORRO PICALDLAKK SWRDDYVIT GIMUGLIGH GTOPOFANCS  KKPPVIRONI HELSPORRO PICALDLAKK SWRDDYVIT GIMUGLIGH GTOPOFANCS  VYDFFWILHY YSVRDTLLGP GEGARDEDP TILISPASSES SURVICUSED DYMHLYTLON  ALPYMPAGT RECONCIDO GEGARDEDP TILISPASSES SURVICUSED DYMHLYTLON  40 LAPIGNBRWY MWDFFPPVY HELFILISDE LOKSTNEPPP GUSTFSFRM LEGFDKADGT ALPYMPAGT GRECONCIDO GEGARDEDP TILISPASSES SURVICUSED DYMHLYTLON  VALVULEVUL AFLOYRRIKK GYPTLMETHL SKRAYTERA  Seq ID NO: 333 Protein Sequence  Protein Accession 8: XP.05942:1  1 11 21  1 11 21  1 11 11  1 11 11  1 11 11  1 1 11  1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		CGSSPVPGTT	DONKPIALAP	USEUMOTTIA	EMSTPEATON	TPARVSIVVL	SGTTAAOVTT	420
GSPSYTLDIV QGISABEILQ AVPSGEDDAP ELTVSCOGGL PREACHERS PCCOPPAGE  COPUPSPAC QUILDIGLING GSGTYCLING LATTINSLAVY STOLINGOG AGLIQVPLIV  GILLVIMAVV LASLIYRRIL MKQDFSVPQL PHSSSMURL PRIFCSCPIG EMSPLLSQQQ  Seq ID NO: 312 Protein Sequence  Protein Accession #: NP_001913.2  1		<b>PEUDIFFADE</b>	LOTOCOCCO	ASSIMSTESI	TGSLGPLLDG	TATLRLVKRO	VPLDCVLYRY	480
GULUMANV LASLIYERRL MKQDFSVPQL PHSSSMALRL PRIFCSCPIG EMSPLLSQQ  Seq ID NO: 332 Protein Sequence  Protein Accession 8: NP_001913.2  1		CCPSVTI.DIV	OGIRSAEILO	AVPSGEGDAP	ELTVSCOGGL	PKEACMEISS	PGCQPPAQRL	540
Seq ID NO: 332 Protein Sequence  Protein Accession 8: NP_001913.2  1	25	CODVI.DSDAC	OLVIHOILKG	GSGTYCLNVS	LADINSLAVV	STOLIMPGOR	MORGOALPIA	600
Seq ID NO: 332 Protein Sequence  Protein Accession 8: NP_001913.2  1 11 21 31 41 51    MSPLMMGPLL SCLGCKILDG AQQGFPRVCM TYDSLVNKEC CPRIGAESAN VCGSQQGRQQ  (CTEVRADTRP WSGPYILRNQ DDRELMPRKP THRICKCTON PAGYNCOGCK FGMTGENCER RKRPVIRONI HSLSPQEREQ FLGALDLAKK RYHDVITT QHMLGLIGEN GTOPGANGS ALPYNNATG RHECDVCTOQ LFGARAPDDP TLISRNSRFS SWETVCOSLD DYNNLTULCN GTYEGLERN QMGRNSMKLP THROTECLE LQKFUNERFF QNSTFSFRNA LEGGPANGTH SCHOOL LONGWINSHLP LTMGIRECLE LQKFUNERFF QNSTFSFRNA LEGGPANGTH SCHOOL LONGWINSHLP LTMGIRECLE LQKFUNERFF QNSTFSFRNA LEGGPANGTH SCHOOL LONGWINSHLP LTMGIRECLE LQKFUNERFF QNSTFSFRNA LEGGPANGTH SCHOOL LAPIGNAMM NWIPFPPFVT NEELFLISDQ LQYSYAIDLP VSVEETPGMP TTLLVVMGTL 461  40 LAPIGNAMM NWIPFPPFVT NEELFLISDQ LQYSYAIDLP VSVEETPGMP TTLLVVMGTL 461  Seq ID NO: 333 Protein Sequence  Protein Accession #: KP_059422.1    MNHLPLFLL ASVTLPSICS HFMPLSHLEL GSNTGIQVFN QIVKSRPHDN IVISPHGIAS VLUMHQLGAD GRIKKQLAMV MRYGVNGVGK ILKKINAIV SKKNKDIVTV ANAMFVKNAS EIEVPFVTHN KVMPCQCYBN NVEEDBASAC DSINAWVINE TEMBINILS PDLIDGVITA 18  50 LVLVNNVYFK GLMKSRFQPE NTKKRTFVAA DGKSVQVPLL AQLSVPCGS TSARNDLMYN 24  FIELPYFTHR KVMPCQCYBN NVEEDBASAC DSINAWVINE TRIMBITISH SPLLIDGVITA 30  GVLLVNNVYFK GLMKSRFQPE NTKKRTFVAA DGKSVQVPL AQLSVPCGS TSARNDLMYN 37  FIELPYHGES ISMLIADTE STFIDATIP HISTKTIDSH MSIMVPKNVQ VILDRFTAVA 30  GVLLVNNVYFK GLMKSRFQPE NTKKRTFVAA DGKSVQVPL AQLSVPCGS TSARNDLMYN 39  55 Seq ID NO: 334 Protein Sequence  Protein Accession #: XP_040512.2  1 11 21 31 41 51    MRQNDTRNGR IVLISGRSF CSIFSVLPYR DSTQVGLKL DGGRGTGAV KIKLIGLEG GSDLGDFMDY DPNLLDDPQN PGCHRKRVLI FPSYMTTVID YMRSDLKKD MNSTFKEKFP HISTKTIDSH MSIMVPKNVQ VILDRFTAVA 30  GSDLGDFMDY DPNLLDDPQN PGCHRKRVLI FPSYMTTVID YMRSDLKKD MNSTFKEKFP HISTKTIDGK AGRICAN STRIFFARDA SCHOOL STRIPP		GILLVLMAVV	LASLIYRRRL	MKQDPSVPQL	PHSSSHWLRL	PRIFCSCPIG	ENSPLLSGQQ	
1 1 21 31 41 51		V						901
1 1 21 31 41 51		Sec ID NO:	332 Protei	n Sequence				
1   1   21   31   41   51	30	Protein Ac	cession #:	NP_001913.2				
SECTEVRADTRP MSGPYILENQ DDRELMPRKF FIRTCKCTCH PAGYNGGOCK FORTGPNCER  KERVYLRONI HSLSPQEREQ FIGALDLAKK RYHEPYVITT QHMIGLIGER GTOPGANCS  VYDFFVMLHY YSVRDTLIGP GRPYBAIDFS HGGPAFVTHH RYHLLCLERD LQRLIGNESF  ALPYMFATG RECDVCTDQ LPGAARPDDP TLISENSRSS SWETUCSUD DYHLHYLLON  GTYEGLIRRN QMGRISMICH TLKDIRDCLS LQRFDNPPFP QNSTFSFRNA LEGFDKADGT  LDSQUMSLEN LVESTLINGTN ALPHSAANDP ITLISENSRSS SWETUCSUD DYHLHYLCN  SEQ ID NO: 333 Protein Sequence  Protein Accession #: XP_055422.1  1 1 21 31 41 51    MNMHLPLFILL ASVILPSICS HFMPLSLEEL GSNTGIQVFN QIVKSRPHDN IVISPHGIAS 100 100 100 100 100 100 100 100 100 10					31	41	51	
SECTEVRADTRP MSGPYILENQ DDRELMPRKF FIRTCKCTCH PAGYNGGOCK FORTGPNCER  KERVYLRONI HSLSPQEREQ FIGALDLAKK RYHEPYVITT QHMIGLIGER GTOPGANCS  VYDFFVMLHY YSVRDTLIGP GRPYBAIDFS HGGPAFVTHH RYHLLCLERD LQRLIGNESF  ALPYMFATG RECDVCTDQ LPGAARPDDP TLISENSRSS SWETUCSUD DYHLHYLLON  GTYEGLIRRN QMGRISMICH TLKDIRDCLS LQRFDNPPFP QNSTFSFRNA LEGFDKADGT  LDSQUMSLEN LVESTLINGTN ALPHSAANDP ITLISENSRSS SWETUCSUD DYHLHYLCN  SEQ ID NO: 333 Protein Sequence  Protein Accession #: XP_055422.1  1 1 21 31 41 51    MNMHLPLFILL ASVILPSICS HFMPLSLEEL GSNTGIQVFN QIVKSRPHDN IVISPHGIAS 100 100 100 100 100 100 100 100 100 10		1	I	1	1		HOCEOOCECO	60
NEMPURION HISLSPORED FIGALDLAKK RYHDYVITT OMMGLIGHN GTOPOFANCE  VENTYMENT SYNDTLIGE FIGALDLAKK RYHDYVITT OMMGLIGHN GTOPOFANCE  ALPYWNPATG RNECDVCTDQ LEGAARPODP TILISRNSRES SWETVCOSLD DYNHLVTLON  GTYEGLIRRN OMERSWKLP TIKDIRCLS LQKPDNPPFP ONSTEPRNA LEGEDPKADGT  GTYEGLIRRN OMERSWKLP TIKDIRCLS LQKPDNPPFP ONSTEPRNA LEGEDPKADGT  LAPIGHRMY NNVPPPPPVT NEELFLITSDQ LGYSVAIDLP VSVEETPGWP TILLVVMGTL  SEQ ID NO: 333 Protein Sequence  Protein Accession #: XP_OS9422.1		MSPLWWGFLL	SCLGCKILPO	AQGQFPRVCM	TVDSLVNKEC	CPRIGAESAN	FCWTCDNCER	120
ALPYMNATO RICCOVCTOQ LEGALARDDS HIGGRAFYTWH RYHLLCLERD LORLIGNESS ALPYWNATOR RICCOVCTOQ LEGALARDDD TLISBNSRS SWETCOSLD DYNHUTLCN GTYEGLIRN QMGRNSMKLP TLKDIRDCLS LQKPONPPFF QNSTESFRNA LEGFDKADGT LDSQVMSLIN LVHSFLAGTN ALPESANDDI ITVULHSFID AIFDEMNKRP NPPADAWPQE LDSQVMSLIN LVHSFLAGTN ALPESANDDI ITVULHSFID AIFDEMNKRP NPPADAWPQE LAFLGNERW MVDPFPPPVT NEELFLISDQ LGYSYAIDLP VSVEETPGWP TTLLVVMGTL SEQUENCE PROTEIN ACCESSION #: XP_059422.1  Seq ID NO: 333 Protein Sequence Protein Accession #: XP_059422.1  MNWHLPLFLL ASVILPSICS HENPLSLEEL GSNTGIQVFN QIVKSRPHDN IVISPHGIAS OVIGMIQUGAD GRTKKQLAMV MRYGVNGVGK ILKKINKAIV SKKNKDIVTV ANAVFVKNAS 12 LEVPFVTRN KDVFQCEVRN VMFPDASACD SINAWVENE TEDMIDNILLS PDLIDGVLFR QTULVMAVYFK GLMKSRFQPE NTKKRTFVAA DGKSYQVPML AQLSVFRCGS TSAPNDLWN QTULKEPLKV LGITDMFDDS KAMFAKITS ENLUNSHILQ KAKIEVSEDG TKASAATTAI GTLAKPSPWF IVDRPFLFFI RHNPTGAVFF MGQINKP  55 Seq ID NO: 334 Protein Sequence Protein Accession #: XP_040512.2  1 11 21 31 41 51    MRQHDTRNGR IVLISGRSF CSIFSVLPYR DSTQVGDLKL DGRQSTGAV SLKELIGLEG GO SELGADGKTV SYTQFLLPTN AFGARRNTID STSSFSQFRN LSHRSLSIGR ASGTQGSLDT GSDLGDFMDY DPHLIDDPOW PCKHKRVLI FPSYMTVID YVKPSDLKKD MNETFFEKFP HIKLTLSKIR SLKEPENKLA QEDCGLEEPT VANAFYFEK LAKKRKINKOM KNETFFEKFP LLANKGSDL KKHEVKHLID KLEEKFPRLNR RELIAFEFPV LVALEPALHL PEHEVMPHYR 30 ACCESSION #: AAHO8826  Seq ID NO: 335 Protein Sequence Protein Accession #: AAHO8826  1 11 21 31 41 51    MTTLAGAVPR MMRPGFQQNY PRSGFPLEVS TPLGGGRVNQ LGGVFINGRP LPMHIRHKIV EMAHAGISPC VISRQLRVSH GCVSKILCRY QETGSIRPGA IGGSKPKVTT PDVEKKLEEP 12 KKAKNSIDGI LSERASAPQS DEGSDIDSEP DLPLKKROR SRTTFTAEQL EELERAFERT 2 GFSSYTDSFV PPSGPSNPNN STRAKSKRA AKKNSLOGG GGGGOSPGG SPSKPPASPG SHSNDDFDNW STRPRTSSN ASTISGRSP AKKNSLOGG GGGGOSPGG SPSKPPASPG SHSNDDFDNW STRPRTSSN ASTISGRSP GAGSYNCAPG CHEKSLETSDS PPHNDIHTPV FORWYTT POVENTER GRAVTOVET PVOKNTENG SKRYNCAPG CHEKSLETSDS PPHNDIHTPV FORWYTT PVOKNTENG SKRYNCAPG SKNYNCAPG SKNYN	35	CTEVRADIRE	, Machaller	DUKELWPKKE	PVHPDYVITT	OHWLGLLGPN	GTOPOFANCS	180
ALPYWNFATG RNECDYCTDQ LEGAARPODF TILISHNSRFS SWETYCOSLD DYNHLVTLOS  GTYEGLIRRN QMGRNSMLP TILKDIRDCLS LQKENDPFF QNSTFSPRNA LEGFDKARGT  LDSQVMSLINI LVHSFLIRGTN ALPHSAANDP IFVVLHSFTD AIFDEMMKRF NPPADAMPQE  LAPIGHRMY NNVPFPPVT NEELFLTSDQ LGYSYAIDLP VSVEETPGWP TILLVVMGTL  SEQ ID NO: 333 Protein Sequence  Protein Accession #: XP_059422.1  1 11 21 31 41 51	33	KKAPATKONI	YSVRDTLIG	GRPYRAIDES	HOGPAFVTWH	RYHLLCLERD	LORLIGNESF	240
TYEGLLERN OMERSHALP TALDIROCLS LOKPENPEFF ONSTESSENA LEGEPANDOE LDSQWMSLEN LUHSFLEGT ALPHSANADD FEVULHSTD ALFDEMMER NEPRADAPQE 40 LAPIGHRRY NWVPPPPPVT NEELFLTSDQ LGYSYAIDLP VSVEETPGHP TTLLVVMGTL  Seq ID NO: 333 Protein Sequence Protein Accession #: xP_059422.1  1 11 21 31 41 51    MRMHLPLFLL ASVTLPSICS HENPLSLEEL GSNTGIQVFN QIVKSRPHDN IVISPHGIAS VIJGMIQIGAD GRTKKQLAMV MRYGNGYGK ILKKINKAIV SKKNKDIVTV ANAVFVKNAS EIEVPFVTRN KDVFQCEVRN VNFEDPASAC DSINAWINE TERDIROLLS BEDLIGVUTR EIEVPFVTRN KOWFQCEVRN VNFEDPASAC DSINAWINE TERDIROLLS STAPHDLMYN QTDLKEPLKV LGITDMFDSS KAMFAKITES ENLEVSHLQ KAKIEVSEDG TKASAATTAI GTDLKEPLKV LGITDMFDSS KAMFAKITES ENLEVSHLQ KAKIEVSEDG TKASAATTAI LIARSSPPHF IVDRPFLFFI RHNPTGAVLF MGQINKP  55 Seq ID NO: 334 Protein Sequence Protein Accession #: XP_040512.2  1 11 21 31 41 51    MRQHDTRNGR IVLISGRRSF CSIFSVLPYR DSTQVGDLKL DGGRQSTGAV SLKEIIGLEG GSDLGDFMDY DPNLLDDPOW PCKHRKVLI FPSYMTUVLD YVKPSDLKKD MNSTFFEKEP HIKLTLSKIR SLKREMRKLA QEDCGLEEPT VAMAPYPSK LAKKGKINNQ NKELCGACV LLAAKIGSDL KKHEVKHLID KLEEKFRLNR RELIAFEFPV LVALEPALHL PEHEVMPHYR RIVQSS  65  Seq ID NO: 335 Protein Sequence Protein Accession #: AAH08826  1 11 21 31 41 51    MTTLAGAVPR MMRPGPGQNY PRSGFPLEVS TPLGGGRVNQ LGGVFINGR LPMHIRHKIV KRENPOMFSM EIRDKLLKDAD VORNTYPSV SISSILRSK FOKGEEEEAD LERKPAERESE INTOLENDAM EIRDKLLKDAD VORNTYPSV SISSILRSK FOKGEEEEAD LERKPAERESE KKAKKSIDGI LSERASAPOS DEGSDIDSEP DLPLKKRORS SRTTFTAEQL EELERAAEESE SHNDDFDNM STPRPRSSN ASTISGRSPN RAMRKQAGAN QMAAPHNILP GOFFPTAMPT SHNDDFDNM STPRPRSSN ASTISGRSPN RAMRKQAGAN GMARPHILP GOFFPTAMPT SHNDDFDNM STPRPRSSN ASTISGRSPN RAMRKQAGAN GMARPHILP GOFFPTAMPT SLSSEINPEN MEALLDININL LSSPTSLTVS TOSSPGTMMQ OTPCYSYAPP NTSLNSPSPN 6 SLSSEINPEN MEALLDININL LSSPTSLTVS TOSSPGTMMQ OTPCYSYAPP NTSLNSPSPN 6 SLSSEINPEN MEALLDININL LS		ALDYWNEATY	RNECDVCTDO	LFGAARPDDP	TLISRNSRFS	SWETVCOSLO	DYNHLVTLON	300
LDSQWASHIN LVHSPLNGTN ALPHISAANDP IFVVLHSFTD AIPDEMMRF NPPADAPPOE 448  LAPIGHNRMY NMVPPPPVT NEELFLISDQ LGYSYAIDLP VSVEETFGMP TILLVVMGTL  Seq ID NO: 333 Protein Sequence Protein Accession #: XP_059422.1		CTYPCLIRRY	OMGRNSMKLI	P TLKDIRDCLS	LOKPONPPFE	? QNSTFSFRNA	LEGFDKADGT	360
Seq ID NO: 333 Protein Sequence Protein Accession #: XP_059422.1  1	40	T.DSOVMST.HD	I LVHSFLNGTI	N ALPHSAANDP	IFVVLHSFT	) AIPDEWMKRE	Nbbadambde	420
Seq ID NO: 333 Protein Sequence Protein Accession #: XP_059422.1  1 11 21 31 41 51    MMMHLPLFLL ASVILPSICS HENPLSLEEL GSNTGIQVEN QIVKSRPHDN IVISPHGIAS VLGMLQLGAD GRTKKQLAMV HRYGVNGYGK ILKKINKAIV SKKNKDIVTV ANAVEVNAS EIEVPFVTRN KDVFQCEVRN VNFEDPASAC DSINAWVKNE TROMINDILS PDLIGGVLTR ELVLVNAVYFK GLMKSRFQPE NTKKRTFVAA DGKSYQVPML AQLSVFRCGS TSAPNDLWYN CTDLKEPLKV LGITDMFDSS KANFAKITRS ENLFWSHILQ KAKIEVSEDG TKASAATTAI  50 EVENTAME GUNDEN FOR STEPLSAIIP HISTKTIDSM MSIMVPRRVQ VILPKTAVA QTDLKEPLKV LGITDMFDSS KANFAKITRS ENLFWSHILQ KAKIEVSEDG TKASAATTAI 36 LIARSSPPWF IVDRPFLFFI RHNPTGAVLF MGQINKP  55 Seq ID NO: 334 Protein Sequence Protein Accession #: XP_040512.2 1 11 21 31 41 51    MRCHDTRNGR IVLISGRRSF CSIFSVLPYR DSTQVGDLKL DGGRQSTGAV SLKEIIGLEG GSDLGDFMDY DFNLLDDPQN PGGKHKRVLI FPSYMTTVID YVKPSDLKKD MNETPKEKEP HIKLTLSKIR SLKEMMRLA QEDCGLEEFT VANAFVYFEK LALKGKLNKQ NRKLCAGACV LLAAKIGSDL KKHEVKHLID KLEEKFRLNR RELIAFEFFV LVALEFALHL PEHEVMPHYR  65 Seq ID NO: 335 Protein Sequence Protein Accession #: AAHO8826 1 11 21 31 41 51    MTTLAGAVPR MWRPDFQONY PRGGFPLEVS TPLCQGRVNQ LGGVFINGFP LPMHIRHKIV KREMPGMFSM EIRDKLLKDA VCDRNTVPSV SSISRILRSK FGKGEEEEAD LERKELEESE 10 KKACHSIGGI LSERASAPGS DEGSDIDSEP DLPLKRKGRR SRTTFTAROL EELERAPERT 2KCACHSTORY TOPTOLOGY SING PLOYESTRE ALGRANDS SAYCLPSTRR CFSSYTDSFV PSSGSNFMN PTIGNGLSPO NSIRNINLSH SKTIFTAROL EELERAPERT 2KCACHSTORY STRPRTSSN ASTISGRLSP NSIRNINLSH SKTIFTAROL EELERAPERT 2KSTIFTSFY PSSGSNFMN PTIGNGLSPO NSIRNINLSH SKTIFTBROL EELERAPERT 2KSTIFTSFY PSSGSNFMN SKPAKSRSRA AKKKASLOSG GEGAGDSGS GPSKMPASPG SHSNODFONM STFRFRTSSN ASTISGRLSP INTEQDLGG COMPANYVPP SAANMASTLP 5SLSEISNPEN MENLLDNIAL LSSPTSTLVS TOSSFCTMOQ OFFCYSFAPP NTSLNSPSPN 6  80 YGKYTYGGSS MSPLEPMPIQ TLQDNKSYG CMSQNNCAPG LLKELLTSDS PPHRDIMTPV PDGVAQRPNS VLQQNVMGCP NSVMSTYGSG ASNNOOMPS SHTHPGHAQQ TSAAVGGPLP 7 PGVAQRPNS VLQQNVMGCP DVMSTYGSG ASNNOOMPS SHTHPGHAQQ TSAAVGGPLP 7 PGVAQRPNS VLQQNVMGCP DVMSTYSTGSG ASSNNOOMPS SHTHPGHAQQ TSAAVGGPLP 7	40	LAPIGHNRM	NMVPPPPPV	r NEELFLTSDQ	LGYSYAIDLE	VSVEETPGWE	TILLVVMGIL	
1 1 21 31 41 51    MNMHLPLFLL ASVILPSICS HFNPLSLEEL GSNTGIQVFN QIVKSRPHDN IVISPHGIAS   VIGMIQICAD GRTKKQLAMV WRYGYNGYGK ILKKINKAIV SKNKKDIVTV ANAVFVKNAS   EIEVPFVTRN KDVFQCEVRN VNFEDPASAC DSINAWVKNE TROMIDNILS PDLIDGVLTR     EIEVPFVTRN KDVFQCEVRN VNFEDPASAC DSINAWVKNE TROMIDNILS PDLIDGVLTR     EIEVPFVTRN KDVFQCEVRN VNFEDPASAC DSINAWVKNE TROMIDNILS PDLIDGVLTR     LVLVUNAVYFK GLMKSRFQPE NTKKRTFVAA DGKSYQVPML AQLSVFRCGS TSAPNDLWYN     FIELPYHGES ISMLIALPTE SSTPLSAIIP HISTKTIDSW MSIMVPKRVQ VILPKFTAVA     QTDLKEPLKV LGITDMFDSS KANFAKITRS ENLHVSHILQ KAKIEVSEDG TKASAATTAI     CONTROL   LIARSSPPWF IVDRPFLFFI RHNPTGAVLF MGQINKP     Seq ID NO: 334 Protein Sequence     Protein Accession #: XP_040512.2     CONTROL   LIARSSPPWF IVDRPFLFFI RHNPTGAVLF MGQINKP     MRQHDTRNGR IVLISGRRSF CSIFSVLPYR DSTQVGDLKL DGGRQSTGAV SLKEIIGLEG     GONTROL   LIARSSPR CONTROL   LIARSSPR CONTROL     CONTROL   LIARSSP CONTROL   LIARSSP CONTROL   LIARSSP CONTROL     CONTROL   LIARSSP CONTROL   LIARSSP CONTROL   LIARSSP CONTROL     CONTROL   LIARSSP CONTROL   LIARSSP CONTROL   LIARSSP CONTROL   LIARSSP CONTROL     CONTROL   LIARSSP CONTROL   LIA		Seq ID NO	: 333 Prote	in Sequence				
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VIGMIQIGAD GRYKKQLAMV MRYGVNGGK ILKKINKAIV SKKNKDIVTV ANAVVYNAS 12 EIEVPFVTRN KDVFQCEVRN VNFEDPASAC DSINAWKNE TRMIDNILS PDLIDGVLTR 18 LVLVNAVYFK GLMKSRFQPE NTKKRTFVAA DGKSYQVPML AQLSVFRCGS TSAPNDLWYN 24 FIELPYHGES ISMLIALPTE SSTPLSAIIP HISTKTIDSW MSIMVPKRVQ VILPKFTAVA 30 QTDLKEPLKV LGITDMFDSS KANFAKITRS ENLHVSHILQ KAKIEVSEDG TKASAATTAI 36 LIARSSPPWF IVDRPFLFFI RHNPTGAVLF MGQINKP 39  Seq ID NO: 334 Protein Sequence Protein Accession #: XP_040512.2  1		MNWHLPLFL	L ASVTLPSIC	S HFNPLSLEEL	GSNTGIQVF	N QIVKSRPHDI	IVISPHGIAS	60
LVLVNAVYFK GLMKSRFQPE NTKKRTFVAA DGKSYQVPML AQLSVFRCGS TSAPNDLWYN 24 FIELPYHGES ISMLIALPTE SSTPLSAIIP HISTKTIDSW MSIMVPKRVQ VILPKFTAVA 30 QTDLKEPLKV LGITDMFDSS KAMFAKITRS ENLHVSHILQ KAKIEVSEDG TKASAATTAI 36 LIARSSPPWF IVDRPFLFFI RHNPTGAVLF MGQINKP 39 SEQ ID NO: 334 Protein Sequence Protein Accession #: XP_040512.2  1		VICMICICA	D GRTKKOLAM	V MRYGVNGVGE	ILKKINKAI'	v skknkdivt	/ ANAVFVKNAS	120
FIELPYHGES ISMLIALPTE SSTPLSAIIP HISTRIIDSW MSIMYPKRVQ VILPKPTAVA JOTDIKEPIKV LGITDMFDSS KANFAKITRS ENLHVSHILQ KAKIEVSEDG TKASAATTAI 36 LIARSSPPWF IVDRPFLFFI RHNPTGAVLF MCQINKP  55 Seq ID NO: 334 Protein Sequence Protein Accession #: XP_040512.2  1 11 21 31 41 51    MRQHDTRNGR IVLISGRRSF CSIFSVLPYR DSTQVCDLKL DGGRQSTGAV SLKEIIGLEG GSDLGDFMDY DPNILLDDPQW PCGKHKRVLI FPSYMTVLD YVKPSDLKKD MNSTFKEKFP 18  GSDLGDFMDY DPNILLDDPQW PCGKHKRVLI FPSYMTVLD YVKPSDLKKD MNSTFKEKFP 18  HIKLTLSKIR SLKREMRKLA QEDCGLEEPT VAMAFYPYEK LALKGKLNG NRKLCAGACV LLAAKIGSDL KKHEVKHLID KLEEKFRLNR RELIAPEFFV LVALEPALHL PEHEVMPHYR 30  RLVQSS  56 Seq ID NO: 335 Protein Sequence Protein Accession #: AAH08826  1 11 21 31 41 51    MTTLAGAVPR MMRPGPGQNY PRSGFPLEVS TPLCQGRVNQ LGGVFINGRP LPNHIRHKIV KRENPGMFSW EIRDKLLKDA VCDNTVPSV SSISRILRSK FGRGEEEEAD LERKEAEESE 11  KKARHSIDGI LSERASAPOS DEGSDIDSEP DLPLKRKQRR SRTTFTAEQL EELERAPERT 24  KKARHSIDGI LSERASAPOS DEGSDIDSEP DLPLKRKQRR SRTTFTAEQL EELERAPERT 25  KKARHSIDGI LSERASAPOS DEGSDIDSEP DLPLKRKQRR SRTTFTAEQL EELERAPERT 26  EPTYGLSETS YQPTSIPQAV SDPSSTVERP QPLPPSTVJO STIPSNPDSS SAYCLPSTHH 30  FPEGGKSGKSP RRRAASMONN SKPAKSRSRA AKKKASLOSG GEGGGDSFGS GFSKMPASFG 45  SHSNDDFDNW STFRPRTSSN ASTISGRLSP IMTEQDDLGE GDVHSMVYPP SAAKMASTLP 76  SLSEISNPEN MENLLDNLNL LSSPTSLTVS TQSSPGTMOQ QTPCYSFAPP NTSLNSSPSN 65  SLSEISNPEN MENLLDNLNL LSSPTSLTVS TQSSPGTMOQ QTPCYSFAPP NTSLNSSPSN 65  SLSEISNPEN MENLLDNLNL LSSPTSLTVS TQSSPGTMOQ TTPCYSFAPP NTSLNSSPSN 65  SQRYNCAPG LLKKLLTDS PPHNDIMTPV 64  FVGNYTYGQSS MSPLPQMPIQ TLQDNKSSYG GMSQYNCAPG LLKKLLTSDS PPHNDIMTPV 64  FVGNYTYGGSS MSPLPQMPIQ TLQDNKSSYG GMSQYNCAPG LLKKLLTSDS PPHNDIMTPV 64  FVGNYTYGGSS MSPLPQMPIQ TLQDNKSSYG GMSQYNCAPG LLKKLLTSDS PPHNDIMTPV 64  FVGNYTYGGSS MSPLPQMPIQ TLQDNKSSYG GMSQYNCAPG SLLKGLLTSDS PPHNDIMTPV 64  FVGNYTYGGSS MSPLPQMPIQ TLQDNKSSYG GMSQYNCAPG SLLKGLLTSDS PPHNDIMTPV 64  FVGNYTYGGSS MSPLPQMPIQ TLQDNKSSYG GMSQYNCAPG SLLKGLTSDA PPHDDIMTPV 64  FVGNYTYGGSS MSPLPQMPIQ TLQDNKSSYG MSSNNOMONPS SHTHQFAQQ TSAVNGRPLP 76  FVGNYTYGGS MSPLPQMPIQ TLQDNKSSYG MSSNNOMONPS	50	EIEVPFVTR	N KDVFQCEVR	N VNFEDPASAC	DSINAWVKN	E TROMIDALL	S PDLIDGVLTK	
OTDLKEPLKV LGITDMFDSS KANFAKITRS ENLHVSHILQ KAKIEVSEDG TKASAATTAI  11	30	LVLVNAVYF	K GLWKSRFQP	E NTKKRIFVAF	DGKSIQVPR	M WOLDALKER	VILPKETAVA	300
Seq ID NO: 334 Protein Sequence Protein Accession #: XP_040512.2  1 11 21 31 41 51		PIECPINGE	S ISMLIALPI V IGITOMFOS	S KANFAKITRS	ENLHVSHIL	O KAKIEVSED	G TKASAATTAI	360
Seq ID NO: 334 Protein Sequence Protein Accession #: XP_040512.2  1 11 21 31 41 51    MRCHDTRNGR IVLISGRRSF CSIFSVLPYR DSTQVCDLKL DGGRQSTGAV SLKEIIGLEG GSDLGDFMDY DPNLLDDPQW PCGKHKRVLI FPSYMTVLD YVKPSDLKKD MRETFREKFP HIKLTLSKIR SLKREMRKLA QEDCGLEEPT VAMAFVYPER LALKGKLNKQ NRKLCAGACV LLAAKIGSDL KKHEVKHLID KLEEKFRLNR RELIAFEFPV LVALEFALHL PEHEVMPHYR RLVQSS  Seq ID NO: 335 Protein Sequence Protein Accession #: AAH08826  1 11 21 31 41 51    MTTLAGAVPR MMRPGPGQNY PRSGFPLEVS TPLGQGRVNQ LGGVFINGRP LPNHIRHKIV EMAHHGIRPC VISRQLRVSH GCVSKILCRY GETGSIRPGA IGGSKPKVTT PDVEKKIEEY KKACHSIDGI LSERASAPQS DEGSDIDSEP DLPLKRKQRR SRTTFTAEQL EELERAPERT KKACHSIDGI LSERASAPQS DEGSDIDSEP DLPLKRKQRR SRTTFTAEQL EELERAPERT LPTYQLSETS YQPTSIPQAV SDPSSTVRP QPLPPSTVO STIPSNPDSS SAYCLPSTHH PEGGKSGKSP RRRAASMONN SKPAKSRSRA AKKKASLOSG QEGGGDSFGS OFSKMPASFG SHSNDDFDNM STPRPRTSSN ASTISGRLSP IMTEQDDLGE GDVHSMVPP SAAKMASTLP SLSEISNPEN MENLLDNLNL LSSPTSLTVS TQSSPGTMOQ QTPCYSFAPP NTSLNSPSPN SUSSIESIENPEN MENLLDNLNL LSSPTSLTVS TQSSPGTMOQ QTPCYSFAPP NTSLNSPSPN SUSSIESIENPEN MENLLDNLNL LSSPTSLTVS TQSSPGTMOQ QTPCYSFAPP NTSLNSPSPN SUSSIESIENPEN MENLLDNLNL LSSPTSLTVS TQSSPGTMOQ GTPCYSFAPP NTSLNSPSPN SUSSIESIESPEN MENLLDNLNL LSSPTSLTVS TQSSPGTMOQ GTPCYSFAPP NTSLNSPSPN SUSSIESIESPEN MENLLDNLNL LSSPTSLTVS TQSSPGTMOQ GTPCYSFAPP NTSLNSPSPN SUSSIESIESPPSN MENLLDNLNL LSSPTSLTVS TQSSPGTMOQ GTPCYSFAPP NTSLNSPSPN SUSSIESPEN MENLLDNLNL LSSPTSLTVS TQSSPGTMOQ GTPCYSFAPP NTSLNSPSPN SUSSIESPEN MENLLDNLNL LSSPTSLTVS TQSSPGTMOQ GTPCYSFAPP NTSLNSPSPN SUSSIESPEN MENLLDNLT PVOVPLPHPH OMSALGGYSS VSSCNGYGRM GLLHQEKLPS 7		LIARSSPPW	F IVDRPFLFF	I RHNPTGAVLI	MGQINKP	•		397
Protein Accession #: XP_040512.2  1 11 21 31 41 51    WRQHDTRNGR IVLISGRRSF CSIFSVLPYR DSTQVGDLKL DGGRQSTGAV SLKEIIGLEG GOVERACKTV SYTOPLLPTN AFGARRNTID STSSFSOFFN LSHRSLSIGG ASGTQGSLDT 12  GSDLGDFMDY DPNLLDDPQW PCGKHKRVLI FPSYMTVID YVKPSDLKKD MNSTFKEKFP HIKLITLSKIR SLKREMRKLA QEDCGLEEFT VAMAVYPEK LALKGKLNKQ NRKLCAGACV LLAAKIGSDL KKHEVKHLID KLEEKFRLNR RELIAFEFPV LVALEPALHL PEHEVMPHYR 30  Seq ID NO: 335 Protein Sequence Protein Accession #: AAH08826  1 11 21 31 41 51    WITLAGAVPR MMRFGPGQNY PRSGFPLEVS TPLCQGRVNQ LGGVFINGRP LPNHIRHKIV GEMANHGIRPC VISRQLRVSH GCVSKILCRY QETGSIRPGA IGGSKPKVTT PDVEKKIEEY 12  KKAKHSIDGI LSERASAPQS DEGSDIDSEP DLPLKRKQRR SRTTFTAEQL EELERAFERT 22  KKAKHSIDGI LSERASAPQS DEGSDIDSEP DLPLKRKQRR SRTTFTAEQL EELERAFERT 23  HYPDIYTREE LAQRAKLTEA RVQVWFSNRR ARMKQAGAN QLMAFNHIG GGFPPTAMPT 36  TO LPTYQLSETS YQPTSIPQAV SDSSTVHRP QPLPPSTVHQ STIPSNPDSS SAYCLPSTH 33  GFSSYTDSFV PPSGPSNPMN PTIGNGLSPQ NSIRHNLSLH SKPIRVQNEG TGKSSWMMLN 43  SHSNDDFDNW STFRPRTSSN ASTISGRLSP IMTEQDDLG GDVFSMYPP SARMASTLP 7  80 YQKYTYGQSS MSPLPQMPIQ TLQDNXSSYG GMSQYNCAPG LLKELLTSDS PPHNDIMTPV 64  FVGNYTYGGSS MSPLPQMPIQ TLQDNXSSYG GMSQYNCAPG LLKELLTSDS PPHNDIMTPV 64  FVGNYTYGGSS MSPLPQMPIQ TLQDNXSSYG GMSQYNCAPG LLKELLTSDS PPHNDIMTPV 64  FVGNYTYGGSS MSPLPQMPIQ TLQDNXSSYG GMSQYNCAPG SLLKELLTSDS PPHNDIMTPV 64  FVGNYTYGGSS MSPLPQMPIQ TLQDNXSSYG GMSQYNCAPG SLLKELLTSDS PPHNDIMTPV 64  FVGNYTYGGSS MSPLPQMPIQ TLQDNXSSYG GMSQYNCAPG SLLKELLTSDS PPHNDIMTPV 64  FVGNYTYGGSS MSPLPQMPIQ TLQDNXSSYG GMSQYNCAPG SLLKGLLTSDS PPHNDIMTPV 64  FVGNYTYGGS MSPLPQMPIQ TLQDNXSSYG GMSQYNCAPG SLLKGLLTSDS PPHNDIMTPV 64  FVGNYTYGGSS MSPLPQMPIQ TLQDNXSSYG GMSQYNCAPG SLLKGLTSDS PPHNDIMTPV 64  FVGNYTYGGS MSPL								
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GSDLGFMDY DPNLLDPQW PCGKHKRVLI FPSYMTTVID YVKPSDLKKD MNSTFKEKFP HIKLTLSKIR SLKREMRKLA QEDCGLEEFT VAMAVYPEK LALKGKLNKQ NRKLCAGACV LLAAKIGSDL KKHEVKHLID KLEEKPRLNR RELIAFEFPV LVALEPALHL PEHEVMPHYR  65  Seq ID NO: 335 Protein Sequence Protein Accession #: AAH08826  1 11 21 31 41 51		1	1	1	1	1	Ì	
GSDLGFMDY DPNLLDPQW PCGKHKRVLI FPSYMTTVID YVKPSDLKKD MNSTFKEKFP HIKLTLSKIR SLKREMRKLA QEDCGLEEFT VAMAVYPEK LALKGKLNKQ NRKLCAGACV LLAAKIGSDL KKHEVKHLID KLEEKPRLNR RELIAFEFPV LVALEPALHL PEHEVMPHYR  65  Seq ID NO: 335 Protein Sequence Protein Accession #: AAH08826  1 11 21 31 41 51		MRQHDTRNG	R IVLISGRRS	F CSIFSVLPY	DSTOVGDLK	L DGGRQSTGA	V SLKEIIGLEG	60
HIKLTLSKIR SLKREMRKLA QEDCGLEEFT VAMAFVYFEK LALKGKLNKQ NRKLCAGACV LLAAKIGSDL KKHEVKHLID KLEEKFRLNR RELIAFEFPV LVALEPALHL PEHEVMPHYR  RLVQSS  Seq ID NO: 335 Protein Sequence Protein Accession #: AAH08826  1 11 21 31 41 51	60	VELGARGET	V SYTOPLLPI	'N AFGARRNTII	) STSSFSOFR	N LSHRSLSIG	R ASGTQGSLDT	120
LLAAKIGSDL KKHEVKHLID KLEEKFRLNR RELIAFEFPV LVALEFALHL PEHEVMPHYR  RLVQSS  Seq ID NO: 335 Protein Sequence Protein Accession #: AAH08826  1 11 21 31 41 51		GSDLGDFMD	Y DPNLLDDPC	W PCGKHKRVL	FPSYMTTVI	D YVKPSDLKK	D MNETPKEKPP	180 240
Seq ID NO: 335 Protein Sequence Protein Accession #: AAR08826  1 11 21 31 41 51		HIKLTLSKI	R SLKREMRKI	A QEDCGLEEP	T VAMAPVIPE	N LAUKGKLAK U 1.VALEPALH	I. DEHEVMDHYR	300
Seq ID NO: 335 Protein Sequence Protein Accession #: AAR08826  1 11 21 31 41 51			E KKHEVKHLI	D KLEEKPRUN	K KELIAPEFF	V DVKDBIAD.		306
Seq ID NO: 335 Protein Sequence Protein Accession #: AAH08826  1 11 21 31 41 51	65	KDVQ33						
Protein Accession #: AAR08826  1 11 21 31 41 51	-	Seg ID NO	: 335 Prote	in Sequence				
TO MTTLAGAVPR WMRPGPGQNY PRSGFPLEVS TPLGQGRVNQ LGGVFINGRP LPNHIRHKIV 60 EMAHNGIRPC VISRQLRVSH GCVSKILCRY QETGSIRPGA IGGSKPKVTT PDVEKKIEEY 12 KRENPGMPSW EIRDKILKODA VCDRNTVPSV SSISRILRSK FGKGEEEEAD LERKEAEESE 14 KKAKHSIDGI LSERASAPQS DEGSDIDSEP DLPLKRKQRR SRTTFTAEQL EELERAFERT 22 LPTYQLSETS YQPTSIPQAV SDPSSTVHRP QRUPPSTVHQ STIPSNPDSS SAYCLPSTRH GFSSYTDSFV PPSGPSNPMN PTIGNGLSPQ NSIRHNLSLH SKPIRVQNEG TGKSSWMLN 45 PEGGKSGKSP RRRAASMONN SKPAKSRSRA AKKKASLQSG QEGAGDSPGS OFSKMPASFG SHSMDDFDNW STFRPRTSSN ASTISGRLSP IMTEQDDLGE GDVHSMYYPP SAAKMASTLP SLSEISINPEN MENLLDNLNL LSSPTSLTVS TQSSPGTMQ QTPCYSFAPP NTSLNSPSPN 65 PGKYYTGQSS MSPLPQMPIQ TLQDNKSSYG GMSQYNCAPG LLKELLTSDS PPHNDIMTEV 66 PGYQYPTS VLGQNVMMGP NSVMSTYGSQ ASSINIMONDS SHTHPGLAQQ TSAVMGRPLP 76 HTVSTMPHTS GMGRILTOVKT PVOVPLPHPM OMSALGGYSS VSSCNGYGRM GLLHQEKLPS 77								
TILAGAVPR MMRPGPGQNY PRSGFPLEVS TPLGQGRVNQ LGGVFINGRP LPRHIRIKIV 61 EMAHHGIRPC VISRQLRVSH GCVSKILCRY GETGSIRPGA IGGSKPKVIT PDVEKKIEEY 1 KRENPGMFSM EIRDKLIKDA VCDRNTVPSV SSISRILRSK FGRGEEEEAD LERKEAEESE 11 KKACHSIGGI LSERASAPQS DEGSDIDSEP DLPLKRKQRR SRTTFTAEQL EELERAPERT 2 HYPDIYTREE LAQRAKLTEA RYQVWFSNRR ARMKQAGAN QLAAFNILIP GGFPFTAHPT 3 LPTYQLSETS YQPTSIPQAV SDPSSTVRP QPLPPSTVHQ STIPSNDES SAYCLPSTRH 3 FGSSYTDSFV PPSGPSNPMN PTIGNGLSPQ NSIRENLSH SKPIRVQNEG TGKSSWMMLN 4 PEGGKSGKSP RRRAASMONN SKPAKSRSRA AKKKASLQSG QEGAGDSPS OFSKMPASFG SHSNDDFDNM STFRPRTSSN ASTISGRLSP IMTEQDDLGE GDVHSMVYPP SAAMASTLP 5 SLSEISNPEN MENLLDNLNL LSSPTSLTVS TQSSPGTMQQ QTPCYSFAPP NTSLNSPSPN 6 YQKYTYGQSS MSPLPQMPIQ TLQDNKSSYG GMSQYNCAPG LLKELLTSDS PPHNDIMTPV 6 DPGVAQPNSR VLGQNVMMGP NSVMSTYGSQ ASSNIMMONPS SHTHPGHAQQ TSAVMGRPLP 7 HYDSTMPHTS GMGRLTOVKT PVOVPLPHPM OMSALGGYSS VSSCNGYGRM GLLMQEKLPS 7		1		-		41	51	
EMAHHGIRPC VISRQLRVSH GCVSKILCRY QETGSIRPGA IGGSKPKVTT PDVEKKIEEY KREMPGMFSM EIRDKLIKDA VCDRNTVPSV SSISRILRSK FGKGEEEAD LERKEAEESE KKAKHSIDGI LSERASAPQS DEGSDIDSEP DLPLKRKQRR SRTIFTAEQL EELERAFERT HYPDIYTREE LAQRAKLTEA RVQVWFSNRR ARWRKQAGAN QLMAFNHLIP GGFPPTAMPT LPTYQLSETS YQPTSIPQAV SDPSSTVHRP QPLPPSTVHQ STIPSNPDSS SAYCLPSTRH GFSSYTDSFV PPSGPSNPNN PTIGNGLSPQ NSIRMILSLH SKPIRVQNEG TGKSSWMMLN PEGGKSGKSP RRAASMDNN SKPAKSRSRA AKKKASLQSG QEGAGDSPGS QFSKNPASFG SHSNDDFDNM STFRRTSSN ASTISGRLSP IMTEQDLIGE GDVHSMVYPP SAAKMASTLP SLSEISNPEN MENLLDNLNL LSSPTSLTVS TQSSPGTMQ QTPCYSFAPP NTSLNSPSPN GYGKTYGGS MSPLEQMPIQ TLQDNKSSYG GMSQYNCAPG LLKELLTSDS PPHNDIMTPV HYGTMPHTS GMGRLTOVKT PVOVPLPHPM OMSALGGYSS VSSCNGYGRM GLLMQEKLPS 7	70	1		ny procest cu	C SEL COCEIA	ICCUPINGE	D I DNIH I BHKIV	60
KRENFGMFSM EIRDKLLKDA VCDRNTVPSV SSISRILRSK FGKGEEEAD LERKABESE 14 KKAKHSIDGI LSERASAPQS DEGSDIDSEP DLPLKRKQR SRTTFTAEQL EELERAFERT 21 HYPDIYTREE LAQRAKLTEA RVQVWFSNRR ARMRKQAGAN QLMAFNHLIP GGFPPTAMPT 31 GFSSYTDSFV PPSGFSNPMN PTIGNGLSPQ NSIRMILSLH SKFIRVQNEG TGKSSWMMLN 41 PEGGKSGKSF RRAASMDNN SKPAKSRRA AKKKASLQSG QEGAGDSPGS QFSKMPASPG 21 SHSNDDFDNM STFRRTSSN ASTISGRLSP IMTEQDDLGE GDVHSMVYPP SAAKMASTLP 5 SLSEISNPEN MENLLDNLNL LSSPTSLTVS TQSSPGTMQ QTPCYSFAPP NTSLNSPSPN 6 YQKYTYGQSS MSPLEQMPIQ TLQDNKSSYG GMSQYNCAPG LLKKLLTSDS PPHNDIMTPV 6 DPGVAQPNSR VLGQNVMMGP NSVMSTYGSQ ASHNOMONPS SHTHPGHAQQ TSAVMGRPLP 7 HTVSTMPHTS GMGRLTOVKT PVQVPLPHPM OMSALGGYSS VSSCNGYGRM GLLMQEKLPS 7	70	MITTLAGAVI	K MMKPGPGQI OC VICDOIDU	SH CCASKII'G AT EKOGERPEA	A UELGGIBBO P ILPOGOKAL	A IGGSKPKVT	T POVEKKIEEY	120
KKAKHSIGGI LSERASAPQS DEGSDIDSEP DLPLKRKORR SRTTFTAEQL EELERAFERT  HYPDIYTREE LAQRAKLTEA RVQVWFSNRR ARWKQAGAN QLMAFNHLIP GGFPPTAMPT  LPTYQLSETS YQPTSIPQAV SDPSSTVHRP QPLPPSTVHQ STIPSNPDSS SAYCLPSTRH  GFSSYTDSFV PPSGPSNPMN PTIGNGLSPQ NSIRHNLSLH SKPIRVQNEG TGKSSWMMLN  SHSNDDFDNW STRPRTSSN ASTISGRLSP IMTEQDDLGE GDVHSMVYPP SAAKMASTLP  SLSEISNPEN MENLLDNLNL LSSPTSLTVS TQSSPGTMQ QTPCYSFAPP NTSLNSPSPN  GYGYTYGQSS MSPLPQMPIQ TLQDNKSSYG GMSQYNCAPG LLKELLTSDS PPHNDIMTPV  HYVSTMPHTS GMGRLTDVKT PVQVPLPHPM OMSALGGYSS VSSCNGYGRM GLLNQEKLPS  7		KDENDOMES	W FIRDKLLK	DA VCDRNTVPS	V SSISRILRS	K FGKGEEEE	D LERKEAEESE	180
HYPDIYTREE LAQRAKLTEA RYQYWFSNRR ARMKQAGAN QLAFAFNLID GGFPFTANFT SYQPTSIPQAV SDPSSTVHRP QPLPPSTVHQ STIPSNPDSS SAYCLPSTRH GFSSYTDSFV PPSGPSNPMN PTIGNGLSPQ NSIRMINLSH SKPIRVQNEG TGKSSWMMLN PEGGKSGKSP RRRAASMONN SKPAKSRSRA AKKKASLQSG QEGAGDSFGS QFSKMPASFG SHSWDDFDNW STFPRFTSSN ASTISGRLSP IMTEQDDLGE GDVHSMVYPP SAAKMASTLPP SLSEISNPEN MENLLDNLNL LSSPTSLTVS TQSSPGTMQQ QTPCYSFAPP NTSLMSSPSN 60 YQKYTYGQSS MSPLPQMPIQ TLQDNKSSYG GMSQYNCAPG LLKELLTSDS PPHDDIMTPV DPGVAQPNSR VLGQNVMMGP NSVMSTYGSQ ASINKMONPS SHTHPGHAQQ TSAVNGRPLP HTVSTMPHTS GMORLTOVKT PVOVPLPHPM OMSALGGYSS VSSCNGYGRM GLLMQEKLPS 7		MARKAGILA	IT LSERASAPO	OS DEGSDIDSE	P DLPLKRKOF	R SRTTFTAEC	L EELERAFERT	240
Typicats yopisipoav sdpsstyhrp opuppstyho stipsydds sayclpstrh Gessytdefv ppsgrenpmn ptignglepo nsirhnlelh skpirvoneg teksemmlin Peggksgksp rraasmonn skpakesrra akkkaslosg oegagderg ofskmpaspg Shsnddfonm stprrtism astisgrlep imteoddleg govhsmyypp saakmastlp Sleeinpen menlldninl lesptsltvs tosepetmog otpcyspapp ntslnepspn Gygktyggs menleompiq tlodnkssyg gmsyncapg llkelleted pphndimtpv Gygktyggs vlggnvmgp nsvmstygsq ashnoones shtheghaoq tsavngrelp HTVSTMPHTS GMGRLTOVKT PVOVPLPHPM OMSALGGYSS VSSCNGYGRM GLLHQEKLPS  31 32 33 34 35 35 36 37 36 37 37 37 37 37 37 37 37 37 37 37 37 37		HYDDIYTE	EE LAORAKLT	ea rvovwfsnr	R ARWRKQAGA	<b>VN QLMAFNHL</b> I	P GGFPPTAMPT	300
PEGGKSGKSP RRRAASMONN SKPAKSRSRA AKKRASLOSG GEGAGDSPSG OFSKNPASFG SHRODFDNW STFRPRTSSN ASTISGRLSP IMTEQDDLGE GDVHSMYYPP SAAKMASTLP SLSEISHPEN MENLLDNLNL LSSPTSLTVS TOSSPGTMON OTPCYSFAPP NTSLNSPSPN 6 YQKYTYGQSS MSPLPOMPIQ TLQDNKSSYG GMSQYNCAPG LLKELLTSDS PPHRDIMTPV 6 DPGVAQPNSR VLGQNVMMGP NSVMSTYGSQ ASINIMMONPS SHTHPGHAQQ TSAVMGRPLP 7 HTVSTMPHTS GMGRLTOVKT PVOVPLPHPM OMSALGGYSS VSSCNGYGRM GLLHQEKLPS 7	75	T.DTVOLSET	rs vortsipo	AV SDPSSTVHR	P OPLPPSTVI	40 STIPSNPDS	S SAYCLPSTRH	360 420
SHSNDDFDNW STFRFRTSSN ASTISGRLSP IMTEQDDLGE GDVHSMYYPP SAARMASTLP  SLSEISNPEN MENLLDNLAL LSSPTSLTVS TQSSPGTMQ QTPCYSPAPP NTSLNSPSPN  YQKYTYQGSS MSPLPQMPIQ TLQDNKSSYG GMSQYNCAPG LLKELLTSDS PPHNDIMTPV  DPGVAQPNSR VLGQNVMMGP NSVMSTYGSQ ASHNOOMPS SHTHPGHAQQ TSAVMGRPLP  TAVSTMPHTS GMGRLTOVKT PVOVPLPHPM OMSALGGYSS VSSCNGYGRM GLLHQEKLPS  7		GFSSYTDSI	PV PPSGPSNP	MN PTIGNGLSP	O NEIRHNLE	PH SYLIKANNI	S OESKMDYEDG TOVDDWWWW	480
SLSEISNPEN MENLLDNLNL LSSPTSLTVS TOSSPGTMON OTPCYSFAPP NTSLNSPSFN 6 YQKYTYGQSS MSPLEOMPIQ TLQDNKSSYG GMSQYNCAPG LLKELLTSDS PPHNDIMTPV 6 DPGVAQPNSR VLGQNVMMGP NSVMSTYGSQ ASHNOONPS SHTHPGHAQQ TSAVNGRPLP 7 HTVSTMPHTS GMORLTOVKT PVOVPLPHPM OMSALGGYSS VSSCNGYGRM GLLHQEKLPS 7		PEGGKSGK	SP RKKAASMD	NN SKYAKSRSR Sn astigodie	A WEEKENDII	SE COVHSMVY	P SAAKMASTLP	540
OV YQKYTYGQSS MSPLEQMPIQ TLQDNKSSYG GMSQYNCAPG LLKELLTSDS PPHNDIMTVV 6 DPGVAQPNSR VLGQNVMMGP NSVMSTYGSQ ASHNMOMONPS SHTHPGHAQQ TSAVMGRPLP HTVSTMPHTS GMGRLTOVKT PVOVPLPHPM OMSALGGYSS VSSCNGYGRM GLLHQEKLPS 7		CLICETENE	EN MENLLDNL	NL LSSPTSLTV	S TOSSPGTM	NO OTPCYSFAI	PP NTSLNSPSPN	
DPGVAQPNSR VLGQNVMMGP NSVMSTYGSQ ASHMOMONPS SHTHPGHAQQ TSAVNGRPLP 7 HTVSTMPHTS GMURLTOVKT PVOVPLPHPM OMSALGGYSS VSSCNGYGRM GLLHQEKLPS 7	80	VOKVTVGO	SS MSPLPOMP	IO TLODNKSSY	'G GMSOYNCAI	PG LLKELLTSI	OS PPHINDIMTPV	660
HTVSTMPHTS GMNRLTOVKT PVOVPLPHPM OMSALGGYSS VSSCNGYGRM GLLHQEKLPS /	_	DOCUADON	SR VLGONVMM	GP NSVMSTYGS	O ASHNIGON	PS SHTHPGHA(	Q TSAVNGRPLP	720
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ATYVLPEPET ASRCNPAASD HDTAIALKDT EGRSLATQEL GRLKLCEGAG SLHFVDAFLM
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CVETGCAWCK SARRCIHPFT ACDPSDYERN QEQCPVAVEK TSGGGRPKEN KGNRTNQALQ
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                                                                                                               1080
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15	RKGSMAEEPR VRLRSGAQVG EGRVEVLMIR QMGTVCDHRM NLISASVVCR QLGFGSAREA LFGARLOGGL GPIHLSEVRC RGYEBTLSCC PALEGSONGC QHENAAAVRC NVPNMGFQNQ VRLAGGRIPE EGLLEVQVEV NGVPRMGSVC SEMMGLTEAM VACRQLGLGF AIHAYKETMF WSGTPRAQEV VMSGVRCSGT ELALQQCQRH GPVHCSHGGG RPLAGVSCMD SAPDLVMIAQ LVQETAYLED RPLSQLYCAH EENCLSKSAD HDWPYGYRR LLAFSTQIYN LGRTDFRKT GRDSWVHOC HRHYHSIEVF THYDLLTLMG SKVAEGHKAS FCLEDTNCPT GLQRRYACAN	360 420 480 540 600 660
20	FGEQGVTVGC WDTYRHDIDC QWVDITDVGP GNYIFQVIVN PHYEVAESDF SNNMLQCRCK YDGHRVWLKN CHTGNSYPAN AELSLEQEQR LRNNLI	720 756
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35	Seq ID NO: 344 Protein Sequence Protein Accession #: NP_439892.1  1 11 21 31 41 51	60
40	PNIVKLLDVI HTENKLYLVF EFLHQDLKKF MDASALTGIP LPLIKSYLFO LLOGLAFCHS HRVLHRDLKP QNLLINTEGA IKLADFGLAR AFGVPVRTYT HEVTRRALFP GDSEIDQLFR IFRTLGTPDE VVWPGVTSMP DYKPSFPKWA RQDFSKVVPP LDEDGRSLLS QMLHYDPYKR ISAKAALAHP PFQDVTKPVP HLRL	120 180 240 264
45	Seq ID NO: 345 Protein Sequence Protein Accession #: NP_116127.1 1	
50	MKLGCVLMAW ALYLSLGVLW VAQMLLAASF STLQCEGPVC TEESSCHTED DITDAREAGF GVKAYTPSEP FHLIVSYDWL ILQGPAKEVF EXDLLVLRCQ AWQDWELTGV TFYROGSALG PEGNREFSI TVVQKADSGH YHCSGIFQSP GPGIPETASV VALTVQELPP APTLRAVPSA EPQAGSPMTL SCQTKLFLQR SAARLLFSFY KDGRIVQSRG LSSEFQIPTA SEDHSGSYWC EAATEDNQVW KQSPQLBIRV QGASSSAAPP TLNPAPQKSA APGTAPSEAP GPLPPPPTPS SEDPGPSSPL GMPDPHLYHQ MGLLLKHHQD VRVLLGHLLM ELRELSGHQK PGTTKATAE	60 120 180 240 300 359
55	Seq ID NO: 346 Protein Sequence   Protein Accession #: NP_002337.1   1	
60	MKIPLPVLLA ALLGVERASS LMCPSCLNQK SNLYCLKPTI CSDQDNYCVT VSASAGIGNL VTFGHSLSKT CSPACPIPEG VNVGVASHGI SCCQSPLCNF SAADGGLRAS VTLLGAGLLL SLLPALLRFG P	60 120 131
65	Seq ID NO: 347 Protein Sequence Protein Accession #: XP_113526.2  1 11 21 31 41 51	60
70	MEDIGENTMV LSTLRSLNNP ISQRVEGGSG LDISTSARGS LQMQYQQSMQ LEERAEQIRS KSHLIQVERE KMQMELSHKR ARVELERAAS TSARNYEREV DRNQELLTRI RQLQEREAGA EEKOQOQUER NQQQQNLDA ASKRLEKED SLAQAGETIN ALKGRISELQ WSVMQQEMRV KRLESEKQEL QEQLDLQHKK CQEANQKIQE LQASQEARAD HEQQIKDLEQ KLSLQEQDAA	60 120 180 240
70	IVKNMKSELV RLPRLERELK QLREESAHLR EMRETNGLLQ EELEGLQRKL GRQEKMQETL VGLELENERL LAKLQSWERL DOTMGLSIRT PEDLSRFVVE LQQRELALKO KNSAVTSSAR GLEKARQOLQ EELRQVSQQL LEERKKRETH EALARRLQKR VLLLTKERDG MRAILGSYDS ELTPAEYSPQ LTRRMREAED MVQKVISHSA EMERQLSQAL EELGGQKQRA DMLEMELWIL KSQSSSABOS FLPSREEADT LRLKVEELEG ERSRLEEEKR MLEAQLERRA LQGDYDQSRT	300 360 420 480 540
75	KSQSSSADOS FLFSREADT LRUKVEELEG ERSKLEEEKK MLEAQLEKKA LAGBINGSKE KVLHMSLMPT SVARGRIRED HSQLQAECER LRGLIRAMER GGTVPADLEA AAASLPSSKE VAELKKQVES AELKNQRLKE VFQTKIQEFR KACYTLTGYQ IDITTENQYR LTSLYABHPG DCLIFKATSP SGSKMQLLET EFSHTVGELI EVHLRRQDSI PAFLSSLTLE LFSRQTVA	600 660 718
80	Seq ID NO: 348 Protein Sequence Protein Accession #: NP_000264.1  1 11 21 31 41 51                      MTQAGRRGPG TPEPRPRTQP MASPRIGTFC CPTRDAATQL VLSFQPRAPH ALCLGSGGLR LALGLIQLLP GRRPAGFGSP ATSPPASVRI LRAAAACDLL GCLGMVIRST VWLGFPNFVD	60 120

5	SVSDMNHTEI NAWGLATLLCV I ASLLKGRQGI N LKPVRTAAKT NHPSPLMPHEN I HGDL	EGAAMLYYPS YTENERRMGA TWFIMGILNP	VSRCERGLDH VIKIRFFKIM AOGFLLSLAF	AIPHYVTMYL LVLIICWLSN YGWTGCSLGP	PLLLVLVANP IINESLLFYL QSPRKEIQWE	ILFOKTVTAV EMOTDINGGS SLTTSAAEGA	180 240 300 360 420 424
10	Ī	ession #: N 11 	IP_647478.1 21 	31 	41 	51	
15	MGPKDSAKCL PLTEEEEEG KVRCPFCYGG EEPEDAAPVA AQLRRLQEER	AGATLSRGPA LQSWKRGDDP PSVPASGYPE	FPGMGSEELR WTEHAKWFPS LPTPRREVQS	LASFYDWPLT CQFLLRSKGR ESAQEPGGVS	AEVPPELLAA DFVHSVQETH PAEAQRAWWV	AGPFHTGHQD SQLLGSWDPW LEPPGARDVE	60 120 180 240 298
20	MGPKDSAKCL	ession #: 1 11     HRGPQPSHWA	NP_071444.1 21   AGDGPTQERC	31   GPRSLGSPVL	41   GLDTCRAWDH	51   VDGQILGQLR	60
25	PLTEEEEEEG KVRCFFCYGG	AGATLSRGPA LQSWKRGDDP PSVPASGYPE	FPGMGSEELR WTEHAKWFPS LPTPRREVQS	LASFYDWPLT CQFLLRSKGR ESAQEPGARD	AEVPPELLAA DFVHSVQETH VEAQLRRLQE	AGFFHTGHQD SQLLGSWDPW	120 180 240 280
30	1	ession #: : 11 	NP_066300.1 21 	31 	41 	51 	
35	KSEDFFYIKV AVRPTAFKPV SLPTHSTSSS HSNKADKGPS RCRDELEGPE TKLRSYEREK	SQKARGSHHP LPRSGAILHS YQLDPLVTPV CVRSPISTDE PKGGNKLKQA TSFGPALEET	DYTALSSGDL SPESASHQLH GPTSRFGGSA CSIQELEQKL SQKSQRAQQV QWEVCQKSGE	GGQAGVDFDP PAPPDKPKEQ HNITQGIVLQ LEREGALQKL LHLQVLQLQQ ISLLKQQLKE	STPPKLMPFS ELKPGLCSGA DSNMMSLKAL QRSFEEKELA EKRQLRQELE SQTEVNAKAS	GHGKSSSKMG NQLEMGSEKG LSDSGRNSMS SFSDGGSKLG SSLAYEERPR SLMKEQDLLE EILGLKAQLK	60 120 180 240 300 360 420
40	QAALARDMGP	PTPPEDVPAL	<b>ORELERLRAE</b>	LREERQGHDQ	MSSGFQHERL LEGADIPYED	LEQELQELRA VWKEEKEKVI IIATEI	480 540 596
45	Protein Acc	352 Proteicession #: 11   ELDDDVTES	AAG41361.1 21     KDLLSNEDAA	31     DOAFKTSELI	41     VDGQEEKDTI	51     VEEGSEVEDE	60
50	VGQRIRRGSI QCPLVKNASH LAMIKGIQSS EAATQVFFAL	GVWNYISPKI TFVEPECEQS GKIIYFSSLI GLGFGGVIAI	GGIGFASCV S SATTYYWYRE F PYVVLICFLI F SSYNKRDNNO	CYFVALYYN ALNISSSISI RAFLLNGSII HFDAVLVSP	/ IIGWSLFYFS E SGGLNWKMT! D GIRHMFTPKI I NFFTSVLAT!	GIPLFFLELS GQSFQQPLPWD CCLLAAWVMVC LEIMLEPKVWR LVVFAVLGPKA	120 180 240 300 360 420
55	LHLNSCKIEE GIVTPIVDTF NIAVCFVYGI AWIEDKASEE RVLKEPVNLE	ELNKAVQGTO KVRKEILTV: DKFMEDLKDI FLSYPTWGL' GDDTSLIHG	G LAFIAFTEM I CCLLAFCIGI M LGFAPSRYYY V VCVSLVVFA	4 THEPASPEW: L IFVQRSGNY! Y YMWKYISPLI L LPVPVVFIV!	S VMFFLMLVNI P VTMFDDYSA: M LLSLLIASV R RFNLIDDSSG	I QKVKEEFPA L GLGSMFGTIE I LPLLIVVILE V NMGLSPPGYN G NLASVTYKRG G RYGIGYLMAD	480 540 600 660 720
60	IMPDMPESDL	•					730
65	Protein Ac 1       MEEGERSPLI	cession #: 11     SQETAGQKP	in Sequence NP_005594. 21   L SVHRPPTSG	31   C LGPVPREDQ	41   A EAWGCSCCP	51   P ETKHQALSGT	60 120
70	MLGLALGGLV SLEHTLRVAI ASCCIDPREI	VSAASLAGC AHYQDDPDL GASVNDQCG	L GALCENTCL R FLLDQVQLG F GVLRLDADA	L RGFSGGILA L RCCGAASYQ A QRVVYLEGC	F LVLEAVAGA D WQQNLYFNC	S DLGGPLPTDP L VVALWGPLQD S SPGVQACSLP N LAASGGYAIA A KPARG	180 240
75			in Sequence AAL84622.1		41	51	
75	WKLAIQILK: DVYDQLIFA	I AMVTIQLVL V NQYLQLYNV	F GLSNQMVVA S VGNHAYENK	F KEENTIAFK G TKQSAMAIC	CH LFLKGYMDR XQ HFYKRGNIY	C EKFWARGRKP M DDTYAVYTQS P GNDTFDIDPE V RHQELPDCYD	120 180
80	PTLTITFDNI ILCIRSVIR EIQAKSLTS MIYLGYCFO	K AHSGRIKIS G LQLQQEFVN Y DVCSILLGT G WIVLGPYHI	L DNDISIREC IF PLLHYKKEV S TMLVWLGVI K PRSLNMVSE	K DWHVSGSIQ S VSDQMEFVN R YLGFFAKYN C LFSLINGDI	OK NTHYMMIPE IG WYIMIIISE IL LILTLQAAI OM PATPAKMQQ	DA FVILTCLVSL DI LTIIGSILKM LP NVIRFCCCAA QK SYLVWLFSRI CD LPNSGKYRLE	300 360 420 480

	DDPPVSLFCC (	CKK					553
	Seq ID NO:	3SS Protein	Sequence				
5	Protein Acc			31	41	51	
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	MEPGLWLLFG						60
	PGEGTVAPTA PEQTVPYGLS						120 180
10	SNSRTAEKTD						238
	Seq ID NO: Protein Acc						
1.0			31	31	41	51	
15	]	]		Deveti I In		 	60
	MGCGCSSHPE :						120
	SLEPEPWPFK	NLSRKDAERQ	LLAPGNTHGS	PLIRESESTA	GSFSLSVRDP	DQNQGEVVKH	180
20	YKIRNLDNGG PRETLKLVER						240 300
20	VRLYAVVTQE						360
	IHRDLRAANI	LVSDTLSCKI	ADFGLARLIE	DNEYTAREGA	KPPIKWTAPE	AINYGTFTIK	420
	SDVWSFGILL PEDRPTFDYL			ONLERGYRMV	RPDNCPEELY	QLMRLCWKER	480 509
25	PEURPIPUIL	KSAMEDLLIM	TEGGIQEQE				307
	Seq ID NO:				•		
	Protein Acc	ession #: N 11	IP_055469.1 21	31	41	51	
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30					FSPDVALAVS		60
					VSTTMATTAA VATARATTPE		120 180
					GTTAPGPTEV		240
35					AAAKASSPPG		300
33		VTYQKPDKQE		VIVGGVVGAL	FAAPLVTLLI	IKMAKADEGS	360 384
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	• .	358 Proteir	•	•			
40	Protein Acc	ession #:	NP_008848.:	31	41	51	
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					SHPSYTDTPV		60 120
					GPFKRTIRKD		180
45	CLIDKRORNR	CQYCRYQKCL	VMGMKREAVQ	EERQRSRERA	ESEAECATSG	HEDMPVERIL	240
					VEWAKRIPHP AGVGSIFDRV		300 360
					LEAYTKOKYP		420
50	LRLPALRSIG	LKCLEHLFFF	KLIGDTPIDT	FLMEMLETPL	QIT.		463
30	Sec ID NO:	359 Protein	o Semience				
		cession #: 1					
	1	11	21	31	41	51	
55	MTILGTTFGM	VPSLLOVVSG	ESGYAONGDL	EDAELDDYSF	SCYSQLEVNG	SOHSLTCAPE	60
	DPDVNTTNLE	FEICGALVEV	KCLNPRKLQE	IYFIETKKFL	LIGKSNICVK	VGEKSLTCKK	120
					KVLMHDVAYR SPSYYPRTPE	QEKDENKWTH	180 240
					KTLEHLCKKP		300
60	ESFLDCQIHR	VDDIQARDEV	EGFLQDTFPQ	QLEESEKQRL	GGDVQSPNCP	SEDVVVTPES	360
		AGNVSACDAP VAQGQPILTS			YOULLLSLGT	TNSTLPPPFS	420 459
	DQ3G1D1E412	TAUGUITETE	Dographic	Tribut Tquq			
65		360 Protei					
05	Protein Acc	cession #: 1	NP_006263.1				
	1	11	21	31	41	51	
		   TOURNOVEC		CELVELINNE	   LEMPLETTE	QEVVDKVMET	60
70		FOEFMAFVAM				40	92
			_				
		361 Protei cession #:	n Sequence NP_006148.	1			
26	TIOCETH AC		-	-			
75	1	11	21	31	41	51	
	MPMDI.TI.VVW	FCVCTARTVV	I GEGMOPOLON	DIVTELDLV	I I TTLGVAOVSO	   MONASKAFLF	60
	QDIEREIHAA	PHVSEKLIQL	FONKSEPTIL	ATVQQKPSTS	GVILSIRELE	HSYFELESSG	120
80						YERVIDPPDT	180 240
30	MDFOEFFYKW	TAKLNYAETR	LSQLENCHCE	KTCQVSGLL	RDQDSWVDGE	SDFLSLVQGI HCRNCTCKSG	300
	AVECRRMSCP	PLNCSPDSLP	VHIAGQCCK\	CRPKCIYGGI	( VLAEGQRILT	KSCRECRGGV	360
						NTKATCECKS DFSCTERDEC	420 480
	AL LOACODON	COULUS CAM	' WART CHANGE	CVNDPGDIR	~ ~~++017KAF	, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	

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GSGQHNCDEN AICTNTVQGH SCTCKPGYVG NGTICRAFCE EGCRYGGTCV APNKCVCPSG
       FTGSHCEKDI DECSEGIIEC HNHSRCVNLP GWYHCECRSG FHDDGTYSLS GESCIDIDEC ALRTHTCWND SACINLAGGP DCLCPSGPSC SGDCPHEGGL KHNGQVWTLK EDRCSVCSCK
                                                                                  600
                                                                                  660
                                                                                  720
       DGKIPCRRTA CDCQNPSADL FCCPECDTRV TSQCLDQNGH KLYRSGDNWT HSCQQCRCLE
 5
       GEVDCWPLTC PNLSCEYTAI LEGECCPRCV SDPCLADNIT YDIRKTCLDS YGVSRLSGSV
                                                                                  780
                                                                                   810
       WTMAGSPCTT CKCKNGRVCC SVDFECLONN
       Seq ID NO: 362 Protein Sequence
       Protein Accession #: NP_057264.1
10
                                                        41
                                                                    51
       MGSNSGOAGR HIYKSLADDG PFDSVEPPKR PTSRLIMHSM AMFGREFCYA VEAAYVTPVL
       LSVGLPSSLY SIVMFLSPIL GPLLQPVVGS ASDHCRSRWG RRRPYILTLG VMMLVGMALY
LNGATVVAAL IANPRRKLVW AISVTMIGVV LFDFAADFID GPIKAYLFDV CSHQDKEKGL
                                                                                  120
                                                                                  180
15
       HYHALFTGFG GALGYLLGAI DWAHLELGRL LGTEFQVMFF FSALVLTLCF
       PLTEVAKGIP PQQTPQDPPL SSDGMYEYGS IEKVKNGYVN PELAMQGAKN KNHAEQTRRA
                                                                                  300
       MTLKSLLRAL VNMPPHYRYL CISHLIGWTA FLSNMLFFTD FMGQIVYRGD PYSAHNSTEF
                                                                                  360
       LIYERGUEVG CMGFCINSVF SSLYSYFOKV LVSYIGLKGL YFTGYLLFGL GTGFIGLFFN
VYSTLVLCSL PGVMSSTLYT VPFNLITEYH REEEKERQQA PGGDPDNSVR GKGMDCATLT
                                                                                  480
20
       CMVQLAQILV GGGLGFLVNT AGTVVVVVIT ASAVALIGCC FVALFVRYVD
                                                                                   530
       Seg ID NO: 363 Protein Seguence
       Protein Accession #: NP_036532.1
                                                                    51
                    11
                               21
25
       MELALLCGLV VMAGVIPIQG GILNLNKMVK QVTGKMPILS YWPYGCHCGL GGRGQPKDAT
                                                                                  120
       DWCCQTHDCC YDHLKTQGCS IYKDYYRYNF SQGNIHCSDK GSWCEQQLCA CDKEVAFCLK
                                                                                  145
       RNLDTYOKRL RFYWRPHCRG QTPGC
30
        Seq ID NO: 364 Protein Sequence
        Protein Accession #: NP_061313.1
                                                                    51
                    11
                                21
        MRLPDLRPWT SLLLVDAALL WLLOGPLGTL LPQGLPGLWL EGTLRLGGLW GLLKLRGLLG
35
        FVGTLLLPLC LATPLTVSLR ALVAGASRAP PARVASAPWS WLLVGYGAAG LSWSLWAVLS
                                                                                   120
        PPGAQEKEQD QVNNKVLMWR LLKLSRPDLP LLVAAFFFLV LAVLGETLIP HYSGRVIDIL
                                                                                   180
        GGDFDPHAFA SAIFFMCLFS FGSSLSAGCR GGCFTYTMSR INLRIREQLF SSLLRQDLGF
        FQETKTGELN SRLSSDTTLM SNWLPLNANV LLRSLVKVVG LYGFMLSISP RLTLLSLLHM
                                                                                   300
                                                                                   360
        PFTIAAEKVY NTRHQEVLRE IQDAVARAGQ VVREAVGGLQ TVRSFGAEEH EVCRYKEALE
40
        QCRQLYWRRD LERALYLLIR RVLHLGVQML MLSCGLQQMQ DGELTQGSLL SFMIYQESVG
                                                                                   420
        SYVQTLVYIY GDMLSNVGAA EKVFSYMDRQ PNLPSPGTLA PTTLQGVVKF QDVSFAYPNR
                                                                                   480
        PDRPVLKGLT FTLRPGEVTA LVGPNGSGKS TVAALLQNLY QPTGGQVLLD EKPISQYEHC
                                                                                   540
        YLHSQVVSVG QEPVLFSGSV RNNIAYGLQS CEDDKVMAAA QAAHADDFIQ EMEHGIYTDV
                                                                                   600
        GEKGSOLAAG OKORLAIARA LVRDPRVLIL
45
        Seq ID NO: 365 Protein Sequence
        Protein Accession #: NP 002407
                    11
50
        MKKSGVLFLL GIILLVLIGV OGTPVVRKGR CSCISTNOGT IHLOSLKDLK OFAPSPSCEK
                                                                                    60
        IEIIATLKNG VQTCLNPDSA DVKELIKKWE KQVSQKKKQK NGKKHQKKKV LKVRKSQRSR
         Seg ID NO: 366 Protein Sequence
55
         Protein Accession #: NP 006524.1
         MARSLVCLGV IILLSAFSGP GVRGGPMPKL ADRKLCADQE CSHPISMAVA LQDYMAPDCR
         FLTIHRGQVV YVFSKLKGRG RLFWGGSVQG DYYGDLAARL GYFPSSIVRE DQTLKPGKVD
 60
         VKTDKWDFYC Q
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It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All publications, sequences of accession numbers, and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.

#### WHAT IS CLAIMED IS:

1 1. A method for determining the presence or absence of a pathological cell in a 2 patient, said method comprising detecting a nucleic acid comprising a sequence at least 80% 3 identical to a sequence as described in Tables 2A-68 in a biological sample from said patient, thereby determining the presence or absence of said pathological cell. 4 1 2. The method of Claim 1, wherein: 2 a) said pathology is described in Table 1, including a cancer; and/or 3 b) said biological sample comprises isolated nucleic acids. 1 3. The method of Claim 1, wherein said biological sample is tissue from an organ 2 which is affected by said pathology of Table 1, including a cancer. 1 4. The method of Claim 2, wherein said nucleic acids are mRNA 1 5. The method of Claim 2: 2 a) further comprising a step of amplifying nucleic acids before said step of detecting 3 said nucleic acid; or 4 b) where said detecting is of a protein encoded by said nucleic acid. 1 6. The method of Claim 1, wherein said nucleic acid comprises a sequence as 2 described in Tables 2A-68. 7. The method of Claim 2, wherein: 1 2 a) said detecting step is carried out by: 3 i) using a labeled nucleic acid probe; 4 ii) utilizing a biochip comprising a sequence at least 80% identical to a sequence 5 as described in Tables 2A-68; or 6 iii) detecting a polypeptide encoded by said nucleic acid; or

- b) said patient is:
- i) undergoing a therapeutic regimen to treat said pathology of Table 1; or
- 9 ii) is suspected of having said pathology or cancer.

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1 8. An isolated nucleic acid molecule comprising a sequence as described in 2 Tables 2A-68.

1	9.	The nucleic acid molecule of Claim 8, which is labeled.				
1	10.	An expression vector comprising the nucleic acid of Claim 8.				
1	11.	A host cell comprising the expression vector of Claim 10.				
1	12.	An isolated polypeptide which is encoded by a nucleic acid molecule				
2	comprising a	sequence as described in Tables 2A-68.				
1	13.	An antibody that specifically binds a polypeptide of Claim 12.				
1	14.	The antibody of Claim 13:				
2	a) con	njugated to an effector component;				
3	b) co	njugated to a detectable label, including a fluorescent label, a radioisotope, or a				
4	су	totoxic chemical;				
5	c) wh	ich is an antibody fragment; or				
6	d) wh	nich is a humanized antibody.				
1	15.	A method for specifically targeting a compound to a pathological cell in a				
2	patient, said r	nethod comprising administering to said patient an antibody of Claim 13,				
3	thereby provi	ding said targetting.				
1	16.	A method for determining the presence or absence of a pathological cell in a				
2	patient, said r	method comprising contacting a biological sample with an antibody of Claim 13.				
1	. 17.	The method of Claim 16, wherein:				
2	a) sai	d antibody is conjugated to:				
3	i)	an effector component; or				
4	ii)	a fluorescent label; or				
5	b) said biological sample is a blood, serum, urine, or stool sample.					

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18.

polypeptide, said method comprising the steps of:

A method for identifying a compound that modulates a pathology-associated

3	a) contacting said compound with a pathology-associated polypeptide, said
4	polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence
5	at least 80% identical to a sequence as described in Tables 2A-68; and
6	b) determining the functional effect of said compound upon said polypeptide.
1	19. A drug screening assay comprising the steps of:
2	a) administering a test compound to a mammal having a pathology of Table 1 or a
3	cell isolated therefrom; and
4	b) comparing the level of gene expression of a polynucleotide that selectively
5	hybridizes to a sequence at least 80% identical to a sequence as described in
6	Tables 2A-68 in a treated cell or mammal with the level of gene expression of said
7	polynucleotide in a control cell or mammal, wherein a test compound that
8	modulates said level of expression of the polynucleotide is a candidate for the
9	treatment of said pathology.
10	

# (19) World Intellectual Property Organization International Bureau





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25138 A

(54) Title: METHODS OF DIAGNOSIS OF CANCER COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF CANCER

(57) Abstract: Described herein are genes whose expression are up-regulated or down-regulated in specific cancers. Related methods and compositions that can be used for diagnosis and treatment of those cancers are disclosed. Also described herein are methods that can be used to identify modulators of selected cancers.



International application No.

PCT/US02/29560

IPC(7) US CL	SSIFICATION OF SUBJECT MATTER : C12Q 1/68 : 435/6	in a land charles and IDC			
According to International Patent Classification (IPC) or to both national classification and IPC  B. FIELDS SEARCHED					
	cumentation searched (classification system followed b 35/6, 7.1, 287.2; 436/63, 64	y classification symbols)			
Documentation	Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched -				
	ta base consulted during the international search (name ontinuation Sheet	of data base and, where practicable, sear	ch terms used)		
C. DOC	UMENTS CONSIDERED TO BE RELEVANT				
Category *	Citation of document, with indication, where ap	propriate, of the relevant passages	Relevant to claim No.		
X,P	US 6,426,186 B1 (JONES et al.) 30 July 2002 (30.0	7.2002), see especially Detailed	1-6		
 Y,P	Description of the Invention and Sequence 62.		7		
х	US 6,194,158 B1 (KROES et al.) 27 February 2001	(27.02.2001), see especially	2-5		
	Background of the Invention and Detailed Description				
Y			1, 6, 7		
X,P	US 6,440,676 B1 (KROES et al.) 27 August 2002 (2		2-5		
	of the Invention and Detailed Description of the Inve	ntion.	167		
Y,P			1, 6, 7		
Y,P	US 6,500,938 B1 (AU-YOUNG et al.) 31 December Summary of the Invention and Description of the Inv		1-7		
Y	SMYTH TEMPLETON et al. Cloning and Character Insterstitial Collagenase. September 1990, Volume 5 especially Figure 2.	rization of Human Tumor Cell	1-7		
:					
	documents are listed in the continuation of Box C.	See patent family annex.	1 101 4		
- s	pecial categories of cited documents:	"T" later document published after the inte date and not in conflict with the applic			
	t defining the general state of the art which is not considered to be llar relevance	principle or theory underlying the invent.  "X" document of particular relevance; the			
"E" cartier ap	plication or patent published on or after the international filing date	considered novel or cannot be consider when the document is taken alone	red to involve an inventive step		
"L" document establish specified)	t which may throw doubts on priority claim(s) or which is cited to the publication date of another citation or other special reason (as	"Y" document of particular relevance; the considered to involve an inventive step	when the document is		
"O" document	t referring to an oral disclosure, use, exhibition or other means	combined with one or more other such being obvious to a person skilled in the	documents, such combination e art		
	r published prior to the international filing date but later than the late claimed	"&" document member of the same patent	family		
	ctual completion of the international search	Date of mailing of the international search	ch report		
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	ailing address of the ISA/US nunlissioner of Patents and Trademarks	KINDUN I I WOOD	res		
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Box	I Obse	rvations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)
This	internati	onal report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:
1.		Claim Nos.: because they relate to subject matter not required to be searched by this Authority, namely:
2.		Claim Nos.: because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3.		Claim Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).
Box	П Оь	servations where unity of invention is lacking (Continuation of Item 2 of first sheet)
		onal Searching Authority found multiple inventions in this international application, as follows: ontinuation Sheet x  As all required additional search fees were timely paid by the applicant, this international search report covers all
2.		searchable claims.  As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite
3.		payment of any additional fee.  As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.
<b>4.</b>	$\boxtimes$	No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-7 for Specie A(hemangiomas) and B (SEQ ID NO: 1)
Rem	ark on F	
		No protest accompanied the payment of additional search fees.

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This application contains the following inventions or groups of inventions, which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional examination fees must be paid.

Groups 1-104,648, claim(s) 1-7, drawn to a method for determining the presence or absence of a pathological (Specie A) cell in a patient via detection of polynucleotides that are at least 80% identical to listed sequences (Specie B). If electing from this Group Set, Applicants are asked to elect one species from A and B. Species A has 254 possibilities (see Table 1). Please note that the sequences in Tables 2A-68 are unsearchable as they are not included in the Sequence Listing. Applicants have supplied 412 nucleic acid sequences from which a selection can be made for Specie B. The total number of individual inventions in this Group Set including all possible combinations of Species A and B is 104,648.

Groups 104,649-105,060, claim(s) 8-12, drawn to an isolated nucleic acid molecules from Tables 2A-68, expression vectors, host cells, and polypeptides encoded by nucleic acid molecules with listed sequences from Tables 2A-68 (Species B). If electing from this Group Set, Applicants are asked to elect one species from Species B. Please note that the sequences in Tables 2A-68 are unsearchable as they are not included in the Sequence Listing. Applicants have supplied 412 nucleic acid sequences from which a selection can be made for Specie B. The total number of individual inventions possible in this Group Set with Specie B is 412.

Groups 105,061-105,472, claim(s) 13-14, drawn to an antibody that binds to a polypeptide encoded by a polynucleotide with sequences from Tables 2A-68 (Species B). If electing from this Group Set, Applicants are asked to elect one species from Species B. Please note that the sequences in Tables 2A-68 are unsearchable as they are not included in the Sequence Listing. Applicants have supplied 412 nucleic acid sequences from which a selection can be made for Specie B. The total number of individual inventions possible in this Group Set with Specie B is 412.

Groups 105,473-105,884, claim(s) 15, drawn to a method for targeting a compound to a pathological cell in a patient via administering an antibody that binds to a polypeptide encoded by a polynucleotide from Tables 2A-68 (Species B). If electing from this Group Set, Applicants are asked to elect one species from Species B. Please note that the sequences in Tables 2A-68 are unsearchable as they are not included in the Sequence Listing. Applicants have supplied 412 nucleic acid sequences from which a selection can be made for Specie B. The total number of individual inventions possible in this Group Set with Specie B is 412.

Groups 105,885-106,296, claim(s) 16-17, drawn to a method for determining the presence or absence of a pathological cell in a patient via contacting the sample with an antibody that binds to a polypeptide encoded by a polynucleotide from Tables 2A-68 (Species B). If electing from this Group Set, Applicants are asked to elect one species from Species B. Please note that the sequences in Tables 2A-68 are unsearchable as they are not included in the Sequence Listing. Applicants have supplied 412 nucleic acid sequences from which a selection can be made for Specie B. The total number of individual inventions possible in this Group Set with Specie B is 412.

Groups 106,297-106,708, claim(s) 18, drawn to a method for identifying a compound that modulates a pathology-associated polypeptide encoded by a polynucleotide that hybridizes to a sequence in Tables 2A-68 (Species B). If electing from this Group Set, Applicants are asked to elect one species from Species B. Please note that the sequences in Tables 2A-68 are unsearchable as they are not included in the Sequence Listing. Applicants have supplied 412 nucleic acid sequences from which a selection can be made for Specie B. The total number of individual inventions possible in this Group Set with Specie B is 412.

Groups 106,709-211,356, claim(s) 19, drawn to drug screening assay by administering a compound to a mammal or cell having a pathology (of Table 1) and comparing the level of gene expression of a polynucleotide that hybridizes to a sequence that is 80% identical to sequences as described in Tables 2A-68 (Species B) to gene expression in control cells or mammals. If electing from this Group Set, Applicants are asked to elect one species from A and B. Species A has 254 possibilities (see Table 1). Please note that the sequences in Tables 2A-68 are unsearchable as they are not included in the Sequence Listing. Applicants have supplied 412 nucleic acid sequences from which a selection can be made for Specie B. The total number of individual inventions in this Group Set including all possible combinations of Species A and B is 104,648.

This International Searching Authority considers that the international application does not comply with the requirements of unity of invention (Rules 13.1, 13.2, and 13.3) for the reasons indicated below:

The inventions listed as all Group Sets (Groups 1-211,356) do not relate to a single general inventive concept under PCT Rule 13.1, because under PCT Rule 13.2 they lack the same or corresponding special technical features for the following reasons:

Groups 1-104,648 and Groups 105,472-211,356 are directed to methods or assays which vary in one or more of the following: reactants, steps, and/or goals which are not coextensive and which do not share the same technical feature. Groups 104,649-105,472 have two separate special technical features, a nucleic acid and an antibody, respectively. These are directed to different chemical entity types regarding the critical limitations featuring different structures and functions. The antibodies undergo recognition and binding reactions

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wherein what is bound is different from what is bound by the compositions including the nucleic acids. Thus, in summary, each Group is directed to a different special technical feature and thus supports this lack of unity.

This application contains claims directed to more than one species of the generic invention. These species are deemed to lack unity of invention because they are not so linked as to form a single general inventive concept under PCT Rule 13.1.

In order for more than one species to be examined, the appropriate additional examination fees must be paid. The species are as follows:

The claims in the Groups 1-104,648 and 106,709-211,356 include a series of species A directed to different pathologies which are listed in Table 1. Each of these types of pathologies are separate entities which affect patients differently, meaning each has its own special technical feature.

The claims in all Groups (1-211,356) include a series of species B directed to nucleic acid sequence listed (412 possibilities) which are considered separate as each defines its own special technical feature.

The first listed pathology (Specie A) and SEQ ID NO: 1 (Species B) will be automatically searched. For each additional Group with a specie combination elected, the fee is an additional \$210.00.

Continuation of B. FIELDS SEARCHED Item 3: WEST, PUBMED, BIOSIS, CAPLUS, MEDLINE, SCISEARCH, EMBASE searching terms: diagnosis, cancer, screen, modulator, pathological cell, patient, nucleic acid, tissue, mRNA, detect, probe, biochip, array, therapeutic

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